

94-199

From: Hamud, Fozia
Sent: Friday, May 16, 2003 9:48 AM
To: STIC-Biotech/ChemLib
Subject: sequence search for 09/912,157

RECEIVED

MAY 16 2003

Please search 09/912,157, SEQ ID NO:2 amino acid residues 36-313, 36-753, 336-753 and 1-753 against commercial data bases and interference data bases. Thank you.

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Point of Contact:
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Technical Info. Specialist
CM1 6A04
703-308-3534

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 5/19
Date Completed: 5/19
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: 4
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: es
WWW/Internet: _____
Other (specify): _____

May 19 09:52:37 2003

us-09-912-157-2_copy_336_753.fpr

Page 1

GenCore version 5.1.4.p5_4578
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OK, protein is protein search, using sw model

Run on: May 19, 2003, 09:16:08 ; Search time 15,4315 seconds
(without alignments)
2604.041 Million cell updates/sec

Title: US-09-912-157-2_COPY_336_753

Perfect score: 2210

Sequence: 1 RKQENIYSHLDESSSTTTAALPRELRPRPKVFLCISKDKQHNNVQCFAYFL 418

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 9613422 residues

al number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

PIR_73: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2210	100.0	564	2 T42695	hypothetical prote
2	150.5	6.8	846	2 T27282	hypothetical prote
3	126	5.7	718	2 T30113	hypothetical prote
4	110	5.0	535	2 T17212	hypothetical prote
5	107.5	4.9	3942	2 T42730	Bassoon protein -
6	105.5	4.8	592	2 I49239	vesicle transport
7	105	4.8	757	2 T09081	telomere-associate
8	105	4.8	901	2 JC6093	dead ringer nuclea
9	105	4.8	1571	2 T14155	zinc finger protei
10	100.5	4.5	901	2 F83781	transposase (08) /
11	99.5	4.5	794	2 S59089	z13 protein - mous
12	98	4.4	1023	2 T48997	epsin-like protein
13	97.5	4.4	291	2 F86451	protein F86451.2 [1
14	97.5	4.4	589	2 F96599	protein F96599.6 [1
15	96.5	4.4	438	2 I38946	melanoma ubiquitin
16	96.5	4.4	981	1 F0NVMG	gag-abl polyprotei
17	96	4.3	660	2 S31437	homeotic protein H
18	95	4.3	933	1 ORHUP	progesterone recep
19	95	4.3	2148	2 A56011	transcription fact
20	94	4.3	469	2 T46929	hypothetical prote
21	94	4.3	469	2 T46930	hypothetical prote
22	93.5	4.2	471	2 B86170	ADK1 [Imported] -
23	93.5	4.2	806	1 JN0612	protein kinase B-r
24	93.5	4.2	807	1 I51153	protein kinase B-r
25	93.5	4.2	1571	2 T00062	hypothetical prote
26	93	4.2	449	2 T34328	hypothetical prote
27	93	4.2	1537	2 T13160	protein CNK - frui
28	92.5	4.2	531	2 T08760	hypothetical prote
29	92.5	4.2	546	2 JC4798	seizure-related me

30	92.5	4.2	2314	1 A46151	protein-tyrosine-p
31	92	4.2	883	2 S57653	brevican precursor
32	92	4.2	985	2 A36777	hypothetical prote
33	92	4.2	3147	2 T21328	hypothetical prote
34	91.5	4.1	348	2 T34266	LIM homeobox prote
35	91	4.1	883	2 S49126	brevican precursor
36	91	4.1	2038	2 A43742	female sterile hom
37	90.5	4.1	828	2 T33481	hypothetical prote
38	90.5	4.1	3788	2 T13960	beige protein homo
39	90	4.1	579	2 JT0494	alpha-glucosidase
40	90	4.1	627	2 T27123	hypothetical prote
41	89.5	4.0	641	2 T05497	hypothetical prote
42	89.5	4.0	766	2 S37894	hypothetical prote
43	89.5	4.0	3507	2 T34513	hypothetical prote
44	89	4.0	357	2 T02785	probable homeotic
45	89	4.0	1337	2 T13948	atypical protein k

ALIGNMENTS

RESULT 1

T42695 hypothetical protein DKFzp434N1928.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000

C:Accession: T42695

R:Blocker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database November 1999

A:Reference number: 222230

A:Accession: T42695

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-564 <AAA>

A:Cross-references: EMBL:AL133097

A:Experimental source: adult testis; clone DKFzp434N1928

C:Genetics:

A:Note: DKFzp434N1928.1

Query Match 100.0%; Score 2210; DB 2; Length 564;

Best Local Similarity 100.0%; Pred. No. 3.6e-170;

Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	RKQENIYSHLDESSSTTTAALPRELRPRPKVFLCISKDKQHNNVQCFAYFL	60
Db	147	RKQENIYSHLDESSSTTTAALPRELRPRPKVFLCISKDKQHNNVQCFAYFL	206
Qy	61	QDFCGCEVALDLWEDFSLCRGQREWIQIHESQFIIVVCSKGMKIFVDKKNKHKGGG	120
Db	207	QDFCGCEVALDLWEDFSLCRGQREWIQIHESQFIIVVCSKGMKIFVDKKNKHKGGG	266
Qy	121	RGSGKGEFLVAVSAIAEKLRQAKQSSAALSXFIATFYDSCGDPGILDLSTKYLRLM	180
Db	267	RGSGKGEFLVAVSAIAEKLRQAKQSSAALSXFIATFYDSCGDPGILDLSTKYLRLM	326
Qy	181	DNLPOLCSHLHSRDHGLQEPQOHTROGSRNRYFSKSGSLTYAICNKHQFIDEEPWF	240
Db	327	DNLPOLCSHLHSRDHGLQEPQOHTROGSRNRYFSKSGSLTYAICNKHQFIDEEPWF	386
Qy	241	KQVFPFPPLRYREPVLKFTDGLVLDVNVCKPGSPDPSDFCLVAVNLTGATGADSOHE	300
Db	387	KQVFPFPPLRYREPVLKFTDGLVLDVNVCKPGSPDPSDFCLVAVNLTGATGADSOHE	446
Qy	301	SOHGLQDQCEARPALDGAALQPLLHTVAVKAGSPDMRPSDGIYDSSVPSSELSLPLMEG	360
Db	447	SOHGLQDQCEARPALDGAALQPLLHTVAVKAGSPDMRPSDGIYDSSVPSSELSLPLMEG	506
Qy	361	LSTDQTTSSLTSEVSSSGIAGEEPPLPSKLLSSGSCRADLGCRSYTDELHVAAPL	418
Db	507	LSTDQTTSSLTSEVSSSGIAGEEPPLPSKLLSSGSCRADLGCRSYTDELHVAAPL	564

RESULT 2

T27282

hypothetical protein Y64G10A.e - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T27282

R:Almsough, R.

submitted to the EMBL Data Library, September 1999

A:Reference number: Z20336

A:Accession: T27282

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-846 <WIL>

A:Cross-references: EMBL:AL110498.1; PIDN:CAB54470.1; CESP:Y64G10A.e

A:Experimental source: clone Y64G10A

C:Genetics:

A:Gene: CESP:Y64G10A.e

A:Introns: 106/1; 198/3; 261/1; 301/3; 386/1; 416/2; 475/1; 510/3; 580/2; 815/3

C:Superfamily: Caenorhabditis elegans hypothetical protein Y64G10A.e

Query Match 6.8%; Score 150.5; DB 2; Length 846;
 Best Local Similarity 22.5%; Pred. No. 0.0065;
 Matches 94; Conservative 57; Mismatches 147; Indels 119; Gaps 24;

QY 2 KQOENIYSHLDSESSSYTAALPRERLRPRPKVFLCYSSKDGQNMVVOCFAYFLQ 61
 DB 448 KKASNI--ELLNENPAPS--HSGSIPL--ILKQISISLVIV--SHDSAQHEAAVLFAELLR 502
 QY 62 DFCGCEVALDWEDFSLCREGQREWIQIHESQFIIVVCSKGMKYFVDKKNKHKGGOR 121
 DB 503 DVFNVLNVLVDWEDDI--ENRATYINSSIVRANKVLIINSIG--AYF--RTVFRHOR--- 555
 QY 122 GSGKGEFLVAVSAIAEKROAKSSAALSKEFIAYFYDSCGDV--PGILDLSKY-- 177
 DB 556 -----EPAIERITTRND-----VIFDMQCELALQHPCVISCHESYTN 593
 QY 178 -----RLMD--NLQICSHLSRDHGLQEPQHTQSGRRNYFRSKSGSLYVAIGN 227
 DB 594 PRYVFPINRLQYISIP---NSLMTWTALTQPARPQLAGNQVFAR---LQAARSR 646
 QY 228 MHQFTDEPDPFEK-----QVFPHPPLPLRYR-----EP 256
 DB 647 KLYTESQPFQFENTHVRVATRVSELAHNIVPL--PPSEVKVVEDAFQGMETLPIDE 705
 QY 257 VLEKF-----DSGLVNDVMCKPGPESDFCLKVEAAVILGATGPADSOHESQH 303
 DB 706 LKEKFAAKRDLEVEVLSDVKLEDDVKACGP-----IHVEPTEPVELEPAEPMEAE 760
 QY 304 GGLDGDGEARALDGSAA---LQPLL--HTVKGSPSPMDRDSGIYDSS--VPSSELS 354
 DB 761 ED--EDEDVDSVSGQTARIEELQRLIVR-----KDMNHDGSLNLSATVSGSDFS 809

RESULT 3

T30113

hypothetical protein F56D1.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000

C:Accession: T30113

R:Chisoe, S.; Wilson, R.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid F56D1.

A:Reference number: Z20737

A:Accession: T30113

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-718 <CHI>

A:Cross-references: EMBL:U39997; PIDN:AAA81100.1; CESP:F56D1.2

C:Genetics:

A:Gene: CESP:F56D1.2

A:Introns: 93/1; 121/2; 163/3; 459/1; 517/3; 555/1; 615/3; 667/3

C:Superfamily: Caenorhabditis elegans hypothetical protein F56D1.2

Query Match

5.7%; Score 126; DB 2; Length 718;

Best Local Similarity 21.1%; Pred. No. 0.049;
 Matches 82; Conservative 64; Mismatches 149; Indels 94; Gaps 19;

QY 28 REERLRPR-----KVFCLYSSKDGQNMVVOCFAYFLQDFCGCEVALDWEDFS 77
 DB 398 KDKVRSREVRNIALTEFVKVIVIAD--DNDLETCTVKLVENLRNCASCDPVFDLEKLIT 456
 QY 78 LCRSGQREWIQIHESQFIIVVCSKGMKYFVDKKNKHKGGKSGKGEFLVAVSAIA 137
 DB 457 AEQIVPSRWLVLDQISSLKKEFIIVSDCAEKILDTSETHQLVQARPPADLFGPANEMI- 515
 QY 138 EKLROAKSSAALSKEFIAYFYDSCGDV---GILDSTKYRLMDNLPQLCSHLRSR 194
 DB 516 --IRDATHNPEARKKYAVVRNYS--PHVPPNLAAILNLT--FILPEQFAQLTALHNVE 570
 QY 195 HGLQEPQHTQSGRRNYFRSKSGSLY---VAICNHQFIDEEPWFKEQFVP----- 245
 DB 571 H-----TERANVTONISEAQIHEWNLCSARMSFFVVRNPWLETWRKPKDELA 619
 QY 246 FHPPLRYRFLVLEKDSGLVNDVMCKPGPESDFCLKVEAAVILGATGPADSOHESQHG 305
 DB 620 LH---LKRQSPVIVPIOT-----EED---RIASIKYNLVPPQALVDS--- 657
 QY 306 LQDGEARALDGSAAALQPLLHTVKGSPSPM---PRDSGIYDSSVPSSELSLPLMEGLST 363
 DB 658 --DED-----DVDLQIP--HASHQNPILLPPEQCG-----PDSD-----SD 690
 QY 364 DOTSSLTSESVSSSGLGEEPPALPSK 392
 DB 691 SESDSSSESESDNBS---EDPKTIIVK 716

RESULT 4

T17212

hypothetical protein DKFZp434P211.1 - human (fragments)

C:Species: Homo sapiens (man)

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T17212

R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, September 1999

A:Reference number: Z18723

A:Accession: T17212

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-488;489-535 <POD>

A:Cross-references: EMBL:AL117401

A:Experimental source: adult testis; clone DKFZp434P211

A>Note: the cDNA sequence contains a -1 frameshift near codon 488

C:Genetics:

A>Note: DKFZp434P211.1

Query Match 5.0%; Score 110; DB 2; Length 535;

Best Local Similarity 23.5%; Pred. No. 0.65;

Matches 70; Conservative 42; Mismatches 108; Indels 78; Gaps 17;

QY 139 KLRQAKSS--SAALSKFIAYFYDSCGDVPGI-----LDLSTKYRLMDNLPQ 185
 DB 103 RYNOTSQTSTWTSSTNRNAISSYSTSTGLPGLRRREGPASSECOITLSSKTVSEDRPQ 162
 QY 186 LCSHLRSRDLQGE--PGQHTQSGRRNYFRSKSGSLYVAICNHQFIDEEPWFKEQF 243
 DB 163 AVSSGHTQCEKAADIARQGTLT--LRNDSSTSEASRP-----STHKP-----PLLPRRG 210
 QY 244 VPFF--PPPL-----RYRPFVLERPDSGLVNDVM---CKPGESDFCLKVEAA 287
 DB 211 EPIALPPLELGYRVTVVEDLDREKAAPQRIINSALQVEDKALSDCRPSRSH---TILSL 267
 QY 288 VLGATG--PADSOHESQHGGLQDGEARALDGSAAALQPLLHTVKGSPSPM-----RD 340
 DB 268 ATGASGLPAYSKAPS---MDAQQETHSKSDCLGLLDPLASA--AGVSTAPMSKKHRP 321
 QY 341 SG--IYDSSVPSSELSLPLMEGLSTDOTSTSLTESVSSSSGLGEEPPALPSKLLSG 397
 DB 341 SG--IYDSSVPSSELSLPLMEGLSTDOTSTSLTESVSSSSGLGEEPPALPSKLLSG 397

A;Gene: munc-18c

RESULT 5

T42730 Mus musculus
 C:Species: Mus musculus (house mouse)
 C:Date: 11-Jan-2000 [sequence revision 11-Jan-2000 text change 21-Jul-2000]
 C:Accession: T42730.1
 C:Direct S.; Sumariwalla, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex, J.; Cullen, B. 147, 499-509, 1998
 A:Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized to the presynaptic cytoskeleton
 A:Reference number: 122242; PMID: 96345363; PMID: 9679147
 A:Accession: T42730
 A:Status: preliminary; translated from GB/EMBL/DBFJ
 A:Molecule type: DNA
 A:Residues: 1-3942 <DIE>
 A:Cross-references: EMBL:X17034; NID:93413809; PIDN:CA476598.1; PID:G3413810
 A:Experimental source: strain 129 SVJ
 A:Genetics:
 A:Map position: 3p1
 A:Introns: 72/2; 208/3; 505/3; 675/3; 2889/3; 3582/1; 3851/3; 3886/1; 3930/1
 A:Note: bassoon
 C:Function:
 A:Description: may be involved in cytomatrix organization at the site of neurotransmitter release
 A:Note: component of the presynaptic cytoskeleton
 C:Keywords: coiled coil; zinc finger

```

Query Match      4.9%  Score 107.5;  DB 2;  Length 3942;
Best Local Similarity 19.1%;  Pred. No. 15;
Matches 58;  Conservative 29;  Mismatches 99;  Indels 117;  Gaps 11;

QY 181 DNLPOLCSHLHSRDHGLQGFQTHGSRRTYFSKSGRSLVAIC-----NMHQFIDEE 235
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3535 DTCQPOCS-----SHSNPDVQEHVKGDPRAHAKREEGYMLDDSHCVVSDSEAYHLQCE 3589
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 236 PDWFKEQYVPFPPPLRYRE-----PVLEKF-----DSGLVLNDVMCKPG 275
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3590 TMTFDK-----PRDARSDFRHHGGHTVSSQKRGPARSHYHDYDEPEGLPHD-----EGG 3643
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 276 PSEDFCLKVEAVLGNATGPADSQHSQHG-----GLDQDG-----EARP- 314
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3644 PGRH-----TSAKEHRHSDHGRSHGAEPPGRRAAKPHARDMGREARPH 3691
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 315 -----ALDGSAAALQPLHRTV 329
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 3692 PQASPAQMKKGCGYPPSSADYSQSSRAPSAVHHASESKGSRQAHTGPSALQPKADTQ 3751
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

330 KAGSPSDMRDSGTYDSSVPSSLSPLMEGLSTDTQTETSSLTESVSSSSGLGSEEPAL 389
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 3752 AQPQWGRQAAPGPQSQPPSSRQT---PSGTASRQPTQKQKQKQKQKQKQKQKQKQKQ 3808
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 390 PSK 392
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3809 PSQ 3811
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 6

I49239 vesicle transport protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I49239
R:Tellam, J.T.; McIntosh, S.; James, D.E.
J. Biol. Chem. 270, 5857-5863, 1995
A:Title: Molecular identification of two novel Munc-18 isoforms expressed in non-neuronal
A:Reference number: I49238; MUID:95197608; PMID:7890715
A:Accession: I49239
A:Status: preliminary; translated from GB/EMBL/DDBT
A:Molecule type: mRNA
A:Residues: 1-392 <RSD>
A:Cross-references: EMBL:U19521; NID:9642027; PIDN:AAA69913.1; PTD:9642028
C:Genetics:

RESULT 7

T09081
telomere-associated recQ-like helicase ~ smut fungus (Ustilago maydis) (fragment)
C:Species: Ustilago maydis (corn smut)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-May-2000
C:Accession: T09081
R:Sanchez-Alonso, P.; Guzman, P.
Genetics 148, 1043-1054, 1998
A:Title: Organization of chromosome ends in Ustilago maydis: recQ-like helicase motif
A:Reference number: Z16557; PMID:98198830; PMID:9539423
A:Accession: T09081
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-757 <S>
A:Cross-references: EMBL:AF030885; NID:g2642221; PID:g2642222
A:Experimental source: strain FH2
C:Genetics:
A:Gene: UTA5recQ
C:Keywords: DNA binding

Query Match

```

Query Match      4.8%; Score 105; DB 2; Length 757;
Best Local Similarity 20.6%; Pred. No. 2.6;
Matches 92; Conservative 42; Mismatches 147; Indels 166; Gaps 23;

QY      11 HLDSESSSESYTAALP-----RRLRPRPRVF-----LCYSKDGQHNNVVQ 54
Db       169 HYRDETQTVLNTATPPEDAFISHKLTPLIVRESTNRSLNCISVRYAEHRNSGMT 228

QY      55 CF-AFFLDPCGCEVALDWEFSLCRGCEQWYQKHESQFIIVWCSSKGMKYFDK-- 111
Db      229 CYDAVRYVD--ECRARTDW-----NQKRD-----RIIVYCTS--RELVARLA 267

QY      112 -----KNYKHKGGRGS-----QKGELFLVAVSAATEKLRAQKQSSAALSFTIA 156
Db      112 -----KNYKHKGGRGS-----QKGELFLVAVSAATEKLRAQKQSSAALSFTIA 156

```


A:Cross-references: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BA04773.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1054

Query Match: 4.5%; Score 100.5; DB 2; Length 901;
Best Local Similarity 22.6%; Pred. No. 7.6;
Matches 66; Conservative 44; Mismatches 103; Indels 79; Gaps 15;

QY 1 RKQOENYSHLDE-----ESSESTYTAALPRERLRPRKPVFLCYSSKQDN 48
DB 482 RTDVSFVGKNGLRRLHKGKSVHIELGLVAL-AHNLKRAIV--DRSKPKN 538
QY 49 ---HAN-----VVOCF---AYFLDPGCEVALDWEFSLREGREW--- 87
DB 539 THQKNNRNRKRSFYVLRFCFNDSPFFIKSDGQYASALFD--KLREGGNNIEVI 596
QY 88 -LQKHESQFIIVVCSKGMKIFVDKKNYKHGGRSGKGEFLVAVSAI----- 136
597 DLSKTYRNRVW---KGINMFKEMGVLLGPNAGAKSTTSMISLIQPTSGDVLK 652
137 ---AKLQKQSSAALSKFTAVFYSCB-----GDVPGILDLSLYRLMDNLPOLC 187
DB 653 GGSIKHQSARLSILGVPOEIAVYHDTARENLAFPGKIYGLKGBELKHR-WESTLQV 711
QY 188 SLHSRDRGLQEPQOHTROGSRNRYFRSKGRSLVIAICNMHQ---FIDPEP 236
DB 712 -----GLEE-----RQNDRVHTFSGMKRRLNIAVALLHEPELIINDEP 750

RESULT 11
S59069
Z13 Protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 28-May-1999
C:Accession: S59069
Biochem. J. 311, 219-224, 1995
Rathjen, P.D.; Wells, J.R.E.
A:Title: An unusual arrangement of 13 zinc fingers in the vertebrate gene z13.
A:Reference number: S59069; PMID:96003919; PMID:7575457
A:Accession: S59069
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-794 <SCH>
A:Cross-references: GB:U14556; NID:g608136; PIDN:AAA85493.1; PID:g608137
C:Superfamily: POZ domain homology
F:10-108/Domain: POZ domain homology <POZ>

Query Match: 4.5%; Score 99.5; DB 2; Length 794;
Best Local Similarity 20.6%; Pred. No. 7.7;
Matches 71; Conservative 41; Mismatches 146; Indels 87; Gaps 15;

QY 64 CGCEVALDWEFSLCREGREWYQKHESQFIIVVCSKGMK-YFVDKKNYKHGGRG 122
DB 24 CDCTFVVD-GVDF-----KAHKA--VLAACSEYFKMLFYDQKDVVHLDISNA 67
QY 123 SGKGEFLVAVSAIAELKROAKOSS-----AALSFKFIATVFDYSCGDVPGILDLS 175
DB 68 AGLGQ-----VLEPMYTKLSLSPENVDDVLAVASFLMQ-----DIVT 106
QY 176 KYRLMDNLPOLCSHL-HSRDHGLQEPQH-----TROGSRNRYFRSKGRSLY 222
DB 107 ACHTLKSLAEPSTTGESADASAAGGDKRANDEKAATMLSLRGQAGSSSTGFGRELK 166
QY 223 VAICNMHQFIDEEDPWEKQFVPEHPPLRYREPVLKFDGLVNDVCMKPKPESDFCL 282
DB 167 EERGQASASSGAEQTEKADAPREPP-----VELKPDPTSSMA- 206
QY 283 KYEAAVATGATCPADSQHESQHGGLDQGEARPDGSAALQPLHTVYKAGSPDMPRSG 342
DB 207 AAEEALSESSEQEMEYEPASK--EDGEEGAGPATVYKEGKH-LDNGEPEEENESA 263
QY 343 IYDSSVSPSELSLP---LMEGLSTQDTETSSLTESVSSSSGLIGE 384

DB 264 GTDS---GQELNGEONLSRSGYGDRTESKAYGSIHKCEGCKE 305

RESULT 12
T48997
epsin-like protein - Arabidopsis thaliana
N:Alternate names: protein F25L23.150
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: T48997
R:D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.
submitted to the Protein Sequence Database, May 2000
A:Reference number: Z55012
A:Accession: T48997
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1023 <DAN>
A:Cross-references: EMBL:AL356014; GSPDB:GN00061; ATSP:F25L23.150
A:Experimental source: cultivar Columbia; BAC clone F25L23
C:Genetics:
A:Gene: ATSP:F25L23.150
A:Map position: 3
A:Introns: 12/2; 29/3; 56/2; 82/3; 110/3; 159/2; 263/2; 277/2; 311/2; 365/1; 443/3; 8

Query Match: 4.4%; Score 98; DB 2; Length 1023;
Best Local Similarity 20.4%; Pred. No. 14;
Matches 76; Conservative 55; Mismatches 146; Indels 96; Gaps 17;

QY 85 EWVQKHESQFIIVVCSKGMKIFVDKKNYKHGGRSGKGEFLVAVSAIAELKROAK 144
DB 96 EVIEVEKEHAYQITLS-GFQY-IDSSG---KQGSNRYKKAQSLVALYNDKERITEVR 150
QY 145 QSSSAALSKP-----TAVTFD-YSCGVDYVGLDLSYKRLMDNLPOLCSHLSDRG 196
DB 151 EKAANRDKYTHSMRHPGSGYGDYDEG-----RYGDRDEGRSGYKEREYIG 198
QY 197 LQEPQOHTROGSRNRYFRSKGRSLVIAICNMHQFIDEEDPWEKQFVPEHPPLRYREP 256
DB 199 YRDDNRNRDGR--YSRDSEDR--YGRDGN---TDDE-----YGRSR 235
QY 257 VLEKFDGLVNDVCMKPKPESDFCLVE-----NAVLGATGPADSQHESQHGGLDQD--- 309
DB 236 SVNYNG-----SRGRSDRERPIEDGSSSDSGADADHSQGRGLERFSE 286
QY 310 ---GEARPDGSAALQPLHTVYKAGSPDMPRSGIYDSSVSPSELSLPMEGLSTDOT 366
DB 287 QNIGAAPPSEYEAVS-----ESRSPVYSERDGETPOVAPPGAAASPLAENISVDNK 338
QY 367 ETSLSLE-----SVSS--SSGLGEPEPALPSKLLSS-----GSKCADLGC 405
DB 339 AADFVNESSPOQVEAFDEDPGVSACAPTAGASVPAPITPVYSTAPPASINAEML 398
QY 406 RSYDELHAYAPL 418
DB 399 LGSLSDFVSENP 411

RESULT 13
F86451
protein F6W18.2 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F86451
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
ansen, N.F.; Hughes, B.; Hulzar, L.
China, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, E.A.; Luros, J.S.; Maitl, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tello
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: F86451
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-391 <STO>
 A:Cross-references: GB:AE005172; NID:g6714285; PIDN:AAF25981.1; GSPDB:GN00141
 A:Genetics: F86451
 A:Map position: 1

Query Match 4.4%; Score 97.5; DB 2; Length 291;
 Best Local Similarity 34.2%; Pred. No. 2.9;
 Matches 47; Conservative 28; Mismatches 76; Indels 43; Gaps 10;
 QY 229 HOFIDEDPWFKEQFPFHPPLKRYREPVL---EKFDGVLNDVMCKPGPSDFCLAYE 285
 DB 92 HEFVARP-----PHEPLP-HGSOPIISHGQDQGSNTAESV-----SVTMYR 133
 286 AAVLGATGPADQSHQSGGLDQ---DGEAR-----PALDGAALQPLHTVKGPSD 336
 134 QSLDGGPNNOMOPSDNQOQVQEGQAQSHNSHNSFRNDSARNTPIPTKFDGPPQ 193
 QY 337 MPRDGGYDSSVPSSELSPLMGLSTDTOTETSSLTSSVSSSGIGEEPPALPKSLSS 396
 DB 194 Q-----MNNSLPS-----PRENGRILPTPTSOYRP--QSPYATNLLSPRSPPLST 241
 QY 397 G-SCRADLCGRSYT 409
 DB 242 GVQYPPPTPPRNT 255

RESULT 14

F96599
 protein F14J16.6 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 A:Accession: F96599
 R:Rheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: F96599
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-589 <STO>
 A:Cross-references: GB:AE005173; NID:g8778302; PIDN:AAF79311.1; GSPDB:GN00141
 A:Genetics: F14J16.6
 A:Map position: 1

Query Match 4.4%; Score 97.5; DB 2; Length 589;
 Best Local Similarity 20.0%; Pred. No. 7.5;
 Matches 60; Conservative 54; Mismatches 123; Indels 63; Gaps 12;
 QY 104 GMYKVFYDKKHKGGGSGKELFVAVSAIAEKLRQAKQSSAALSFIAYFYDSC 163
 DB 88 GRNFASNSVQSGSGRNASFEKE---NGANHVTGSTRAPAKNSATVTVNETKVS 144
 QY 164 EGDVGLDLSKTYRLMDNLPLQ---CSHLHSRDHGLQPGQHTGRRNYFRSKGRSL 221
 DB 145 PASIFSEV---SNHKAQDD-PSLISASRCSSKSDQAIETATSKQGNQSL----- 191
 QY 222 IYVACNMHGFIDEQPFWEKQFV---PFHPPLRYREPVLKFDGLNDVMCKPGPSD 279
 DB 192 -----PRPDYSESHVTFPH-----IQVAKGLQNLGTFGSP-----DSN 226

QY 280 FCLKEAAVLGATGPADQSHQSGGLDQGEARPALDGSAAALQPL-----LFTYKA 331
 DB 227 FVKEVSSS-NGASGGYDSNFESSHGTGDDRESSTTNGITGVASARFVTELTSLYLEE 285
 QY 332 GSPDMRDSGYDSS-----VPSSELSPLMGLSTDTOTETSSLTSSVSSSGIGEEPP 386
 DB 286 TSTVSEKDKIGISNATGAEPVVSDDHIVPPVEVPKEALSNTETHQIA-----TQDAP 341
 RESULT 15
 138946
 melanoma ubiquitous mutated protein - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 31-May-1996 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
 A:Accession: 138946
 R:Coulie, P.G.; Lehmann, F.; Lethe, B.; Herman, J.; Lurquin, C.; Andrawiss, M.; Boon,
 Proc Natl. Acad. Sci. U.S.A. 92, 7976-7980, 1995
 A:Title: A mutated intron sequence codes for an antigenic peptide recognized by cytol
 A:Reference number: 138944; MUID:95377402; PMID:7644523
 A:Accession: 138945
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-438 <RES>
 A:Cross-references: EMBL:U20897; NID:g1046222; PIDN:AAC50240.1; PID:g1046223
 A:Accession: 138946
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 'G', 1-74 <RE2>
 A:Cross-references: EMBL:U20908; NID:g1046218; PIDN:AAC50238.1; PID:g1046219
 C:Genetics:
 A:Introns: 46/3

Query Match 4.4%; Score 96.5; DB 2; Length 438;
 Best Local Similarity 20.8%; Pred. No. 6.1;
 Matches 94; Conservative 39; Mismatches 135; Indels 103; Gaps 24;
 QY 65 GCEVALDMDWDFSLCREGQREWIQIIESOFIIVCSKMKYFDKKNYKHGGGSG 124
 DB 30 GCK-----TYLCRWKRLPAKVLARTA-----TSTRKRRK----- 61
 QY 125 KGEFLVA-----VSAIAEKLRQAKQSSAALSFI-----IA 156
 DB 62 --EYFLAVQILSLEEKIKVKSTEVEILEKSKQIAIASLASQNEVPAAPLEAYRSLR 119
 QY 157 VFDYSCGQV-----PGILDLSKTYRLMDNLPLQ-----SHLSR 193
 DB 120 VALDVLSEGSINSQESSAGTGRADSKLRGKPMHEVSSPCDSNSSSLPRGDLVGSRRPHR 179
 QY 194 -----DH--GLQEP-----GQHTQGRS-----RNY- 212
 DB 180 RPYVQSSLSSTCEKDPCKVDHKKLRKSENPRGLVLPAGGGAQDSGRIHKNT 239
 QY 213 FRSKGR--SLYVAICNNHQFI---DEPDWFEK---QFVPEPPPLRYREPVP---LEKFD 262
 DB 240 LAKRGNRNSAKASICLINGSSEDDTERDMGSGGSAAPSLPSGVREDDDPCANAGSD 299
 QY 263 SGLVLDVMCKPGPSDFCLKYAAVATGATGPADQSHQSGGLDQGEARPALDGS--- 319
 DB 300 PGLPLGSLTAPPAEPSAC-----SEPG--ECPAKRPRLDGSRP 338
 QY 320 --AALQPLHTVKGPSDMPDRSDGYDSSVPSSELS-PLMEGLSTDTOT----- 366
 DB 339 PAVOLEPH---AGAAPSQCP--GCPRESVTPRTARLGPSPSHASADATRLCPDPSQK 394
 QY 367 ---ETSSLTSSVSSSGLG-----EEPP 387
 DB 395 LEKESQSEESMGNSNRSLDEDEDEPP 425

Search completed: May 19, 2003, 09:25:32
 Job time : 22.4315 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 19, 2003, 09:07:58 ; Search time 56.6401 Seconds
(without alignments)
1771.498 Million cell updates/sec

Title: us-09-912-157-2
Perfect score: 4013
Sequence: 1. MAPWLQCSVFFVACNLG.....GKADLCGRSYTDELHVAFL 753

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A.Geneseq_101002.*
1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
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10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
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13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
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22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4013	99.8	753	AB07626	Human cytokine rec
2	4003	97.8	738	AB07628	Human cytokine rec
3	3925	97.2	738	AB07628	Human cytokine rec
4	3801	97.1	738	AA009904	Human Interleukin
5	3897	97.1	738	AA009953	Human Interleukin
6	3896	97.1	738	AA009954	Human Interleukin
7	3894	97.0	738	AA009951	Human Interleukin
8	3894	97.0	738	AA009952	Human Interleukin
9	3894	97.0	738	AA009956	Human Interleukin
10	3890	96.9	738	AA009955	Human Interleukin

11	3890	96.9	738	22	AAU09957	Human Interleukin
12	3830.5	95.5	738	23	AAU11355	Human DNAX cytokin
13	3703	92.3	728	22	AAU04958	Human Interleukin
14	3703	92.3	739	22	AAU10602	Human Interleukin
15	3387	84.4	739	23	ABB07630	Murine cytokine re
16	2699.5	67.3	554	23	AAU91330	Human novel secret
17	1337	33.3	296	22	AAU10601	5' portion of Huma
18	312	7.8	866	17	AAW04185	Human Interleukin-
19	312	7.8	866	19	AAW61272	Human Interleukin-
20	312	7.8	866	20	AAW92409	Human IL-17R prote
21	312	7.8	866	21	AAV99941	Human IL-17R prot
22	312	7.8	866	21	AAV97181	Human Interleukin-
23	312	7.8	866	21	AAV97131	Human Interleukin-
24	312	7.8	866	21	AAU03807	Human Interleukin-
25	312	7.8	866	22	AAU62066	Human IL-17R (HCTL
26	312	7.8	866	22	AAV72754	Human Interleukin-
27	306	7.6	864	17	AAW04184	Murine Interleukin
28	306	7.6	864	19	AAW61271	Mouse Interleukin-
29	306	7.6	864	20	AAW92408	Murine IL-17R prot
30	306	7.6	864	21	AAV99935	Murine IL-17R prot
31	306	7.6	864	21	AAV97130	Murine Interleukin
32	306	7.6	864	21	AAV97180	Murine Interleukin
33	306	7.6	864	21	AAU03806	Murine Interleukin
34	306	7.6	864	22	AAU62060	Murine IL-17R Poly
35	306	7.6	864	22	AAV72748	Murine Interleukin
36	271.5	6.8	539	23	AAW47457	Human IL-17 recept
37	135.5	3.4	238	20	AAV31624	Human IL-17RH matu
38	135.5	3.4	385	21	AAU25795	Human secreted pro
39	135.5	3.4	385	22	AAU75381	Human secreted pro
40	135.5	3.4	385	23	AAW47459	Human IL-17 recept
41	135.5	3.4	502	22	AAU72923	Human PRO polypept
42	135.5	3.4	502	22	AAU24349	Human EST encoded
43	135.5	3.4	502	22	AAU04955	Human Interleukin
44	135.5	3.4	502	22	AAE06586	Human protein havi
45	135.5	3.4	502	22	AAAB7604	Human PRO5801. HO

ALIGNMENTS

RESULT 1
AB07626
ID AB07626 standard; Protein; 753 AA.

XX AC AB07626;

XX DT 20-MAY-2002 (first entry)

XX DE Human cytokine receptor, zcytor18 amino acid sequence.

XX KW Cytokine receptor; zcytor18; cell proliferation; antiproliferative; human;
pulmonary alveolar proteinosis; familial periodic fever; antitumor;
erythroleukemia; chromosome 3p14.3; gene therapy.

XX OS Homo sapiens.

XX PN WO200208259-A2.

XX PD 2002-05-20

XX PF 23-JUL-2001; 2001WO-US23253.

XX PR 26-JUL-2000; 2000US-220747P.

XX XX (ZYMO) ZYMOGENETICS INC.

XX PI Presnell SR, Kuestner RE, Gao Z;

XX DR WPI; 2002-217048/27.

XX PT N-PSDB; ABA95031, ABA95032.

XX New cytokine receptor polypeptide designated zcytor18, useful for
inhibiting cell proliferation associated with psoriasis or tumor.

QY 1 MAPWLQCSVFTVNAACNGSOLAAGGSGRAGADTCGRMKAAARPRCLVANEGVGP 60
 DB 1 MAPWLQCSVFTVNAACNGSOLAAGGSGRAGADTCGRMKAAARPRCLVANEGVGP 60
 QY 61 ASRNSGLYNITFKYDNCITTLNPKGVKHIADDAQNTISQYACHDQVAVTILWSPGALGIE 120
 DB 61 ASRNSGLYNITFKYDNCITTLNPKGVKHIADDAQNTISQYACHDQVAVTILWSPGALGIE 120
 QY 121 FLKGFVILLEKSGRCCOOLILKDPKQNSFKRTGMSQFFLNMKFETDIFVKVVPF 180
 DB 121 FLKGFVILLEKSGRCCOOLILKDPKQNSFKRTGMSQFFLNMKFETDIFVKVVPF 180
 QY 181 PSIKNESNYHPPFFTRACDILLOPNLACKPFWKPRNLNISQHSQDMQVSDHAPNFG 240
 DB 181 PSIKNESNYHPPFFTRACDILLOPNLACKPFWKPRNLNISQHSQDMQVSDHAPNFG 240
 QY 241 FRFFYLHYLKLHKGPFKRTCKBOTETTSCLLQNVSPGDIYIELVDYDNTTRKVMHYA 300
 DB 241 FRFFYLHYLKLHKGPFKRTCKBOTETTSCLLQNVSPGDIYIELVDYDNTTRKVMHYA 300
 QY 301 LKPVHSPWAGPIRAVAITVPLWISAFATLFTVCKRKKQENIYSHLDESSSESYTAA 360
 DB 301 LKPVHSPWAGPIRAVAITVPLWISAFATLFTVCKRKKQENIYSHLDESSSESYTAA 360
 QY 361 LPRERLRPRKPVLCYSSKQDNHNVVQCFAFYFLQDFCGCEVALDLWEDFSLCREGORE 420
 DB 361 LPRERLRPRKPVLCYSSKQDNHNVVQCFAFYFLQDFCGCEVALDLWEDFSLCREGORE 420
 QY 421 WVIQKHESQFIIVVCSKGMKIFVCKNKYKHGSGRSGKGELELVAVSAIAEKLRAQK 480
 DB 421 WVIQKHESQFIIVVCSKGMKIFVCKNKYKHGSGRSGKGELELVAVSAIAEKLRAQK 480
 QY 481 SSSAALSKEFIATFDYSCGDVPGILDSTKYRLMDNLPOLCSHLHSDHGLQEPGQTR 540
 DB 481 SSSAALSKEFIATFDYSCGDVPGILDSTKYRLMDNLPOLCSHLHSDHGLQEPGQTR 540
 QY 541 QGSRNRYFRKSGSLYVAICNMHQFIDEEPDWFERKQFPPFPPLRYREPVEKFDOSGL 600
 DB 541 QGSRNRYFRKSGSLYVAICNMHQFIDEEPDWFERKQFPPFPPLRYREPVEKFDOSGL 600
 QY 601 VLNDVCKPGPESDCLVEAVILGATGPADSOHESQHGGLDODGEARPALDGSAAQPL 660
 DB 601 VLNDVCKPGPESDCLVEAVILGATGPADSOHESQHGGLDODGEARPALDGSAAQPL 660
 QY 661 LFTVKAQSPDMRDSGIYDSSVPSSELSPLAMEGLSTQDTETSSLTSESVSSGLGEE 720
 DB 661 LFTVKAQSPDMRDSGIYDSSVPSSELSPLAMEGLSTQDTETSSLTSESVSSGLGEE 720
 QY 721 PPALPKLLSSGSKRADLGCRSYTDLRAVAPL 753
 DB 721 PPALPKLLSSGSKRADLGCRSYTDLRAVAPL 753

RESULT 3

ID ABB07628 standard; Protein; 739 AA.
 XX AC ABB07628;
 XX AC ABB07628;

20-MAY-2002 (first entry)

Human cytokine receptor, Zcytor18 splice variant.

Cytokine receptor; Zcytor18; cell proliferation; antiproliferative; human;
 pulmonary alveolar proteinosis; familial periodic fever; antitumor;
 erythroleukemia; chromosome 3p14.3; gene therapy; splice variant.

Homo sapiens.

W0200208259-A2.

31-JAN-2002.

PF 23-JUL-2001; 2001MO-US23253.
 XX 26-JUL-2000; 2000US-220747P.
 PR (ZYMO) ZYMOGENETICS INC.
 XX Presnell SR, Ruestner RE, Gao Z;
 PI WPI; 2002-217048/27.
 XX N-PSDB; ABA95035, ABA95036.
 PT New cytokine receptor polypeptide designated zcytor18, useful for
 PT inhibiting cell proliferation associated with psoriasis or tumor
 PT growth, and modulating immune system by binding to endogenous zcytor18
 PT ligand
 XX Claim 1; Page 102-106; 119pp; English.
 XX The invention relates to an isolated cytokine receptor polypeptide
 CC designated Zcytor18. The Zcytor18 polypeptides can be expressed by
 CC standard recombinant methodology. The polypeptides can be used to inhibit
 CC cell proliferation associated with psoriasis or tumor growth. The
 CC encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
 CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
 CC vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
 CC and localize Zcytor18 gene expression in tissue samples. The probes are
 CC also useful for detecting gross aberrations in chromosome 3 in which
 CC Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
 CC linkage-based testing of pulmonary alveolar proteinosis, familial
 CC periodic fever and erythroleukemia, and erythroleukemia associated with
 CC polymorphisms of cytokine receptors. The present sequence represents a
 CC human Zcytor18 splice variant.
 XX Sequence. 739 AA;

Query Match 97.8%; Score 3925; DB 23; Length 739;
 Best Local Similarity 98.1%; Pred. No. 0;
 Matches 739; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MAPWLQCSVFTVNAACNGSOLAAGGSGRAGADTCGRMKAAARPRCLVANEGVGP 60
 DB 1 MAPWLQCSVFTVNAACNGSOLAAGGSGRAGADTCGRMKAAARPRCLVANEGVGP 60
 QY 61 ASRNSGLYNITFKYDNCITTLNPKGVKHIADDAQNTISQYACHDQVAVTILWSPGALGIE 120
 DB 61 ASRNSGLYNITFKYDNCITTLNPKGVKHIADDAQNTISQYACHDQVAVTILWSPGALGIE 120
 QY 121 FLKGFVILLEKSGRCCOOLILKDPKQNSFKRTGMSQFFLNMKFETDIFVKVVPF 180
 DB 121 FLKGFVILLEKSGRCCOOLILKDPKQNSFKRTGMSQFFLNMKFETDIFVKVVPF 180
 QY 181 PSIKNESNYHPPFFTRACDILLOPNLACKPFWKPRNLNISQHSQDMQVSDHAPNFG 240
 DB 181 PSIKNESNYHPPFFTRACDILLOPNLACKPFWKPRNLNISQHSQDMQVSDHAPNFG 240
 QY 241 FRFFYLHYLKLHKGPFKRTCKBOTETTSCLLQNVSPGDIYIELVDYDNTTRKVMHYA 300
 DB 241 FRFFYLHYLKLHKGPFKRTCKBOTETTSCLLQNVSPGDIYIELVDYDNTTRKVMHYA 300
 QY 301 LKPVHSPWAGPIRAVAITVPLWISAFATLFTVCKRKKQENIYSHLDESSSESYTAA 360
 DB 301 LKPVHSPWAGPIRAVAITVPLWISAFATLFTVCKRKKQENIYSHLDESSSESYTAA 360
 QY 361 LPRERLRPRKPVLCYSSKQDNHNVVQCFAFYFLQDFCGCEVALDLWEDFSLCREGORE 420
 DB 361 LPRERLRPRKPVLCYSSKQDNHNVVQCFAFYFLQDFCGCEVALDLWEDFSLCREGORE 420
 QY 421 WVIQKHESQFIIVVCSKGMKIFVCKNKYKHGSGRSGKGELELVAVSAIAEKLRAQK 480
 DB 421 WVIQKHESQFIIVVCSKGMKIFVCKNKYKHGSGRSGKGELELVAVSAIAEKLRAQK 480
 QY 481 SSSAALSKEFIATFDYSCGDVPGILDSTKYRLMDNLPOLCSHLHSDHGLQEPGQTR 540
 DB 481 SSSAALSKEFIATFDYSCGDVPGILDSTKYRLMDNLPOLCSHLHSDHGLQEPGQTR 540

Db 467 SSSAALSRLFIATFYDSCGDVPCILDLSTKYRLMDNLPLQCSHLHSRDLQEPQOHR 526
 QY 541 QGSRNRYFRSGSLVYACNMHQFIDEPOWFEKQVFPHPPLPRFVLEKFDGSL 600
 Db 527 QGSRNRYFRSGSLVYACNMHQFIDEPOWFEKQVFPHPPLPRFVLEKFDGSL 586
 QY 601 VLNDVCKPSPESDFCLKVEAAVLGATGADQSHQSGGLDQGEARPALDGSAAQLPL 660
 Db 587 VLNDVCKPSPESDFCLKVEAAVLGATGADQSHQSGGLDQGEARPALDGSAAQLPL 646
 QY 661 LHTVAGSPDPRSGIYDSSVPSSELSPLMEGLSTDTQTSLSFESSSSGLGEE 720
 Db 647 LHTVAGSPDPRSGIYDSSVPSSELSPLMEGLSTDTQTSLSFESSSSGLGEE 706
 QY 721 PPALPSKLLSSGCKADLCGRSYTDELHVAAPL 753
 Db 707 PPALPSKLLSSGCKADLCGRSYTDELHVAAPL 739

RESULT 4
 AAU09904
 ID AAU09904 standard; Protein; 738 AA.
 XX
 AC AAU09904;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human Interleukin 17 (hIL-17) receptor like protein.
 XX
 KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KW vascular; cycostatic; anti-leukaemic; anti-infertility; ophthalmological;
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone disease; vascular disorder; eye disorder; cancer; human.
 XX
 OS Homo sapiens.
 XX
 XX WO200168859-A2.
 XX
 XX 20-SEP-2001.
 XX
 XX 15-MAR-2001; 2001WO-0508678.
 XX
 XX 16-MAR-2000; 2000US-189816P.
 XX
 XX 28-NOV-2000; 2000US-0724460.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX Jing S;
 XX
 XX WPI; 2001-611392/70.
 XX
 XX N-PSDB; AAS15346.
 XX
 XX Nucleic acids encoding Interleukin 17 receptor like polypeptides,
 XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
 XX diabetes, psoriasis and glaucoma -
 XX
 XX Claim 2; Page 152-154; 158pp; English.
 XX
 XX The invention describes novel nucleic acids encoding Interleukin (IL) 17
 XX receptor like polypeptides useful as vaccines and in gene therapy. These
 XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
 XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 XX osteopathic, vascular, cycostatic, anti-leukaemic, anti-infertility and
 XX ophthalmological activities. The IL-17 receptor like nucleic acids and
 XX proteins may be used to prevent and treat diseases associated with
 XX inappropriate IL-17 receptor like polypeptide (hIL17r) expression. These
 XX include, for example immune disorders (e.g. inflammation, diabetes and
 XX transplant rejection), infections (e.g. hepatitis and septicemia),
 XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal

CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
 CC breast cancer), reproductive disorders (e.g. infertility and
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 CC DNA and its complements may also be used as diagnostic probes to detect and
 CC quantitate the presence of similar nucleic acids in samples and identify
 CC patients needing restorative therapy. The IL17rIP may also be used as
 CC antigens in the production of antibodies against the proteins and in
 CC assays to identify modulators of expression and activity. The
 CC anti-IL17rIP antibodies and antagonists may also be used to down regulate
 CC expression and activity. This is the amino acid sequence of the human
 CC Interleukin 17 (IL-17) receptor like protein described in the method of
 CC the invention.
 XX
 XX Sequence 738 AA;
 SQ
 Query Match 97.2%; Score 3901; DB 22; Length 738;
 Best Local Similarity 97.6%; Pred. No. 0;
 Matches 734; Conservative 1; Mismatches 3; Indels 14; Gaps 1;
 QY 1 MAPWLQCSVFFTVNACLNGSLAVAAGSGRARGADTCGRMKAAARPLCVANEGVGP 60
 Db 1 MAPWLQCSVFFTVNACLNGSLAVAAGSGRARGADTCGRMKAAARPLCVANEGVGP 60
 QY 61 ASRNSGLINTFYKDYKCTTLYLPVCKHVIADQNTISQYACHDQVAVTILMSPGALGIE 120
 Db 47 ASRNSGLINTFYKDYKCTTLYLPVCKHVIADQNTISQYACHDQVAVTILMSPGALGIE 106
 QY 121 FLKGFVILEELASGEGCOQILKDPQLNSSFRTGMSQPLNKKETDYFKVYVPP 180
 Db 107 FLKGFVILEELASGEGCOQILKDPQLNSSFRTGMSQPLNKKETDYFKVYVPP 166
 QY 181 PSIKNESNTHPPFFTRACDLLOPDNLCKPFWKPRNINISQSGSDAQVSDHAPHNFG 240
 Db 167 PSIKNESNTHPPFFTRACDLLOPDNLCKPFWKPRNINISQSGSDAQVSDHAPHNFG 226
 QY 241 FRFFLYHLKHEGPPKRTCKEQTTTTSCLQNVSPGDYIIELVDDTNTTRKRVHYA 300
 Db 227 FRFFLYHLKHEGPPKRTCKEQTTTTSCLQNVSPGDYIIELVDDTNTTRKRVHYA 286
 QY 301 LKPVHSPWAGPIRAVAITVPLVVISAPATLFTVCKKQKQENIYSHLDESSESTYTA 360
 Db 287 LKPVHSPWAGPIRAVAITVPLVVISAPATLFTVCKKQKQENIYSHLDESSESTYTA 346
 QY 361 LPRERLRPRKVFCLYSSKDGQNHNVVQCFAFYFLQDFGCEVALDLMEDFSLCREGORE 420
 Db 347 LPRERLRPRKVFCLYSSKDGQNHNVVQCFAFYFLQDFGCEVALDLMEDFSLCREGORE 406
 QY 421 WVIQKHESQFIIVWCCKGMYFVDKKNYKGGGSGGKGLFVAVSATAEKLQAKQ 480
 Db 407 WVIQKHESQFIIVWCCKGMYFVDKKNYKGGGSGGKGLFVAVSATAEKLQAKQ 466
 QY 481 SSSAALSRLFIATFYDSCGDVPCILDLSTKYRLMDNLPLQCSHLHSRDLQEPQOHR 540
 Db 467 SSSAALSRLFIATFYDSCGDVPCILDLSTKYRLMDNLPLQCSHLHSRDLQEPQOHR 526
 QY 541 QGSRNRYFRSGSLVYACNMHQFIDEPOWFEKQVFPHPPLPRFVLEKFDGSL 600
 Db 527 QGSRNRYFRSGSLVYACNMHQFIDEPOWFEKQVFPHPPLPRFVLEKFDGSL 586
 QY 601 VLNDVCKPSPESDFCLKVEAAVLGATGADQSHQSGGLDQGEARPALDGSAAQLPL 660
 Db 587 VLNDVCKPSPESDFCLKVEAAVLGATGADQSHQSGGLDQGEARPALDGSAAQLPL 646
 QY 661 LHTVAGSPDPRSGIYDSSVPSSELSPLMEGLSTDTQTSLSFESSSSGLGEE 720
 Db 647 LHTVAGSPDPRSGIYDSSVPSSELSPLMEGLSTDTQTSLSFESSSSGLGEE 706
 QY 721 PPALPSKLLSSGCKADLCGRSYTDELHVAAPL 753
 Db 707 PPALPSKLLSSGCKADLCGRSYTDELHVAAPL 739

DB 707 PPALPSKLLSSGCKADLCGRSTTDELHAPV 738

RESULT 5

AA009953

ID AA009953 standard; Protein; 738 AA.

XX

AC AA009953;

XX

DT 14-FEB-2002 (first entry)

XX

DE Human Interleukin 17 (hIL-17) receptor like protein substitution #3.

XX

KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathologic; vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmologic; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant; mutein.

KW

OS Homo sapiens.

OS

XX Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 363

FT /label= Ser, Thr, Ala, Cys

FT

PN WO200168859-A2.

XX

XX 20-SEP-2001.

XX

PF 15-MAR-2001; 2001WO-0508678.

XX

PR 16-MAR-2000; 2000US-189816P.

PR

XX 28-NOV-2000; 2000US-0724460.

XX

PA (AMGE-) AMGEN INC.

XX

XX Jing S;

XX

DR WPT; 2001-611392/79.

XX

PT Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma.

PT

PS Claim 20; Page -: 158pp; English.

PS

XX The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, osteopathologic, vascular, cytostatic, anti-leukemic, anti-infertility and ophthalmologic activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (hIL17) expression. These include, for example immune disorders (e.g. hepatitis and diabetes and transplant rejection), infections (e.g. hepatitis and septicemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis), cancers (e.g. leukemia and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also be used as diagnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17rIP may also be used as antigens in the production of antibodies against the proteins and in

CC assays to identify modulators of expression and activity. The anti-IL17rIP antibodies and antagonists may also be used to down regulate expression and activity.

CC

CC Note: This sequence is not given in the specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AA009904) and has been created according to information given in claim 20.

CC

XX

XX Sequence 738 AA:

Query Match 97.18; Score 3897; DB 22; Length 738;

Best Local Similarity 97.58; Pred. No. 0;

Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;

QY 1 MAPWQLQCSVFTVAVNACLSQALVAVAGSGRAGADTCGNMKAAAPRLCVANEGVGP 60

DB 1 MAPWQLQCSVFTVAVNACLSQALVAVAGSGRAGVDTGCMR-----GVGP 46

QY 61 ASRNSGLNITEKYNCTTYLNPVGVKHVIADAQNIITISQACHDOVAVTILWSPGALGIE 120

DB 47 ASRNSGLNITEKYNCTTYLNPVGVKHVIADAQNIITISQACHDOVAVTILWSPGALGIE 106

QY 121 FLKGFVILVLEELKSGRQCOQLILKDPKLNSSFKTKGHSOPFLMKFFTDYFKVVPF 180

DB 107 FLKGFVILVLEELKSGRQCOQLILKDPKLNSSFKTKGHSOPFLMKFFTDYFKVVPF 166

QY 181 PSIKNESNTHPFFTRACDLQLQPDNLACKPFWKPRNLNISOHSGDMQVDFHAPNFG 240

DB 167 PSIKNESNTHPFFTRACDLQLQPDNLACKPFWKPRNLNISOHSGDMQVDFHAPNFG 226

QY 241 FREFFLYHLKHEGPFKTKCKQBOQTETTSCLLQNVSPGDIYIELVDOTNTTKVHYA 300

DB 227 FREFFLYHLKHEGPFKTKCKQBOQTETTSCLLQNVSPGDIYIELVDOTNTTKVHYA 286

QY 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCKKQOENIYSHLDESESSYTTAA 360

DB 287 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCKKQOENIYSHLDESESSYTTAA 346

QY 361 LPRERLRPRKPVLCYSSKQONEMVNVQCFAFYLFQDFCGCEVALDLWEDFSLCREGORE 420

DB 347 LPRERLRPRKPVLCYSSKQONEMVNVQCFAFYLFQDFCGCEVALDLWEDFSLCREGORE 406

QY 421 WTIQKHESQFIIVVCSEKMTFYVDKKNYKHGGSGKSGKGLFVLVAVSAIAEKLRQAKQ 480

DB 407 WTIQKHESQFIIVVCSEKMTFYVDKKNYKHGGSGKSGKGLFVLVAVSAIAEKLRQAKQ 466

QY 481 SSSAALSKEFIATVDFYCEGDPVCGILDSTKYRLMDNLPLQCSHLRSRDLGLOPQGHTR 540

DB 467 SSSAALSKEFIATVDFYCEGDPVCGILDSTKYRLMDNLPLQCSHLRSRDLGLOPQGHTR 526

QY 541 QGSRNRYFKSGRSLTYAICNMQHFDDEPDWFEKQFVFPHPPLRYREPVLEKFGSL 600

DB 527 QGSRNRYFKSGRSLTYAICNMQHFDDEPDWFEKQFVFPHPPLRYREPVLEKFGSL 586

QY 601 VLNDVCKPSPDSCLVAVLAVGATGADPSQHSQHGGLDQDGEARPDALDGAALQPL 660

DB 587 VLNDVCKPSPDSCLVAVLAVGATGADPSQHSQHGGLDQDGEARPDALDGAALQPL 646

QY 661 LHTVAGSPDMPSRGIYDSSVPSSELSPLMBGLSTDTOTETTSITVESVSSGLGEE 720

DB 647 LHTVAGSPDMPSRGIYDSSVPSSELSPLMBGLSTDTOTETTSITVESVSSGLGEE 706

QY 721 PPALPSKLLSSGCKADLCGRSTTDELHAPV 752

DB 707 PPALPSKLLSSGCKADLCGRSTTDELHAPV 738

RESULT 6

AA009954

ID AA009954 standard; Protein; 738 AA.

XX

XX AA009954;

XX

DT 14-FEB-2002 (first entry)

XX DE Human Interleukin 17 (hIL-17) receptor like protein substitution #4.
 XX KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 XX KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 XX KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 XX KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 XX KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;
 XX KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 XX KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 XX KW muten.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX OS Key Location/Qualifiers
 XX OS Misc-difference 374
 XX OS /label- Val, Ile, Met, Leu, Phe, Ala, Nle
 XX PN WO200168859-A2.
 XX PD 20-SEP-2001.
 XX PF 15-MAR-2001; 2001WO-US08678.
 XX PR 16-MAR-2000; 2000US-189816P.
 XX PR 28-NOV-2000; 2000US-0724460.
 XX PA (AMGE-) AMGEN INC.
 XX PI Jing S;
 XX DR WPI; 2001-611392/70.
 XX PT Nucleic acids encoding interleukin 17 receptor like polypeptides,
 XX PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
 XX PT diabetes, psoriasis and glaucoma
 XX PS Claim 21; Page -; 158pp; English.
 XX CC The invention describes novel nucleic acids encoding interleukin (IL) 17
 XX CC receptor like polypeptides useful as vaccines and in gene therapy. These
 XX CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 XX CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
 XX CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 XX CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and
 XX CC ophthalmological activities. The IL-17 receptor like nucleic acids and
 XX CC proteins may be used to prevent and treat diseases associated with
 XX CC inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These
 XX CC include, for example immune disorders (e.g. inflammation, diabetes and
 XX CC transplant rejection), infections (e.g. hepatitis and septicemia),
 XX CC weight disorders (e.g. Alzheimer's disease, Parkinson's disease and obesity), neuronal
 XX CC dysfunction (e.g. Alzheimer's disease, cachexia and anorexia), lung
 XX CC disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 XX CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 XX CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 XX CC (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
 XX CC breast cancer), reproductive disorders (e.g. infertility and
 XX CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 XX CC DNA and its complements may also be used as diagnostic probes to detect and
 XX CC quantitate the presence of similar nucleic acids in samples and identify
 XX CC patients needing restorative therapy. The IL17rp may also be used as
 XX CC antigens in the production of antibodies against the proteins and in
 XX CC assays to identify modulators of expression and activity. The
 XX CC anti-IL17rp antibodies and antagonists may also be used to down regulate
 XX CC expression and activity.
 XX CC Note: This sequence is not given in the specification but is based on the
 XX CC human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)
 XX CC and has been created according to information given in claim 21.
 XX SQ Sequence 738 AA;
 XX Query Match 97.1%; Score 3896; DB 22; Length 738;

Best Local Similarity 97.5%; Pred. No. 0;
 Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;
 QY 1 MAPWQLQCSYFFVFNACLSGSLAAAGSGGARGADTCGRMKAAARPRCLVANEVGP 60
 DB 1 MAPWQLQCSYFFVFNACLSGSLAAAGSGGARGADTCGRMKAAARPRCLVANEVGP 46
 QY 61 ASRNSGLNITFYDNCITLYMPVKHVIADAQNTISOTACHDQVAVTILWSPGALGIE 120
 DB 47 ASRNSGLNITFYDNCITLYMPVKHVIADAQNTISOTACHDQVAVTILWSPGALGIE 106
 QY 121 FLKGFVILEELKSGRQCOQLILKDPQLNSFKRTGMSQFPLNMFETDYFKVYVPF 180
 DB 107 FLKGFVILEELKSGRQCOQLILKDPQLNSFKRTGMSQFPLNMFETDYFKVYVPF 166
 QY 181 PSIKNESNTHPPFFTRACDILLQPDNLAKPKPKPRLNLSQHSQSDQVSDHAPNFG 240
 DB 167 PSIKNESNTHPPFFTRACDILLQPDNLAKPKPKPRLNLSQHSQSDQVSDHAPNFG 226
 QY 241 FRFFLYHLKHEGPFKRTCKEQTTTSCLLQNSPGDYIIELVDDTTRKVAHYA 300
 DB 227 FRFFLYHLKHEGPFKRTCKEQTTTSCLLQNSPGDYIIELVDDTTRKVAHYA 286
 QY 301 LKPVHSPWAGPIBAVAITVPLVVISAFATLFTVMCRKQENIYSHLDESESESTYAA 360
 DB 287 LKPVHSPWAGPIBAVAITVPLVVISAFATLFTVMCRKQENIYSHLDESESESTYAA 346
 QY 361 LPRERLPRKVELCYSSKQGNHNVVQCFAFLQDFCCEVALDLMEDFSLCREGORE 420
 DB 347 LPRERLPRKVELCYSSKQGNHNVVQCFAFLQDFCCEVALDLMEDFSLCREGORE 406
 QY 421 WVIQKHESOFIIVCCKGMYFVDKKNYKHKGGRSGKGEFLVAVSATAELKRAQK 480
 DB 407 WVIQKHESOFIIVCCKGMYFVDKKNYKHKGGRSGKGEFLVAVSATAELKRAQK 466
 QY 481 SSSAALSKEFTAVFYDSCBDDVPGILDISTKYRLMNLPLQCSHLASRDGLOEPGQTR 540
 DB 467 SSSAALSKEFTAVFYDSCBDDVPGILDISTKYRLMNLPLQCSHLASRDGLOEPGQTR 526
 QY 541 QGSRNFRKSGRSILYAIACNMHOFIDEEFDWFEKQFVFPFPPPLRYREPVLKFKFSGL 600
 DB 527 QGSRNFRKSGRSILYAIACNMHOFIDEEFDWFEKQFVFPFPPPLRYREPVLKFKFSGL 586
 QY 601 VLNDVCKCPESDCLKVEAAVLGATGADSPADSOESQHGGLDQGEARPALDGSAAQPL 660
 DB 587 VLNDVCKCPESDCLKVEAAVLGATGADSPADSOESQHGGLDQGEARPALDGSAAQPL 646
 QY 661 LHTYKAGSPDMPSGDIYDSVPSSELSPLMEGLSTDTQTTSSLTSSVSSSSGLGEE 720
 DB 647 LHTYKAGSPDMPSGDIYDSVPSSELSPLMEGLSTDTQTTSSLTSSVSSSSGLGEE 706
 QY 721 PPALPSKLLSSGCKRADLGCRSYTDELHAPVAP 752
 DB 707 PPALPSKLLSSGCKRADLGCRSYTDELHAPVAP 738
 RESULT 7
 AAU09951
 ID AAU09951 standard; Protein; 738 AA.
 XX AC AAU09951;
 XX DT 14-FEB-2002 (first entry)
 XX DE Human Interleukin 17 (hIL-17) receptor like protein substitution #1.
 XX KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 XX KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 XX KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 XX KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 XX KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;
 XX KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 XX KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;

KW muteln.
 XX Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 45
 FT /label= Gly, Pro or Ala
 XX
 PN WO200168859-A2.
 PD 20-SEP-2001.
 XX
 PF 15-MAR-2001; 2001WO-US08678.
 XX
 PR 16-MAR-2000; 2000US-189816P.
 PR 28-NOV-2000; 2000US-0724460.
 XX
 PA (AMGE-); AMGEN INC.
 XX
 PI Jing S;
 XX
 DR WPI; 2001-611392/70.
 XX
 PT Nucleic acids encoding interleukin 17 receptor like polypeptides,
 PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
 PT diabetes, psoriasis and glaucoma
 XX
 PS Claim 18; Page 1; 158pp; English.
 XX
 CC The invention describes novel nucleic acids encoding interleukin (IL) 17
 CC receptor like polypeptides useful as vaccines and in gene therapy. These
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-alzheimer's, renal,
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-asthmatic, dermatological,
 CC anti-parkinsonian, anti-convulsant, anti-leukemic, anti-infertility and
 CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and
 CC proteins may be used to prevent and treat diseases associated with
 CC inappropriate IL-17 receptor like polypeptide (IL17rip) expression. These
 CC include, for example immune disorders (e.g. inflammation, diabetes and
 CC transplant rejection), infections (e.g. hepatitis and septicemia),
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
 CC breast cancer), reproductive disorders (e.g. infertility and
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 CC DNA and its complements may also be used as diagnostic probes to detect and
 CC quantitate the presence of similar nucleic acids in samples and identify
 CC patients needing restorative therapy. The IL17rip may also be used as
 CC antigens in the production of antibodies against the proteins and in
 CC assays to identify modulators of expression and activity. The
 CC anti-IL17rip antibodies and antagonists may also be used to down regulate
 CC expression and activity.
 CC Note: This sequence is not given in the specification but is based on the
 CC human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)
 CC and has been created according to information given in claim 18.
 XX
 XX Sequence 738 AA:

Query Match 97.0%; Score 3894; DB 22; Length 738;
 Best Local Similarity 97.5%; Pred. No. 0;
 Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;
 OY 1 MAPWLQICSVFFTVNACLSQLAVAAGSGCRAGATCCWRMKAAAPRLCVANEGVGP 60
 DB 1 MAPWLQICSVFFTVNACLSQLAVAAGSGRAGVDTCCWR-----GYXP 46
 OY 61 ASRNSGLNITTFKNDCTTYPNPKVGHVIAQAQNTITISQYACHDQVAVTILWSPGALGIE 120
 DB 47 ASRNSGLNITTFKNDCTTYPNPKVGHVIAQAQNTITISQYACHDQVAVTILWSPGALGIE 106

OY 121 FLAGFVILIELKSGROCOOLILKDPKQLNSSFKTKHESOPFLNMFETDIFVKVVPF 180
 DB 107 FLAGFVILIELKSGROCOOLILKDPKQLNSSFKTKHESOPFLNMFETDIFVKVVPF 166
 OY 181 PSTKNESYHPFFFRTRACDILLQPDNLACKPFWKPRNLNLSQHGSDMOVDFHAPNFG 240
 DB 167 PSTKNESYHPFFFRTRACDILLQPDNLACKPFWKPRNLNLSQHGSDMOVDFHAPNFG 226
 OY 241 FREFYLYLKLKGGPFRKTKCKQQTETTSCLQNVSPGDYIIELVDVDTNTTKVMHYA 300
 DB 227 FREFYLYLKLKGGPFRKTKCKQQTETTSCLQNVSPGDYIIELVDVDTNTTKVMHYA 286
 OY 301 LKPVHSPWAGPIRAVAITPVLVVISAFATLFTVNCRKQENIYSHLDEESSESYTAA 360
 DB 287 LKPVHSPWAGPIRAVAITPVLVVISAFATLFTVNCRKQENIYSHLDEESSESYTAA 346
 OY 361 LPRERLRPRKPVFLCYSSKDGONEMVYVQCFAFYFLQDFCGCEVALDLWEDFSLCREGORE 420
 DB 347 LPRERLRPRKPVFLCYSSKDGONEMVYVQCFAFYFLQDFCGCEVALDLWEDFSLCREGORE 406
 OY 421 WYQKHESQFIIVVCSGKMYFVDKKNYKHGGRGSGKGFELFLVAVSAIAEKLRQAKQ 480
 DB 407 WYQKHESQFIIVVCSGKMYFVDKKNYKHGGRGSGKGFELFLVAVSAIAEKLRQAKQ 466
 OY 481 SSSAALSKEFIATFYDSCGDPVPGILDLSYKYLMDNLPLQALSHLSRDHGLQPGQHTR 540
 DB 467 SSSAALSKEFIATFYDSCGDPVPGILDLSYKYLMDNLPLQALSHLSRDHGLQPGQHTR 526
 OY 541 QGSRNRYFSKSGSLYVAICNMHQFIDEEPDMFQFVPPHPPRLRYREPLEKFDGSL 600
 DB 527 QGSRNRYFSKSGSLYVAICNMHQFIDEEPDMFQFVPPHPPRLRYREPLEKFDGSL 586
 OY 601 VLNDVNCKPGPESDFCLAVEANVLGATGPADSQHESQHGGLDQDGEARPDALDQSAALQPL 660
 DB 587 VLNDVNCKPGPESDFCLAVEANVLGATGPADSQHESQHGGLDQDGEARPDALDQSAALQPL 646
 OY 661 LHTVKAQSPDMPRDSGIYDSSVPSSELSPLMEGLSTDTQETSSLTSSVSSSGLGEER 720
 DB 647 LHTVKAQSPDMPRDSGIYDSSVPSSELSPLMEGLSTDTQETSSLTSSVSSSGLGEER 706
 OY 721 PPALPSKLLSSGCKADIGCRSYTDELHAPV 752
 DB 707 PPALPSKLLSSGCKADIGCRSYTDELHAPV 738

RESULT 8
 AAU09952
 ID AAU09952 standard; Protein: 738 AA.
 XX
 AC AAU09952;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human Interleukin 17 (hIL-17) receptor like protein substitution #2.
 XX
 KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 KW muteln.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 227
 FT /label= Phe, Leu, Val, Ile, Ala, Tyr
 XX
 PN WO200168859-A2.

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XX PD      20-SEP-2001
XX PF      15-MAR-2001; 2001WO-US08678.
XX PR      16-MAR-2000; 2000US-189816P.
XX PR      28-NOV-2000; 2000US-0724460.
XX PA      (AMGE-) AMGEN INC.
XX PI      Jing S.
XX DR      WPI; 2001-611392/70.
XX PT      Nucleic acids encoding interleukin 17 receptor like polypeptides,
XX FT      useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
XX TT      diabetes, psoriasis and glaucoma -
XX PS      Claim 19; Page -: 158pp; English.
CC CC      The invention describes novel nucleic acids encoding interleukin (IL) 17
CC CC      receptor like polypeptides useful as vaccines and in gene therapy. These
CC CC      have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
CC CC      immunosuppressive, hepatic, anabolic, anorectic, anti-asthmatic, dermatological,
CC CC      anti-parkinsonian, anti-convulsant, anti-stimulant, anti-infertility and
CC CC      osteopathic, vascular, cytostatic, anti-leukemic, anti-infectivity and
CC CC      ophthalmological activities. The IL-17 receptor like nucleic acids and
CC CC      proteins may be used to prevent and treat diseases associated with
CC CC      inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
CC CC      include, for example immune disorders (e.g. inflammation, diabetes and
CC CC      transplant rejection), infections (e.g. hepatitis and septicemia),
CC CC      weight disorders (e.g. anorexia, cachexia and obesity), neuronal
CC CC      dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
CC CC      lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
CC CC      (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
CC CC      bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
CC CC      (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
CC CC      breast cancer), reproductive disorders (e.g. infertility and
CC CC      miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
CC CC      DNA and its complements may also used as diagnostic probes to detect and
CC CC      quantitate the presence of similar nucleic acids in samples and identify
CC CC      patients needing restorative therapy. The IL17rlp may also be used as
CC CC      antigens in the production of antibodies against the proteins and in
CC CC      assays to identify modulators of expression and activity. The
CC CC      anti-IL17rlp antibodies and antagonists may also be used to down regulate
CC CC      expression and activity.
CC CC      Note: This sequence is not given in the specification but is based on the
CC CC      human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)
CC CC      and has been created according to information given in claim 19.
XX XX
XX SQ      Sequence   738 AA:
Query Match          97.0%; Score 3894; DB 22; Length 738;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 733; Conservative    4; Mismatches    4; Indels    14; Gaps    1
QY      1 MAPWLQLCSVFYFVNACLSGSLAVAAGSGRARGADTCGRNKAAAPRLCVANEGVGP 60
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      61 ASRNSGLYNITFYDNCTYTLNPNVGKRVHVAIDAQNITISOTACHDQAVTILWSPGALGIE 120
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      47 ASRNSGLYNITFYDNCTYTLNPNVGKRVHVAIDAQNITISOTACHDQAVTILWSPGALGIE 106
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      121 FLAKFRVILEELSEKRGCOQQLIKDKPQLNSFKKTGMESQFLNMKFETDYFVKVVFP 180
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      107 FLAKFRVILEELSEKRGCOQQLIKDKPQLNSFKKTGMESQFLNMKFETDYFVKVVFP 166
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      181 PSINKSNHYIPFFTRACDLLLPDLNLACKPKPWPRNLNISQHSMDQMVSFDIAPHNFG 240
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      167 PSINKSNHYIPFFTRACDLLLPDLNLACKPKPWPRNLNISQHSMDQMVSFDIAPHNFG 226
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      241 FRFTLYHLKLKHGPPKRTCKEQTTTSCLLQNYSQGYIIELVDVTNTTKVMHYA 300

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DB	227	XXXXXXFLYTKLKHBPFPFKTKQBDTETTSCLLQNSPGDYIELVDNTNTRKPHYA	286
QY	301	LKPVHSPWAGPIRAVAITVPLVVIYSAFATLFTVCKRKQKQENIYSHLDSESSSTYTA	360
DB	287	LKPVHSPWAGPIRAVAITVPLVVIYSAFATLFTVCKRKQKQENIYSHLDSESSSTYTA	346
QY	361	LPRELRPRPKVFLCTSSKDGQNHNNVQCAYFLQDPCCCEVALDLWEDFSLCREQRE	420
DB	347	LPRELRPRPKVFLCTSSKDGQNHNNVQCAYFLQDPCCCEVALDLWEDFSLCREQRE	406
QY	421	WYQIKIHESQPIIVVCGSKMKYFVDKKNTKHKGGRGSGKGELPLVAVSAIAEKLRQAK	480
DB	407	WYQIKIHESQPIIVVCGSKMKYFVDKKNTKHKGGRGSGKGELPLVAVSAIAEKLRQAK	466
QY	481	SSSAALSFKTAVFDYSCGDVPGILDISTKYRLMDNLPLQCSHLHSRDBGLQEPQSTR	540
DB	467	SSSAALSFKTAVFDYSCGDVPGILDISTKYRLMDNLPLQCSHLHSRDBGLQEPQSTR	526
QY	541	QGSRENTFRSKGSLYVAICNNHQFIDDEPDWPEKQFVPFHPPLRYREPVLKFDGSL	600
DB	527	QGSRENTFRSKGSLYVAICNNHQFIDDEPDWPEKQFVPFHPPLRYREPVLKFDGSL	586
QY	601	VLVNDVCKPGPESDFCLKVEAAVLGATGPADQSHQSHQGGGLDQGEARPALDGSAAQLPL	660
DB	587	VLVNDVCKPGPESDFCLKVEAPVLGATGPADQSHQSHQGGGLDQGEARPALDGSAAQLPL	646
QY	661	LHTVKAQSPDMPRDSCGYDSSVPSSELSLPLMBGLSTDTQTSSLTESVSSSSGLGEE	720
DB	647	LHTVKAQSPDMPRDSCGYDSSVPSSELSLPLMBGLSTDTQTSSLTESVSSSSGLGEE	706
QY	721	PPALPSKLLSSGCKADLCGRSYTDELHNAV 752	
DB	707	PPALPSKLLSSGCKADLCGRSYTDELHNAV 738	
RESULT 9			
AAU009956			
ID	AAU009956	standard; Protein; 738 AA.	
AC	AAU009956;		
DT	14-FEB-2002	(first entry)	
DE	Human Interleukin 17 (hIL-17)	receptor like protein substitution #6.	
KW	Interleukin 17; hIL-17	receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant; mutein.	
OS	Homo sapiens.		
XX	Synthetic.		
FH	Key	Location/Qualifiers	
FT	Misc-difference 515	/Label= Asp, Glu	
FT	XX		
PN	WO200168859-A2.		
PD	20-SEP-2001.		
PF	15-MAR-2001; 2001WO-US08678.		
PR	16-MAR-2000; 2000US-189816P.		
XX	28-NOV-2000; 2000US-0724460.		
XX	(AMGE-) AMGEN INC.		

Jing S;

WPI; 2001-611392/70.

Nucleic acids encoding interleukin-17 receptor-like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma.

Claim 23: Page -; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17rip) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also be used as diagnostic probes to detect and quantify the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17rip may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-IL17rip antibodies and antagonists may also be used to down regulate expression and activity.

Note: This sequence is not given in the specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 23.

Sequence 738 AA:

Query Match 97.0%; Score 3894; DB: 22; Length 738;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 733; Conservative: 1; Mismatches 4; Indels 14; Gaps 1;

1 MAPWLQCSVFTVNAQLNGSQLAAGGSGRAGADTCGRWKAARPRICVANEGVGP 60
1 MAPWLQCSVFTVNAQLNGSQLAAGGSGRAGVDTGWR-----GVGP 46
61 ASRNSGLYNTFKYDNCITLNPVKVVIADQNTISYACHDOVAVTILWSPCALGIE 120
47 ASRNSGLYNTFKYDNCITLNPVKVVIADQNTISYACHDOVAVTILWSPCALGIE 106
121 FLGFRVILEELKSGROCOOLILKDPKQLNSSFKRTGMESQFFLMKFETDIYKVVVF 180
107 FLGFRVILEELKSGROCOOLILKDPKQLNSSFKRTGMESQFFLMKFETDIYKVVVF 166
181 PSIKNSNTHPFFFTFRACDILLQDNLACKPFWKPNLNISQSGDMQVDFHAPNFG 240
167 PSIKNSNTHPFFFTFRACDILLQDNLACKPFWKPNLNISQSGDMQVDFHAPNFG 226
241 FRFFYLHYKLKHEGFKRTCKQEGTETTSCLLQNVSPGDYIIELVDDTNTTRVHYA 300
227 FRFFYLHYKLKHEGFKRTCKQEGTETTSCLLQNVSPGDYIIELVDDTNTTRVHYA 286
301 LKPVHSPWAGPIRAVAITVPLWISAFATLFTVCKRKKQENIYSHLDEESSESTTAA 360
287 LKPVHSPWAGPIRAVAITVPLWISAFATLFTVCKRKKQENIYSHLDEESSESTTAA 346
361 LPRERLRPRKPVFLCYSSKDSQNHNVVQCFAFYFLQDFGCEVALDWEDFSICREGORE 420
347 LPRERLRPRKPVFLCYSSKDSQNHNVVQCFAFYFLQDFGCEVALDWEDFSICREGORE 406

QY 421. WTIQKHESQFIIVVCSKGMKIFVDKKNYKHGGRSGKGLFLVAVSAEKLRAQK 480
DB 407. WTIQKHESQFIIVVCSKGMKIFVDKKNYKHGGRSGKGLFLVAVSAEKLRAQK 466
QY 481. SSSAALSKEFIIVVCSKGMKIFVDKKNYKHGGRSGKGLFLVAVSAEKLRAQK 540
DB 467. SSSAALSKEFIIVVCSKGMKIFVDKKNYKHGGRSGKGLFLVAVSAEKLRAQK 526
QY 541. QGSRNRYFRSKSGSLYVAICNQHOFIDEPDFEKFQVPPHPPPLRYREPVLEKFDGSL 600
DB 527. QGSRNRYFRSKSGSLYVAICNQHOFIDEPDFEKFQVPPHPPPLRYREPVLEKFDGSL 586
QY 601. VLVNWKCPGSPESDCLKVEANVLGATGPDADSOHESQHGGLDQGEARPAALDGSALQPL 660
DB 587. VLVNWKCPGSPESDCLKVEANVLGATGPDADSOHESQHGGLDQGEARPAALDGSALQPL 646
QY 661. LETVAGSPDMRDSGIYDSSVSELSLPLMEGLSTDTSTSLTSVSSSSGLGEE 720
DB 647. LETVAGSPDMRDSGIYDSSVSELSLPLMEGLSTDTSTSLTSVSSSSGLGEE 706
QY 721. PPALSKLLSSGCKADLCGRSTYDELHAYAP 752
DB 707. PPALSKLLSSGCKADLCGRSTYDELHAYAP 738
RESULT 10
AAU09955
ID AAU09955 standard; protein; 738 AA.
AC AAU09955;
XX 14-FEB-2002 (first entry)
DT Human Interleukin 17 (hIL-17) receptor like protein substitution #5.
DE Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
mutin.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FT Misc-difference 385 /label= Cys, Ser, Ala
FT WO200168859-A2.
XX 20-SEP-2001.
PD 15-MAR-2001; 2001WO-US08678.
PF 16-MAR-2000; 2000US-189816P.
PR 28-NOV-2000; 2000US-0724460.
XX (AMGE-) AMGEN INC.
PA Jing S;
PI WPI; 2001-611392/70.
DR Nucleic acids encoding interleukin 17 receptor like polypeptides,
XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
XX diabetes, psoriasis and glaucoma -
XX Claim 22; Page -; 158pp; English.

CC The invention describes novel nucleic acids encoding interleukin (IL) 17
 CC receptor like polypeptides useful as vaccines and in gene therapy. These
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, and
 CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infectivity and
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and
 CC proteins may be used to prevent and treat diseases associated with
 CC inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These
 CC include, for example immune disorders (e.g. inflammation, diabetes and
 CC transplant rejection), infections (e.g. hepatitis and septicemia),
 CC weight disorders (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and obesity), neuronal
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 CC (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
 CC breast cancer), reproductive disorders (e.g. infertility and
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 CC DNA and its complements may also be used as diagnostic probes to detect and
 CC quantitate the presence of similar nucleic acids in samples and identify
 CC patients needing restorative therapy. The IL17rp may also be used as
 CC antigens in the production of antibodies against the proteins and in
 CC assays to identify modulators of expression and activity. The
 CC anti-IL17rp antibodies and antagonists may also be used to down regulate
 CC expression and activity.
 CC Note: This sequence is not given in the specification but is based on the
 CC human Interleukin 17 (IL-17) receptor like protein sequence (AA009904)
 CC and has been created according to information given in claim 22.

XX SQ Sequence: 738 AA;

Query Match 96.9%; Score 3890; DB 22; Length 738;
 Best Local Similarity 97.5%; Pred. No. 0;
 Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;

QY 1 MAPVLQCSVFTVNAQLNGSOLAVAGSGGRAGNDTCGWRMAAARPLCVANGVGP 60
 DB 1 MAPVLQCSVFTVNAQLNGSOLAVAGSGGRAGNDTCGWRMAAARPLCVANGVGP 60
 QY 61 ASNSGLYNITFKYDNCITVLPVGHVADAGNITISQYACHDQVAVTILWSPGALGIE 120
 DB 47 ASNSGLYNITFKYDNCITVLPVGHVADAGNITISQYACHDQVAVTILWSPGALGIE 106
 QY 121 FLKGFVILEELKSGRCQOLILKOPKOLNSFKETGNSOPFLNKKFTDYFKVVPF 180
 DB 107 FLKGFVILEELKSGRCQOLILKOPKOLNSFKETGNSOPFLNKKFTDYFKVVPF 166
 QY 181 PSIKNESNYHPFFTRACOLLQPNLACKPFWKPRNLINSQHSQDMQVSDRAHPNFG 240
 DB 167 PSIKNESNYHPFFTRACOLLQPNLACKPFWKPRNLINSQHSQDMQVSDRAHPNFG 226
 QY 241 FRFFYLTKLHKGPFKKTKCKBOTETTSCILLONVSPGDYIILEVDNTTFRKVMYA 300
 DB 227 FRFFYLTKLHKGPFKKTKCKBOTETTSCILLONVSPGDYIILEVDNTTFRKVMYA 286
 QY 301 LKPVHSPWAGPIRAVATVPLVWISAFATLFTVCKKQKQENIYSHLDESSESYTTAA 360
 DB 287 LKPVHSPWAGPIRAVATVPLVWISAFATLFTVCKKQKQENIYSHLDESSESYTTAA 346
 QY 361 LPRERLRPRPKVFLCYSSKQDMNVMVQCFAFLQDFGCEVALDLWEDFSLCRGORE 420
 DB 347 LPRERLRPRPKVFLCYSSKQDMNVMVQCFAFLQDFGCEVALDLWEDFSLCRGORE 406
 QY 421 WYQKIHESQFTIIVVCSKGMKYFVDKNTKHKGGGSGKGEFLVAVSAIAELKRAQK 480
 DB 407 WYQKIHESQFTIIVVCSKGMKYFVDKNTKHKGGGSGKGEFLVAVSAIAELKRAQK 466
 QY 481 SSSAALSXFIIVYDSCGDVPGILDSTKYRLMDNLPOLCSHLHSDHGLQPKQHR 540
 DB 467 SSSAALSXFIIVYDSCGDVPGILDSTKYRLMDNLPOLCSHLHSDHGLQPKQHR 526
 QY 541 QGSRNRYFRSKSGSLVATCNMHQFIDEPDWEKQFVFPFPPPLRYREPVLKFDGSL 600

DB 527 QGSRNRYFRSKSGSLVATCNMHQFIDEPDWEKQFVFPFPPPLRYREPVLKFDGSL 586
 QY 601 VLNDVCKPESDFCLKVEAVLGTATGPADQSHESQGGGLDGDGARGALDGSAAQPL 660
 DB 587 VLNDVCKPESDFCLKVEAVLGTATGPADQSHESQGGGLDGDGARGALDGSAAQPL 646
 QY 661 LHTVAGSPSPDPRSGIYDSSVPSSELSPLMEGLSTDTSTSSITSSVSSSGIGREE 720
 DB 647 LHTVAGSPSPDPRSGIYDSSVPSSELSPLMEGLSTDTSTSSITSSVSSSGIGREE 706
 QY 721 PPALPSKLLSGGCKADLCGRSTYTDLHAVAP 752
 DB 707 PPALPSKLLSGGCKADLCGRSTYTDLHAVAP 738

RESULT 11

AA009957
 ID AA009957 standard; Protein; 738 AA.

XX AC AA009957;

XX DT 14-FEB-2002 (first entry)

XX DE Human Interleukin 17 (hIL-17) receptor like protein substitution #7.

XX KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KW vascular; cytostatic; anti-leukemic; anti-infectivity; ophthalmological;
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 KW mutein.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 XX FT Misc-difference 602 /label= Cys, Ala, Ser

XX PN WO200168859-A2.

XX PD 20-SEP-2001.

XX PF 15-MAR-2001; 2001WO-0508678.

XX PR 16-MAR-2000; 2000US-189816P.

XX PR 28-NOV-2000; 2000US-0724460.

XX PA (AMGE-) AMGEN INC.

XX PI Jing S;

XX DR WPI; 2001-611392/70.

XX PT Nucleic acids encoding interleukin 17 receptor like polypeptides,
 XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
 XX diabetes, psoriasis and glaucoma.

XX PS Claim 24; Page -; 159pp; English.

XX CC The invention describes novel nucleic acids encoding interleukin (IL) 17
 CC receptor like polypeptides useful as vaccines and in gene therapy. These
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infectivity and
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and
 CC proteins may be used to prevent and treat diseases associated with
 CC inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These
 CC include, for example immune disorders (e.g. inflammation, diabetes and

xx The sequence is PRO20026 which is the human Interleukin 17 receptor, IL-17RH4, encoded by DNA 154095-2998. A composition containing ant/agonists to the PRO polypeptides or individual components are useful for treating a mammal with an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, an juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease, an autoimmune or immune-mediated skin disease, contact dermatitis, an allergic disease e.g. food hypersensitivity, asthma, a transplantation associated disease, or a chronic inflammatory demyelinating polyneuropathy. Treating a PRO1031 or degenerative cartilaginous disorder comprising administering a PRO1031 or PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous examples of the diseases and disorders are given in the specification.

xx Sequence 728 AA;

Query Match 92.3%; Score 3703; DB:22; Length 728;
 Best Local Similarity 96.7%; Pred. No. 0;
 Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

QY 42 RMAAARPRCLYANE-CYGPASRNSGLYNITFKDNCITYLNPVGHVIAQAQNTISQY 100
 Db 3 RASAGVPALFVSGGOGVGPASRNSGLYNITFKDNCITYLNPVGHVIAQAQNTISQY 62

QY 101 ACHDOVAVITLSPGALGIEFLKGFVILEELKSEGRQCOQLILADPKQLNSFKRGTME 160
 Db 63 ACHDOVAVITLSPGALGIEFLKGFVILEELKSEGRQCOQLILADPKQLNSFKRGTME 122

QY 161 SQPLNKKETDIFVKKVPPFSIKNESNYHFFETFEACDILLODNLACPKFKPNLN 220
 Db 123 SQPLNKKETDIFVKKVPPFSIKNESNYHFFETFEACDILLODNLACPKFKPNLN 182

QY 221 ISO-----HGSOMOVSDHAPHNFGFRFFYLHYKLKHEGPFKRKTCQSGYT 267
 Db 183 ISOHGSOMOVSDHAPHNFGFRFFYLHYKLKHEGPFKRKTCQSGYT 242

QY 268 ETSCLLQNVSPDIIELVDVDTNTRKVMHYALKPVHSPWAGPTRAIVATVPLVLSAF 327
 Db 243 ETSCLLQNVSPDIIELVDVDTNTRKVMHYALKPVHSPWAGPTRAIVATVPLVLSAF 302

QY 328 ATLFTVCKRKQENIYSHLDESESESTTAALPRERLRPRKPVFLCYSSKDGQGNHNV 387
 Db 303 ATLFTVCKRKQENIYSHLDESESESTTAALPRERLRPRKPVFLCYSSKDGQGNHNV 362

QY 388 VOCFAIFLQDFCGCEVALDLMEDFSLCREGQREWVQIKIHESQFIIVVCSKGMKFFYDKK 447
 Db 363 VOCFAIFLQDFCGCEVALDLMEDFSLCREGQREWVQIKIHESQFIIVVCSKGMKFFYDKK 422

QY 448 NYKHGGSGSGEGLEFLVAVSAEKLQAKOSSAALSRIYVDFYCEGDPVGLD 507
 Db 423 NYKHGGSGSGEGLEFLVAVSAEKLQAKOSSAALSRIYVDFYCEGDPVGLD 482

QY 508 LSTKYRLMDNLPLCALSHLSRDHGLQEPGQHTQGRSRRNYFRSKGSRSLYVAICNMHQFI 567
 Db 483 LSTKYRLMDNLPLCALSHLSRDHGLQEPGQHTQGRSRRNYFRSKGSRSLYVAICNMHQFI 542

QY 568 DEEPDFWEKQFVFPFPPPLRREPVLKFKFSGVLNDVMCKGPGSDCLKVEAVLIGAT 627
 Db 543 DEEPDFWEKQFVFPFPPPLRREPVLKFKFSGVLNDVMCKGPGSDCLKVEAVLIGAT 602

QY 628 GPADSQSHQGLQDGEARPDALDGSAAQLPLHHTVKAQSPDMRPSGIYDVSVPSS 687
 Db 603 GPADSQSHQGLQDGEARPDALDGSAAQLPLHHTVKAQSPDMRPSGIYDVSVPSS 662

QY 688 LSLPLMEGLSTQDTETTSLSVESVSSGLGEERPPALPKLLSSGSCADLGCSTYDEL 747
 Db 663 LSLPLMEGLSTQDTETTSLSVESVSSGLGEERPPALPKLLSSGSCADLGCSTYDEL 722

QY 748 HAVAPL 753

Db 723 HAVAPL 728

|||||

RESULT 14

AAU10602

ID AAU10602 standard; Protein; 739 AA.

XX AC AAU10602;

DT 14-FEB-2002 (first entry)

XX Human Interleukin 17 (hIL-1) receptor-like protein version 2.

XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 hepatic; anabolic; anorectic; anti-alzheimer's; renal; parkinsonian;
 anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
 hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 bone disease; vascular disorder; eye disorder; cancer; human.

XX Homo sapiens.

OS WO200168859-A2.

XX 20-SEP-2001.

XX 15-MAR-2001; 2001WO-US08678.

XX 16-MAR-2000; 2000US-189816P.

XX 28-NOV-2000; 2000US-0724460.

XX (AMGE-) AMGEN INC.

XX Jing S;

XX WPI; 2001-611392/70.

XX N-PSDB; AAS16201.

XX Nucleic acids encoding interleukin 17 receptor like polypeptides useful for preventing, diagnosing and treating, e.g. leukaemia, asthma, diabetes, psoriasis and glaucoma.

Claim 2: Fig 1; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis, cancers (e.g. leukaemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also be used as diagnostic probes to detect and quantify the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17rlp may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-IL17rlp antibodies and antagonists may also be used to down regulate expression and activity. This is the amino acid sequence of human Interleukin 17 (IL-17) receptor like protein described in the method of

CC the invention.

CC Note: Residues 1-288 of this sequence correspond to residues 8-296 of the sequence shown in AAU10601 which is incomplete in the specification.

XX

SQ Sequence 739 AA;

Query Match 92.3%; Score 3703; DB 22; Length 739;
 Best Local Similarity 93.7%; Pred. No. 0;
 Matches 704; Conservative 5; Mismatches 22; Indels 20; Gaps 3;

QY 3 PWLQLCSVFFVTNACLSQSLAAGSGRARGADTCGRKMAAARPRLCVANEVGPAS 62
 Db 9 PGSOQC-----CLHDSMGLCVG-----RANWLSASCS---LVFPQGVGPAS 48

QY 63 RNSGLNITFKYDNCITFLAPVGRVIAQAQNTISQYACHQDVAVTILMSPGALGIEL 122
 Db 49 RNSGLNITFKYDNCITFLAPVGRVIAQAQNTISQYACHQDVAVTILMSPGALGIEL 108

QY 123 KGRVILEELKSEGRQCOQLILKDPKOLNSFKRTGMSQPFLLMKFETDYFKVVPFPPS 182
 Db 109 KGRVILEELKSEGRQCOQLILKDPKOLNSFKRTGMSQPFLLMKFETDYFKVVPFPPS 168

QY 183 IKNESNYHPPFFRACDILLOPDNLACKPFWKPRNLNISOHSDMOVSFDHAPHNFGFR 242
 Db 169 IKNESNYHPPFFRACDILLOPDNLACKPFWKPRNLNISOHSDMOVSFDHAPHNFGFR 228

QY 243 FYLHKYKLGHPFKRTCKQBOTTTSCILLQNVSPGDIYIELVDNTNTRKMYALK 302
 Db 229 FYLHKYKLGHPFKRTCKQBOTTTSCILLQNVSPGDIYIELVDNTNTRKMYALK 288

QY 303 PVESWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESSSESTYTAALP 362
 Db 289 PVESWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESSSESTYTAALP 348

QY 363 RERLRPRKPVLCYSSKQGNHNVQCFAYFLQDFCCFVALDOLWEDSLCEGQRENV 422
 Db 349 RERLRPRKPVLCYSSKQGNHNVQCFAYFLQDFCCFVALDOLWEDSLCEGQRENV 408

QY 423 IOKIHESQFIIVGSKMGYFDKKNYKKGGRSGKGLFLVAVSAIAEKLRAQKSS 482
 Db 409 IOKIHESQFIIVGSKMGYFDKKNYKKGGRSGKGLFLVAVSAIAEKLRAQKSS 468

QY 483 SAALSKFIATVDFSCGDPVGLDLSLTKYRLMDNLPOLCSHLHSRDBGLQEPQTRQG 542
 Db 469 SAALSKFIATVDFSCGDPVGLDLSLTKYRLMDNLPOLCSHLHSRDBGLQEPQTRQG 528

QY 543 SRRTFRKSGRSILYVAICNHQFIDEEPDPWEKOFVFPFPPPLRYREPVELEKFDGLVL 602
 Db 529 SRRTFRKSGRSILYVAICNHQFIDEEPDPWEKOFVFPFPPPLRYREPVELEKFDGLVL 588

QY 603 NDVMCKPGPESDFCLKYEAVALGATPADSQHESQHGGLQDQGEARPALDGSAAALQPLH 662
 Db 589 NDVMCKPGPESDFCLKYEAVALGATPADSQHESQHGGLQDQGEARPALDGSAAALQPLH 648

QY 663 TVKAGSPDMRDSGIYDSSVPSSLSPLMEGLSTQDTETSSLTESVSSSSGLBEEPP 722
 Db 649 TVKAGSPDMRDSGIYDSSVPSSLSPLMEGLSTQDTETSSLTESVSSSSGLBEEPP 708

QY 723 ALPSKLLSGSGCKADLCGRSYTDELHVAAPL 753
 Db 709 ALPSKLLSGSGCKADLCGRSYTDELHVAAPL 739

RESULT 15

ABB07630

ID ABB07630 standard; Protein; 739 AA.

XX

AC ABB07630;

XX

DT 20-MAY-2002 (first entry)

XX

DE Murine cytokine receptor, Zcytor18.

XX

KW

Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;
 pulmonary alveolar proteinosis; familial periodic fever; antitumour;
 erythroleukemia; chromosome 3p14.3; gene therapy; mouse.

XX

OS Mus sp.

XX WO200208259-A2.

PN 31-JAN-2002.

XX

XX 23-JUL-2001; 2001WO-US23253.

PF 26-JUL-2000; 2000US-220747P.

PR (2TMO) ZYMOGENETICS INC.

XX Presnell SR, Kuestner RE, Gao Z;

XX WPI; 2002-217048/27.

DR N-PSDB; ABA95037, ABA95038.

XX

XX New cytokine receptor polypeptide designated zcytor18, useful for

PT inhibiting cell proliferation associated with psoriasis or tumor

PT growth, and modulating immune system by binding to endogenous zcytor18

PT ligand

XX

XX Claim 1; Page 111-115; 119pp; English.

XX

XX The invention relates to an isolated cytokine receptor polypeptide

CC designated Zcytor18. The Zcytor18 polypeptides can be expressed by

CC standard recombinant methodology. The polypeptides can be used to inhibit

CC cell proliferation associated with psoriasis or tumor growth. The

CC encoding nucleic acids are useful for providing Zcytor18 in vivo by gene

CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in

CC vivo diagnosis, and the Zcytor18 probes and primers can be used to detect

CC and localize Zcytor18 gene expression in tissue samples. The probes are

CC also useful for detecting gross aberrations in chromosome 3 in which

CC Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in

CC linkage-based testing of pulmonary alveolar proteinosis, familial

CC periodic fever and erythroleukemia, and erythroleukemia associated with

CC polymorphisms of cytokine receptors. The present sequence represents a

CC murine Zcytor18 amino acid sequence.

CC

XX Sequence 739 AA;

SQ

Query Match 84.4%; Score 3387; DB 23; Length 739;
 Best Local Similarity 85.2%; Pred. No. 0;
 Matches 645; Conservative 37; Mismatches 53; Indels 22; Gaps 6;

QY 1 MAPWLQCSVFFVTNACLSQSLAAGSGRARGADTCGRKMAAARPRLCVANEVGP 60
 Db 1 MAPWLQCSVFFVTNACLSQSLAAGSGRARGADTCGRKMAAARPRLCVANEVGP 46

QY 61: ASRNSGLNITFKYDNCITFLAPVGRVIAQAQNTISQYACHQDVAVTILMSPGALGI 119
 Db 47 ASRNSGLNITFKYDNCITFLAPVGRVIAQAQNTISQYACHQDVAVTILMSPGALGI 106

QY 120 EFLAGFRVILEELKSEGRQCOQLILKDPKOLNSFKRTGMSQPFLLMKFETDYFKVVP 179
 Db 107 EFLAGFRVILEELKSEGRQCOQLILKDPKOLNSFKRTGMSQPFLLMKFETDYFKVVP 166

QY 180 FPSIKNESNYHPPFFRACDILLOPDNLACKPFWKPRNLNISOHSDMOVSFDHAPHN 239
 Db 167 FPSIKNESNYHPPFFRACDILLOPDNLACKPFWKPRNLNISOHSDMOVSFDHAPHN 226

QY 240 GFRFFLYLHKYKLGHPFKRTCKQBOTTTSCILLQNVSPGDIYIELVDNTNTRKMYALK 299
 Db 227 GFRFFLYLHKYKLGHPFKRTCKQBOTTTSCILLQNVSPGDIYIELVDNTNTRKMYALK 286

QY 300 ALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESSSESTYTA 359
 Db 287 VKSVQSFVWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESSSESTYTA 346

```

QY 360 ALPRERLRPRKVFYLCYSSKQDNHNNVQCFAYFLQDFCGCEVALDLWEDFSLCRBQOR 419
Db 360 ALPRERLRPRKVFYLCYSSKQDNHNNVQCFAYFLQDFCGCEVALDLWEDFSLCRBQOR 419
QY 347 ALPRERLRPRKVFYLCYSSKQDNHNNVQCFAYFLQDFCGCEVALDLWEDFSLCRBQOR 406
Db 347 ALPRERLRPRKVFYLCYSSKQDNHNNVQCFAYFLQDFCGCEVALDLWEDFSLCRBQOR 406
QY 420 EWLQKIHESOFIIVVCSKGMKIFVDRKKNFRHKGSGRGEAQGEFFLVAVAAIAEKLRQAK 479
Db 420 EWLQKIHESOFIIVVCSKGMKIFVDRKKNFRHKGSGRGEAQGEFFLVAVAAIAEKLRQAK 479
QY 407 EWLQKIHESOFIIVVCSKGMKIFVDRKKNFRHKGSGRGEAQGEFFLVAVAAIAEKLRQAK 466
Db 407 EWLQKIHESOFIIVVCSKGMKIFVDRKKNFRHKGSGRGEAQGEFFLVAVAAIAEKLRQAK 466
QY 480 QSSSAALSKFIAYIDYSCGDVPGILDSTKYRLADNLFQCSHLHSDRGLQEP-QQH 538
Db 480 QSSSAALSKFIAYIDYSCGDVPGILDSTKYRLADNLFQCSHLHSDRGLQEP-QQH 538
QY 467 QSSSAALSKFIAYIDYSCGDVPGILDSTKYRLADNLFQCSHLHSDRGLQEP-QQH 523
Db 467 QSSSAALSKFIAYIDYSCGDVPGILDSTKYRLADNLFQCSHLHSDRGLQEP-QQH 523
QY 539 TROGSRNTFRSKGSLVVAICNNHOFIDEEPDMFEKQIPFQHPVPVRYQEPVLEKFD 598
Db 539 TROGSRNTFRSKGSLVVAICNNHOFIDEEPDMFEKQIPFQHPVPVRYQEPVLEKFD 598
QY 524 PGSSSRNTFRSKGSLVVAICNNHOFIDEEPDMFEKQIPFQHPVPVRYQEPVLEKFD 583
Db 524 PGSSSRNTFRSKGSLVVAICNNHOFIDEEPDMFEKQIPFQHPVPVRYQEPVLEKFD 583
QY 599 GLVNDVMCKPGPESDFCLKVEAAVIGATGPADSQH--ESOHGGLDQGEARPALDGSAA 656
Db 599 GLVNDVMCKPGPESDFCLKVEAAVIGATGPADSQH--ESOHGGLDQGEARPALDGSAA 656
QY 584 GLVNDVSKPGPESDFCLKVEAAVIGATGPADSQH--ESOHGGLDQGEARPALDGSAA 643
Db 584 GLVNDVSKPGPESDFCLKVEAAVIGATGPADSQH--ESOHGGLDQGEARPALDGSAA 643
QY 657 LQPLHTVAVAGSPDMPDSDGIYDSSVPSSELSLPLMEGLSTQETSLTESVSSSGL 716
Db 657 LQPLHTVAVAGSPDMPDSDGIYDSSVPSSELSLPLMEGLSTQETSLTESVSSSGL 716
QY 644 LQPLHTVAVAGSPDMPDSDGIYDSSVPSSELSLPLMEGLSTQETSLTESVSSSGL 703
Db 644 LQPLHTVAVAGSPDMPDSDGIYDSSVPSSELSLPLMEGLSTQETSLTESVSSSGL 703
QY 717 GEEPPALPSKLLSSGCKADLQCRSYTDELHVAFL 753
Db 717 GEEPPALPSKLLSSGCKADLQCRSYTDELHVAFL 753
QY 704 GEEDPTLPKLFASGVSR-EHGCHSHTDELQALAPL 739
Db 704 GEEDPTLPKLFASGVSR-EHGCHSHTDELQALAPL 739

```

Search completed: May 19, 2003, 09:20:05
Job time : 59.6401 secs

GenCore version 5.1.4.p5.4578
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CM protein - protein search, using sw model

Run on: May 19, 2003, 09:14:29 ; Search time 32.7919 Seconds
(without alignments)
2626.495 Million cell updates/sec

Title: US-09-912-157-2_COPY_336_753

Perfect score: 2210
Sequence: 1 RKQOENIYSHLDESSES.....CFADLCGRSYTDELHVAAPL 418

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp.archaea:*
- 2: sp.bacteria:*
- 3: sp.fungi:*
- 4: sp.human:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mhc:*
- 8: sp.organelle:*
- 9: sp.phage:*
- 10: sp.plant:*
- 11: sp.rodent:*
- 12: sp.virus:*
- 13: sp.invertebrate:*
- 14: sp.unclassified:*
- 15: sp.rvirus:*
- 16: sp.bacteriap:*
- 17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2210	100.0	564	Q9UFA0	Q9UFA0 homo sapien
2	1817.5	82.2	582	Q8R5J8	Q8R5J8 mus musculus
3	1065.5	48.2	745	Q8QJ39	Q8QJ39 brachydanio
4	1065.5	48.2	745	Q8QJ36	Q8QJ36 brachydanio
5	150.5	6.8	846	Q9NA64	Q9NA64 caenorhabdi
6	111.5	5.0	348	Q9HA60	Q9HA60 homo sapien
7	111.5	5.0	370	Q96KN9	Q96KN9 homo sapien
8	110	5.0	428	Q9NTU6	Q9NTU6 homo sapien
9	108	4.9	1058	Q9AY10	Q9AY10 oryza sativ
10	107.5	4.9	3942	Q88737	Q88737 mus musculus
11	107	4.8	1322	Q9QZP6	Q9QZP6 mus musculus
12	105	4.8	757	Q13399	Q13399 ustilago ma
13	105	4.8	901	Q24573	Q24573 drosophila
14	105	4.8	1571	Q54978	Q54978 mus musculus
15	104.5	4.7	707	Q96SK7	Q96SK7 homo sapien
16	102.5	4.6	593	Q99PV2	Q99PV2 rattus norv

17	102.5	4.6	1545	5	Q9BHW7	Q9BHW7 leishmania
18	102.5	4.6	2031	5	Q9N9I8	Q9N9I8 leishmania
19	102	4.6	4169	4	Q8TCU4	Q8TCU4 homo sapien
20	101.5	4.6	341	6	Q9NOB3	Q9NOB3 macaca fasc
21	101	4.6	539	5	Q9V490	Q9V490 drosophila
22	100.5	4.5	372	2	Q9RNP2	Q9RNP2 zymononas m
23	100.5	4.5	901	16	Q9KE04	Q9KE04 bacillus ha
24	100.5	4.5	1406	4	Q9Y2I6	Q9Y2I6 homo sapien
25	99.5	4.5	1024	10	Q93YP4	Q93YP4 arabidopsis
26	98.5	4.5	804	4	Q9UP86	Q9UP86 homo sapien
27	98	4.4	1023	10	Q9LX42	Q9LX42 arabidopsis
28	97.5	4.4	279	10	Q9ZWI4	Q9ZWI4 sea mayas m
29	97.5	4.4	291	10	Q9LFX0	Q9LFX0 arabidopsis
30	97.5	4.4	589	10	Q9LPG3	Q9LPG3 arabidopsis
31	97.5	4.4	2221	5	Q9NKV1	Q9NKV1 halocynthia
32	97	4.4	245	4	Q14596	Q14596 homo sapien
33	96.5	4.4	438	4	Q13109	Q13109 homo sapien
34	96.5	4.4	981	15	Q92809	Q92809 abelson mur
35	96	4.3	584	4	Q9H4J6	Q9H4J6 homo sapien
36	96	4.3	873	5	Q9W1M0	Q9W1M0 drosophila
37	96	4.3	920	11	Q91VL3	Q91VL3 mus musculu
38	96	4.3	934	13	Q9DER4	Q9DER4 gallus gall
39	96	4.3	1012	4	Q9BWV4	Q9BWV4 homo sapien
40	96	4.3	1060	10	Q9LFP2	Q9LFP2 arabidopsis
41	95.5	4.3	347	11	Q9R0B7	Q9R0B7 mus musculu
42	95.5	4.3	365	4	Q9H1L9	Q9H1L9 homo sapien
43	95.5	4.3	419	4	Q9H1L8	Q9H1L8 homo sapien
44	95.5	4.3	494	4	Q96HR8	Q96HR8 homo sapien
45	95.5	4.3	553	4	Q13517	Q13517 homo sapien

ALIGNMENTS

RESULT 1
Q9UFA0
ID Q9UFA0 PRELIMINARY; PRT: 564 AA.
AC Q9UFA0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE Hypothetical 63.1 kDa protein (fragment).
GN DKFZP434N1928.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC MISCUT-TESTIS;
RA Bloembergen H., Boecher M., Brandt P., Mewes H.W., Gassenhuber J.,
RA Wiemann S., et al. 1996. The EMBL/GenBank/DBJ databases.
RL Sequence alignment with the EMBL/GenBank/DBJ databases.
DR EMBL, AL133097, CAB61708.1,
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 564 AA; 63134 MW; 6B3AA5BD4523E88C CRC64;

Query Match 100.0%; Score 2210; DB 4; Length 564;
Best Local Similarity 100.0%; Pred. No. 1.3e-181;
Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	RKQOENIYSHLDESSESSTYTAALPRRLPRKVFELCYSSKDGQNHNNVQCFAFL	60
Db	147	RKQOENIYSHLDESSESSTYTAALPRRLPRKVFELCYSSKDGQNHNNVQCFAFL	206
QY	61	QDFCCEVALDLWDFSLCBEGREWVIOKIHESOFILVCSKGRKVFYDKNKYHKGKG	120
Db	207	QDFCCEVALDLWDFSLCBEGREWVIOKIHESOFILVCSKGRKVFYDKNKYHKGKG	266
QY	121	RGSGKGEFLVAVSAIAEKLRQAKQSSAALSFKTAVTFDYSCBQDVPGLDLSKTYRLM	180
Db	267	RGSGKGEFLVAVSAIAEKLRQAKQSSAALSFKTAVTFDYSCBQDVPGLDLSKTYRLM	326

QY 181 DNLPCSHLSRDRGLQEPGQTRGSRNRYFRSKSGSLYVAICNMHOFIDEEPWF 240
 DB 327 DNLPCSHLSRDRGLQEPGQTRGSRNRYFRSKSGSLYVAICNMHOFIDEEPWF 386
 QY 241 KQVFPHPPPLRYREPVLKFDGSLVNDVCKPESDCLKVAAYLGATGAPDSQHE 300
 DB 387 KQVFPHPPPLRYREPVLKFDGSLVNDVCKPESDCLKVAAYLGATGAPDSQHE 446
 QY 301 SQRGGLDGGEARPALDGSAAQLPILHTVYKAGSPDPRDSGIYDSSVPSSELSPLMBG 360
 DB 447 SQRGGLDGGEARPALDGSAAQLPILHTVYKAGSPDPRDSGIYDSSVPSSELSPLMBG 506
 QY 361 LSTDTQTSLSLTSVSSSSGLGEEPPALPSKLLSSGSCADLCGRSYDDELHVAAPL 418
 DB 507 LSTDTQTSLSLTSVSSSSGLGEEPPALPSKLLSSGSCADLCGRSYDDELHVAAPL 564
 RESULT 2
 Q8R5J8
 ID Q8R5J8 PRELIMINARY: PRT: 582 AA.
 AC Q8R5J8
 DT 01-JUN-2002 (TREMELrel. 21, Created)
 DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
 DE 01-JUN-2002 (TREMELrel. 21, Last annotation update)
 DE Similar expression to FGF protein (Fragment).
 GN SEP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21824237; PubMed-11802165;
 RA Furthauer M., Lin W., Ang S.L., Thisse B., Thisse C.;
 RT "Sef is a feedback-induced antagonist of Ras/MAPK-mediated FGF
 RT signalling";
 RL Nat. Cell Biol. 4:170-174(2002).
 DR EMBL; AF244804; AAL79530.1; -;
 FT NON-TER
 SQ SEQUENCE 582 AA; 65263 MW; 56663B2981C4268E CRC64;

Query Match 82.2%; Score 1817.5; DB 11; Length 582;
 Best Local Similarity 83.4%; Pred. No. 8e-148;
 Matches 351; Conservative 25; Mismatches 38; Indels 7; Gaps 4;
 QY 1 RKQOENITSHLDESSSTYTAALPRERLRPRPKVFLCYSSKQGNHNVVQCFAYFL 60
 DB 166 RKQOENITSHLDESSSTYTAALPRERLRPRPKVFLCYSSKQGNHNVVQCFAYFL 225
 QY 61 QDFCGCEVALDWEFSLCREGOREWVQIKHESQFIIVVCSKGMKIFVYDKNKHKG 120
 DB 226 QDFCGCEVALDWEFSLCREGOREWVQIKHESQFIIVVCSKGMKIFVYDKNKHKG 285
 QY 121 RSGSGELFLVAVSAIAELKRAKSSAALSKFTAVTDYSCGDVPGILDLSTYK 180
 DB 286 RSGSGELFLVAVSAIAELKRAKSSAALSKFTAVTDYSCGDVPGILDLSTYK 345
 QY 181 DNLPCSHLSRDRGLQEPGQTRGSRNRYFRSKSGSLYVAICNMHOFIDEEPWF 239
 DB 346 DELPELCAHLHS---GEQVYLGQHPCHSSRRNRYFRSKSGSLYVAICNMHOFIDEEPWF 402
 QY 240 EKQVFPHPPPLRYREPVLKFDGSLVNDVCKPESDCLKVAAYLGATGAPDSQ 299
 DB 403 EKQVFPHPPPLRYREPVLKFDGSLVNDVCKPESDCLKVAAYLGATGAPDSQ 462
 QY 300 --ESQHGGLDGGEARPALDGSAAQLPILHTVYKAGSPDPRDSGIYDSSVPSSELSPL 357
 DB 463 TLESQVGLDQDTEAOPSCDAPALQPLHVAVKAGSPSEMPRDSGIYDSSVPSSELSPL 522
 QY 358 MEGLSTQDTFTSLSVSSSSGLGEEPPALPSKLLSSGSCADLCGRSYDDELHVAAP 417
 DB 523 MEGLSPQDTFTSLSVSSSSGLGEEPPALPSKLLSSGSCADLCGRSYDDELHVAAP 581

QY 418 L 418
 DB 582 L 582
 RESULT 3
 Q8QHJ9
 ID Q8QHJ9 PRELIMINARY: PRT: 745 AA.
 AC Q8QHJ9
 DT 01-JUN-2002 (TREMELrel. 21, Created)
 DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
 DE Sef.
 GN SEP.
 OS Brachydanio rerio (Zebrafish) (Zebra dario).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21824236; PubMed-11802164;
 RA Teagui M., Friesel R., Kudoh T., David I.;
 RT "Identification of Sef, a novel modulator of FGF signalling";
 RL Nat. Cell Biol. 4:165-169(2002).
 DR EMBL; AF364103; AAL76112.1; -;
 SQ SEQUENCE 745 AA; 83431 MW; 56FE1F0B9D98DB4 CRC64;
 Query Match 48.2%; Score 1085.5; DB 13; Length 745;
 Best Local Similarity 52.6%; Pred. No. 5.6e-83;
 Matches 222; Conservative 63; Mismatches 104; Indels 33; Gaps 7;
 QY 1 RKQOENITSHLDESSSTYTAALPRERLRPRPKVFLCYSSKQGNHNVVQCFAYFL 60
 DB 321 RKQOENITSHLDESSSTYTAALPRERLRPRPKVFLCYSSKQGNHNVVQCFAYFL 380
 QY 61 QDFCGCEVALDWEFSLCREGOREWVQIKHESQFIIVVCSKGMKIFVYDKNKHKG 120
 DB 381 QDFCGCEVALDWEFSLCREGOREWVQIKHESQFIIVVCSKGMKIFVYDKNKHKG 440
 QY 121 R-----GSGGELFLVAVSAIAELKRAKSSAALSKFTAVTDYSCGDVPG 169
 DB 441 KENREPSASDSSSSRDLFIVASALISEKLKVEHQSS-DLSRFSVYFDYSHETDPT 499
 QY 170 ILDLSTYKRLDNLPCSHLSRDRGLQEPGQTRGSRNRYFRSKSGSLYVAICNMH 229
 DB 500 SLSLAPKFLMDQLPOLFARLHSQLSLTDREPPPNVSKRNIFCYSKSGSLYVAIY 559
 QY 230 QFIDEEPWFQKQVFPFHPPLRYREPVLKFDGSLVNDVCKPESDCLKVAAYL 289
 DB 560 QHVTQEPDWLEKELM---PPPLPNKRTIPEKVDGLVNEVLEKLGSESE-CPVRSNVL 615
 QY 290 -----GATGPADSHESQHGGLDGGEARPALDGSAAQLPILHTVYKAGSPDPRDSG 342
 DB 616 ILPQTQVGVSVLSLSDRGSSSQD-----AGSCRPLVHTDGSASPPPRDSG 666
 QY 343 IYDSSVPSSELSPLMDGLSDTFTSLSVSSSSGLGEEPPALPSKLLSSGSC-CKA-401
 DB 667 IYDSSVPSSELSPLMDGLSDTFTSLSVSSSSGLGEEPPALPSKLLSSGSC-CKA-401
 QY 402 DL 403
 DB 727 DL 728
 RESULT 4
 Q8QHJ6
 ID Q8QHJ6 PRELIMINARY: PRT: 745 AA.
 AC Q8QHJ6
 DT 01-JUN-2002 (TREMELrel. 21, Created)
 DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)

DE FGF signalling antagonist Sef.
 GN Sef.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21824337; PubMed=11802165;
 RA Furrthauer M., Lin W., Siew-Lan A., Thisse B., Thisse C.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF401232; AAL78817.1;
 SQ SEQUENCE 745 AA; 83437 MW; 75BB9EDCC08A4652 CRC64;
 Query Match 48.2%; Score 1065.5; DB 13; Length 745;
 Best Local Similarity 52.6%; Pred. No. 5.6e-83;
 Matches 222; Conservative 63; Mismatches 104; Indels 33; Gaps 7;
 QY 1 RKQOENIYSHLDESSSTYTAALPRELRPRPKVFLCYSSKDGQHNHNVQCFAIFL 60
 DB 321 RKQOENIYSHLDESSSTYTAALPRELRPRPKVFLCYSSKDGQHNHNVQCFAIFL 60
 QY 61 QDFCGCEVALDLWEDFSLCRGQREWVIOKHESQFIIVVCSKGMKYPVCKNKYKGGG 120
 DB 381 QDFCGCEVALDLWEDFSLCRGQREWVIOKHESQFIIVVCSKGMKYPVCKNKYKGGG 120
 QY 121 R-----GSGKGEFLVAVSAIAEKLQAKQSSAALSKEFIATFYDSCGVDV 169
 DB 441 RKNRPSADSSSSSSDLFVASAIISEKLEKVKHQS--DLRFMSYFIDSHETDPT 499
 QY 170 ILDTKYRLMDNLPLGSLHSDHGLQEPGQHTQGSRRNYFRSKGRSLYVAIGNH 229
 DB 500 SLSLAPKFLMDQLPLQFARLHRSQSLTDREPQPNVSKRNYFRSKGRSLYVAIGNH 559
 QY 230 QFTDEPDMFERQFVPPPPPLRYREPVEKEDSGLVNDVCKPGPESDCLKVEAVL 289
 DB 560 QHTQEPDWLEKELM---PPPLPNKRTYPEKVDGSLVNLKVGKGESE--CPPVRSNVL 615
 QY 290 -----GATGPDQSQESQHGGLDQGEARPALDGSAAALQPLHTYKAGSPDMPD 342
 DB 616 ILPQTQVGVSLSLSDREDLGGSSQD-----AGSCRPLVLTGDSASPPMPD 656
 QY 343 IYDSSVPSSELSPLMGLSLDQETSSILTESVSSSGSGEGEPPALPSKLLSSG--CKA 401
 DB 667 IYDSSVPSSELSPLMGLSLDQETSSILTESVSSSGSGEGEPPALPSKLLSSG--CKA 401
 QY 402 DL 403
 DB 727 DL 728
 RESULT 5
 Q9NA64 PRELIMINARY; PRT; 846 AA.
 AC Q9NA64;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Y64GI0A.6 protein.
 GN Y64GI0A.6
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6339;
 RN [1]
 RP SEQUENCE FROM N.A.
 Query Match 5.0%; Score 111.5; DB 4; Length 348;

RA Ainscough R.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology."
 RL Science 282:2012-2018(1998).
 DR EMBL; AL110498; CAB54470.1;
 SQ SEQUENCE 846 AA; 94852 MW; 613AEF55EBB89EA4 CRC64;
 Query Match 6.8%; Score 150.5; DB 5; Length 846;
 Best Local Similarity 22.5%; Pred. No. 0.00035;
 Matches 94; Conservative 57; Mismatches 147; Indels 119; Gaps 24;
 QY 2 KQOENIYSHLDESSSTYTAALPRELRPRPKVFLCYSSKDGQHNHNVQCFAIFL 61
 DB 448 KQASNI--HLLNENPAPS--HSGSIPL--ILKQISISLVIV--SHDSAQHAAVLAFAELR 502
 QY 62 DFCGCEVALDLWEDFSLCRGQREWVIOKHESQFIIVVCSKGMKYPVCKNKYKGGG 121
 DB 503 DFNKLVHLDVWEDDI--EENRAETINSSIVRANKVIIINSIG--AYF--RTVFRHQ 555
 QY 122 GSGKGEFLVAVSAIAEKLQAKQSSAALSKEFIATFYDSCGVDV--PGILDLSKY-- 177
 DB 556 -----EPAIERITGRND-----VIFDMQCELALQHPVCISCHESYTN 593
 QY 178 -----RLMD--NLPLGSLHSDHGLQEPGQHTQGSRRNYFRSKGRSLYVAIGN 227
 DB 594 PXYVFPINRLQYSIP---NSLMTNTALTQPARPEQLAGFNQVFA---LQAISR 646
 QY 228 MQFTDEPDMFER---QVPPHPPPLRYR-----EP 256
 DB 647 KUNYTESDPQFENTHVRVATRVSELAHNIVPL--PPSLEVRYVEDDAPGOMETLPIDE 705
 QY 257 VLEK-----DSGLVNDVCKPGPESDCLKVEAVLQATGPDQSQESQH 303
 DB 706 LKEKFAAKRDLEVEVLDSQEDVKLEDKVCAQGP-----IHVEPTEPVEPAEPEEAE 760
 QY 304 GGLDQGDGAREPALDGSAA---LQPLL--HTYKAGSPDMPDSDGIYDSS--VPSELS 354
 DB 761 ED--EEDDDVDSVGGQTARTEELQLIVH-----KDNHDSGLNLSATVSGSDFS 809
 RESULT 6
 Q9H460 PRELIMINARY; PRT; 348 AA.
 AC Q9H460;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE BA425A6.2 (Similar to connexin) (Fragment).
 GN BA425A6.2
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Heath P.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL121749; CAC10186.1;
 DR InterPro; IPR000500; Connexin.
 DR Pfam; PF00029; connexin; 1.
 DR PRINTS; PR00206; CONNEXIN.
 DR SMART; SM00037; CNX; 1.
 DR PROSITE; PS00407; CONNEXINS_1; 1.
 DR PROSITE; PS00408; CONNEXINS_2; 1.
 FT NON_TER 1
 SQ SEQUENCE 348 AA; 37805 MW; 07EB6478067F8995 CRC64;
 Query Match 5.0%; Score 111.5; DB 4; Length 348;

Best Local Similarity 28.9%; Pred. No. 0.24; Mismatches 25; Indels 25; Gaps 8;
Matches 43; Conservative 25; Mismatches 56; Indels 25; Gaps 8;

QY 265 LVLDVNC-----KPGPESDFCLKVEAVLGTGPDQSQHSQGGLDQGEARPAL 316
DB 189 LGLADLVCSLRRMRPPGPTSPSRKQS---GASGHAEGRTDEGGREEG--APAP 243
QY 317 DGSAAQLPLHTVAGSPDMRPSGIYDSSVP---SELSLPLMEGLSTDTQTSSLTE 373
DB 244 PGARA-----GGGAGSPRTSRVSG--HTKIPDESEVTSSASEKLGR-QPRGRPHRE 295
QY 374 SVSSSSGIG-EEPPALPSKLLSSGCKA 401
DB 296 MAQDPGRSGSEQPSAAPSRLAAPSCSS 324

RESULT 7

Q96KN9 PRELIMINARY; PRT; 370 AA.
AC Q96KN9
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Connexin40.1.
GN CX40.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Eiberger J., Soehl G., Willecke K.;
RT "Structural and functional diversity of connexin genes in the mouse
RT and human genome."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ141564; C93846.1;
DR InterPro; IPR000500; Connexin.
DR Pfam; PF00029; connexin_1.
DR PROSITE; PS00407; CONNEXINS_1; UNKNOWN_1.
DR PROSITE; PS00408; CONNEXINS_2; UNKNOWN_1.
SQ SEQUENCE 370 AA; 40140 MW; CD49F31743A7F7C2 CRC64;

Query Match 5.0%; Score 111.5; DB 4; Length 370;
Best Local Similarity 28.9%; Pred. No. 0.26;
Matches 43; Conservative 25; Mismatches 56; Indels 25; Gaps 8;

QY 265 LVLDVNC-----KPGPESDFCLKVEAVLGTGPDQSQHSQGGLDQGEARPAL 316
DB 211 LGLADLVCSLRRMRPPGPTSPSRKQS---GASGHAEGRTDEGGREEG--APAP 265
QY 317 DGSAAQLPLHTVAGSPDMRPSGIYDSSVP---SELSLPLMEGLSTDTQTSSLTE 373
DB 266 PGARA-----GGGAGSPRTSRVSG--HTKIPDESEVTSSASEKLGR-QPRGRPHRE 317
QY 374 SVSSSSGIG-EEPPALPSKLLSSGCKA 401
DB 318 MAQDPGRSGSEQPSAAPSRLAAPSCSS 346

RESULT 8

Q9NTU6 PRELIMINARY; PRT; 428 AA.
AC Q9NTU6
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical 45.4 kDa protein.
GN KFEZP434P11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

SEQUENCE FROM N.A.

RP TISSUE-TESTIS;
RC MEDLINE-21154917; PubMed-11230166;
RX Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glasel S.,
RA Anorgue W., Boecker M., Bloecher H., Bauersachs S., Blum H.,
RA Lauber J., Duestenroft A., Beyer A., Koehler K., Strack N.,
RA Meves H.W., Ottenwaelder B., Oberwiler B., Tampe J., Heubner D.,
RA Wandutt R., Korn B., Klein M., Poustka A.;
RT "Towards a Catalog of Human Genes and Proteins: Sequencing and
RT Analysis of 500 Novel Complete Protein Coding Human cDNAs";
RL Genome Res. 11:422-435(2001).
DR EMBL; AL117401; CAB55902.2;
KW Hypothetical protein.
SQ SEQUENCE 428 AA; 45443 MW; FA75BAC1A3FDB3EE CRC64;

Query Match 5.0%; Score 110; DB 4; Length 428;
Best Local Similarity 23.5%; Pred. No. 0.42;
Matches 70; Conservative 42; Mismatches 108; Indels 78; Gaps 17;

QY 139 KLRQKQSS-SAALSXFIAYFYDSCGDVPGI-----LDSTKYRLMDNLPQ 185
DB 103 RYNTQTSWTSSCTNRNAISSYSTGCLPKLRRRGPASSHCQLTSSSKTVSDRPO 162
QY 186 LCSHLSEDRHGLQE--PGQHTQSGSRNYFSGSRSLVAICNMHQFIDEQWFEKQF 243
DB 163 AVSGHFOCEKAADIAPGQTLT--LRNDSYSTSEASRP-----STHKF----PLLPRRRG 210
QY 244 VPFF-PPPL-----RYREPVLKFDGLVINDVM--CKPGPESDFCLKVEAA 287
DB 211 EPLMLPPLELGYRVTVEDLREKEAQRINSALQVEDKAISSDCRPSRSH--TLSSL 267
QY 288 VLGATG-PADSOESQHGGLQDGEARPDGSAALQPLLTFTKAGSPDMP-----RD 340
DB 268 ATGASGLPAVSKAPS-----ADAQETHSKDCLGLDPLASA--AGVSTAPMSGKKHRP 321
QY 341 SG-IYSSVSPSELSLPLMEGLSTDTQTSSLTESVSSSGGLGEEPPALPSKLLSSG 397
DB 322 PGLFSSSDP-----LPATSSDSQDSQAQVTSLI-----PAPFFAASNDAG 361

RESULT 9

Q9AYIO PRELIMINARY; PRT; 1058 AA.
AC Q9AYIO
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative gag-pol polyprotein.
GN OSJNBA0087H07.4.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]

SEQUENCE FROM N.A.

RP Wing R.A., Frisch D., Presting G., Wood T., Yu Y., Soderlund C.,
RA Kim H.-R., Rambo T., Henry D., Simmons J.;
RT "Rice Genomic Sequence."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC074283; AAK02020.2;
KW Polyprotein.

QY SEQUENCE 1058 AA; 115228 MW; 9E39B2C564FC6CE7 CRC64;

Query Match 4.9%; Score 108; DB 10; Length 1058;
Best Local Similarity 22.1%; Pred. No. 2.2;
Matches 85; Conservative 52; Mismatches 131; Indels 116; Gaps 21;

QY 116 HKGGSGSGKGEFLVAVSAIAEKL-----BOAKQSSAALSFEVAV-- 157
DB 204 NRGGSGRGSGKGEFLVAVSAIAEKL-----BOAKQSSAALSFEVAV-- 263
QY 158 --YFYDSCGDVPGIIL-LSTKYRLMDNLPQLCSHLSRDLGLOPQGHTRQGSRRNY-- 212

Db 264 NWYDSNADTHITGEMKSLVKDYHGS-----EQVHAGGTGHDANPARQNLRYNH 318
 QY 213 -----FRSKGRSLYVAICMHO-----FIDEPPWFKEQVFF--HP-PPLR 252
 Db 319 RLEFRSK--QCAFGLYSTLHGFCILDISTGRVYISROW-VDEQIYFFANLHPNAGAR 375
 QY 253 YREPVL-----EKDT-SGLVNDVCKPGP-----ESDFCLKVE 285
 Db 376 LRSEVLVLPDLPPPTQFOGSAIYNOPMIDDPNHTNOTAETDADRGAONSEPTGENN 435
 QY 286 AAVLGATGP-----ADSHESQGGGLQDGEARPALDGSAAQLPILHTVAKG-----332
 Db 436 ASNGETEPGGHDFKHGTESGGQHTGSHPEDAALASDAVA-----ESGNDGT 487
 QY 333 SPDMPPDSG-IYDSVPSSKSLPLMEGLSTDTQTTSSLTSSVSSSGL-----GEREPP 387
 Db 488 SPGAGPTAGHAESQESSLSAP-----HDSFASSTPGSDASSDGAESGEGQQP 540
 QY 388 AL-PSKLLSGGCKADLCRSTYD 410
 Db 541 MLGPATRSRGIHKP-----KKYTD 560

RESULT 10

ID O88737 PRELIMINARY; PRT; 3942 AA.
 AC O88737
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Bassoon.
 GN BSN OR BASSOON.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129 SVJ;
 RX MEDLINE=98345363; PubMed=9679147;
 RA Dieck S., Sammarti-Villa L., Languese K., Richter K., Kindler S.,
 RA Soyke A., Wex H., Smalla K.H., Kampf U., Franzer J.T., Stumm M.,
 RA Garner C.C., Gundelfinger E.D.;
 RT "Bassoon, a novel zinc-finger CAG/glutamine-repeat protein selectively
 RT localized at the active zone of presynaptic nerve terminals.";
 RL J. Cell Biol. 142:499-509(1998).
 DR EXBL; Y17034; CAA76598.1;
 DR EXBL; Y17035; CAA76598.1; JOINED.
 DR EXBL; Y17036; CAA76598.1; JOINED.
 DR EXBL; Y17037; CAA76598.1; JOINED.
 DR EXBL; Y17038; CAA76598.1; JOINED.
 DR MGD; MGI:1277955; Bsn.
 SQ SEQUENCE 3942 AA; 418739 MW; 150267E636C4DAB CRC64;

Query Match 4.94; Score 107.5; DB 11; Length 3942;
 Best Local Similarity 19.13; Pred. No. 15;
 Matches 58; Conservative 29; Mismatches 99; Indels 117; Gaps 11;
 QY 181 DNLPLCLSHLRDGLQEPQHTROGSRNIFRSKGRSLVVAIC-----NMGEFIDE 235
 Db 3535 DTCPQCS-----SHSMFDVQEHVDGPRAHAYKREGYMLDSDHCYVSDSEAHVHQEE 3589
 QY 236 PDWFEKQVFFHPPLRTRE-----PVLEKF-----DSGLVNDVCKPG 275
 Db 3590 TDFDK-----PRDARSDFRHHGHTVSSQKGRPARSHYDEPPEGLPHD---EGG 3643
 QY 276 PESDFCLKVEAVLGGATGAPDSQHSQHG-----GLDQD-----EAPR 314
 Db 3644 PGRH-----TSKAEHRHSDGRSGRPHAGEPRGAAPKPHARDMGREARPH 3691
 QY 315 -----ALDGSAAQLPILHTV 329

Db 3692 PQASPAPAKKQGGYGPSSADYSQSRAPSAHYHASEKKGSRQARTGPSALQPKADTQ 3751
 QY 330 KAGSPDNPRDSGIYDSSVPSSELSLPLMEGLSTDTQTTSSLTSSVSSSGSGEPEPPAL 389
 Db 3752 AQPMQGRQAAPGPGQSQPPSSRGT---PSCITASRQPTQCCOQOQOQOGLGQAPOQA 3808
 QY 390 PSK 392
 Db 3809 PSQ 3811

RESULT 11

QOQZP6 PRELIMINARY; PRT; 1322 AA.
 ID OQOZP6
 AC QOZHP6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Neuronal IL-16.
 GN IL16.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kurschner C., Yuzaki M.;
 RT "Neuronal interleukin-16 (NIL-16): a dual function PDZ domain
 RT protein.";
 RL ENBL; AF175292; AAD55393.1;
 DR J. Neurosci. 19:0-0(1999).
 DR HSP; Q14005; I116.
 DR MGD; MGI:1270855; IL16.
 DR InterPro; IPR001478; PDZ.
 DR Pfam; PF00595; PDZ; 4.
 DR SMART; SM00228; PDZ; 4.
 DR PROSITE; PS0106; PDZ; 4.
 SQ SEQUENCE 1322 AA; 141434 MW; DDB94003A5DCB738 CRC64;

Query Match 4.89; Score 107; DB 11; Length 1322;
 Best Local Similarity 22.58; Pred. No. 3.6;
 Matches 71; Conservative 29; Mismatches 117; Indels 98; Gaps 13;

QY 138 EKLQAKQSSAALSKFIANYFYDSGQVPGILDLSIKYRLMDNLPLCSHL-----190
 Db 282 QKFKQAK-----GLLTUTVTEL-TTPPSILCSHSLPCLRS 317
 QY 191 -----HSRDHGLQEPQHTROGSRNIFRSKGRSLVVAICNMHOFIDE 234
 Db 318 LSSSTCGAQDSSPFSLESFAS-PASTAKPNYRMVEVSLKKEAGVGLGICLSPYF---373
 QY 235 EPDWEKQVFFHPD-----PLVREPVLEKDSG---LVLNDVM---CKCP--276
 Db 374 --QCISGIFVHTLSPGVAHLDRGLRCGDEIVINDSPVHCLTNEVTLILSHCDGPVP 431
 QY 277 -----ESDFCLKVEAVLGGATGAPDSQHSQHG---GLDQDGEARPALDGSAA 322
 Db 432 IIVSRHPDPQVSEQOLKEAQAQAVEGVKFGKDRHQSLEGVKRLSSWHGRTLEKERE-490
 QY 323 QPLHTVTKAGSPDMPPDSGLTSSVPSSELS-----LPLMEGLSTDTQTTSSLTSSVSS 377
 Db 491 -----KHSAPPHRAKIMVRSSDSSVYNSGSPGSPCSAGAPQPSREGSTHPSL 543
 QY 378 SSGLGEPEPPALPSK 392
 Db 544 SPGEQEPGQVPSR 558

RESULT 12

O13399 PRELIMINARY; PRT; 757 AA.
 ID O13399
 AC O13399;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)


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RA Ishino F., Surani M.A.;
RT Peg3 imprinted gene on proximal chromosome 7 encodes for a zinc
RT finger protein.;
RL Nat. Genet. 12:186-190(1996).
RN [2]
RR
SEQUENCE FROM N.A.
RX PubMed=11331620;
RY
RT Hibi S.E., Lough M., Keverne E.B., Surani M.A., Loke Y.W., King A.;
RT "Paternal monoallelic expression of PEG3 in the human placenta.";
RL Run. Genet. 10:1093-1100(2001).
RN [1]
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF038939; AB369221; -
DR MGD; MG1:104748; Peg3.
DR InterPro; IPR000822; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 11.
DR PRINTS; PRO0048; ZINCINGER.
DR SMART; SM00355; Znf_C2H2; 11.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 11.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 12.
DR DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.
SQ SEQUENCE 1571 AA; 178923 MW; CF31243613942A8D CR664;

Query Match 4.88; Score 105; DB 11; Length 1571;
Best Local Similarity 19.28; Pred.No. 6.8;
Matches 73; Conservative 49; Mismatches 135; Indels 124; Gaps

QY 71 DLWEDFSLC---REGQREWVIOKHIESQPIIVGCSKGMKTFVDKKNYK---HKGGRSGSGK 125
DB 496 ELGEPFLTCPNPNFPRKMYRKDIYECK---VCGESFLHLSLREHQKHITRGNPNENK 551
QY 126 GELFLVAVASIAEKLRQAKOSSAALSKYFIAYVDYSCGDVPGILDLSLYRLMDNLQ 185
DB 552 -----SRNCEETFPVPSLSRRKQIYREKLDFNNARDA-----LGN----- 589
QY 186 LCHSLHSRDRGLQEPQHTRQGRNRYFSGSLVLAICNMHOFIDEPDMFEKQFVP 245
DB 590 -----SSSSEHQNRSRNRFPEGRG-----FEKPPVE 616
QY 246 FHPPLRYREPLYEKFDSGLVL-----NDVMCKP---GPESDFCLKVEAAVLGATGPA 297
DB 617 SQKSHYITRPENKDDDKPTTISVNPNDKLKLPFWNGSGKSC---ERSVIHSLGSAEA 673
QY 298 QHESQHGGLDQDGEARP-----ALDGSAAQLPLLTHTYKAGS 333
DB 674 Q---KSGGL---GFSKPRPVAESSTQSSSIYFPAUSGNGYEGKTDKSIHSLGAPR 728
QY 334 P-----SDMPDSDGITYDSSVPSESLPLMPGLSTQDTTSLTSVESSSSSGLG 382
DB 729 PLKRRANDHIQDGGESSIYIPDINKGRKIPAREDAYEGSSSSNTHYTPVNSRA----- 784
QY 383 EEEFPALPSSLKSSGCKADL 403
DB 785 --EPPSLSGE---SHDSKQDV 800

```

RESULT 15

	Q96SK7	PRELIMINARY;	PRT;	707 AA.
AD	Q96SK7;			
IC	01-DEC-2001	(TREMBLrel. 19, Created)		
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)		
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
DE	CDNA FLJ14796 fis, clone NTJRP4001235.			
DE	Homo sapiens (Human).			
OS	Homo sapiens			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
OX	[1]			
RN				
RP	SEQUENCE FROM N.A.			
RA	ISOq1.T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,			
RA	Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,			
RA	Tanai H., Kinata M., Watanabe M., Hirooka S., Ishii S., Kawai Y.,			
RA	Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K.,			

```

RA Masuho Y., Kanehori K.;
RT "NEBO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027702; BAB55308.1; -.
DR InterPro; IPR001878; znf.CCEC.
DR Pfam; PF00098; zf-CCEC; 1.
DR SEQUENCE 707 AA; 78475 MW; ED4E954EA2672F56 CRC64;
SQ
Query Match 4.7%; Score 104.5; DB 4; Length 707;
Best Local Similarity 19.6%; Pred. No. 2.5;
Matches 107; Conservative 61; Mismatches 180; Indels 197; Gaps
QY 7 NIYSHLDSESSSSTITAAFLPRELRPRP-----KYFLCTSSKDCQNMNMVQCF 573
DB 118 NLVRFPEQKNDVKTSF-----NLLPQPSVTLREOHKVEECSAKNNKEAFSVGSGVL 173
QY 58 YFLQDFCGEVALDWEFSLCRGORENWIOKHESQFIIVCSKGKFIYVDKNTK-- 115
DB 174 YF-TNFCLDKLGPIILNPNLSEG--WEIPKYHQ-VFSHIVSLGCEIQVAKRKP 228
QY 116 -----HGGGRSGKGELFIVAV----- 133
DB 229 CFNGSSEHOMKCPMPNNAARISEKRKBTNDACGEANNONFOORYHAEVEERGRFKP 288
QY 134 SATAEKLRAQKSSAALSKFI----- 155
DB 289 GVISEELQALGWTDKSLPPIYMRQLGYPGWLKEAENSLGALYDGKDGTDGETV 348
QY 156 -----AVTFYSCGSDVPGCILDST-----KYRLMDNLP-QLCSHL- 190
DB 349 GEIQNKSVTYLDLKLNVFG-FNISTPGIPDENRIFGSIPMQACQKQDFANLFSNF 407
QY 191 -----HSRDHGLQEPQHTQGGRRNYFRSKSGRSLTVACNMHQITDEPDWTEKQ 242
DB 408 QAPGVKSGNKRSSHSSPGSPKKQKNESAGSPADMELDSMEVPHGSGSEGFQFP 467
QY 243 FVPFHPPLRYREPLYEFKDFSGLVLDNMVCKPGPESDFCLKVEAAVLGATGPAOS-QHES 301
DB 468 LPDPTPLPRGTPP-----PVFTPLPKGTPLT-----PSDSPQTRT 505
QY 302 QHGGLDQDGEARNALDGS-----AALQPLEHVKAGSPDMRDSIGTYDSSVPSS--E 352
DB 506 ASGAVDEALTLEEEQORHAALE---QAESVNSDSQVPTDTLGTNSVASSPCPNE 562
QY 353 LSLPLMEGLSTQDTTSLSLTSVSSSGIGEEPPALPSKLLSGGSKADLCGRSTYDEL 412
DB 563 LDLEVPFEG-KTSEKOT-----LDPEVPEIFTRK-----KSEAG----- 594
QY 413 HAVAP 417
DB 595 HASSP 599

```

Search completed: May 19, 2003, 09:24:00
Job time : 38.7919 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2003, 09:16:08 ; Search time 27.7988 Seconds

(without alignments)

2604.041 Million cell updates/sec

Title: US-09-912-157-2

Perfect score: 4013

Sequence: 1 MAPWLQCSVFTVACLVG.....CQADLCGRSYTDELHVAVL 753

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: piri:*

2: piri:*

3: piri:*

4: piri:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3005	74.9	564	T42695	hypothetical prote
2	170.5	4.2	846	T27282	hypothetical prote
3	126.5	3.2	718	T30113	hypothetical prote
4	117	2.9	757	T09081	telomere-associate
5	117	2.9	917	T04661	hypothetical prote
6	117	2.9	2946	T00867	hypothetical prote
7	116.5	2.9	901	F83781	transposase (08) /
8	115.5	2.9	938	T49071	protein kinase - m
9	115	2.9	998	S37627	protein-tyrosine k
10	110	2.7	535	T17212	hypothetical prote
11	110	2.7	592	T49239	vesicle transport
12	108.5	2.7	3788	T13960	belge protein hemo
13	107.5	2.7	3942	T42730	Bassoon protein -
14	107	2.7	3788	T30851	lysosomal traffick
15	106.5	2.7	638	D86477	protein F1504.27 [
16	106	2.6	1448	A12007	Subtilase family p
17	105	2.6	901	JC5093	dead ringer nuclea
18	105	2.6	1571	T14155	zinc finger protei
19	104	2.6	1462	B36182	protein-tyrosine-p
20	103.5	2.6	663	A39897	GTPase-activating
21	103.5	2.6	930	A84668	Argonaute (AGO1)-1
22	102	2.5	813	A47485	ABR protein 2 - hu
23	102	2.5	859	A49307	ABR GTPase-activat
24	101.5	2.5	822	A47485	ABR protein 1 - hu
25	101.5	2.5	1639	T50119	probable sensory t
26	101	2.5	641	T05497	hypothetical prote
27	101	2.5	664	T51247	ARR2 protein [Impo
28	101	2.5	1275	A38985	nucleotide exchang
29	100.5	2.5	938	T05533	hypothetical prote

30	100.5	2.5	974	2	E59434	Rho GTPase activat
31	100.5	2.5	1007	2	T24643	hypothetical prote
32	99.5	2.5	657	2	E56949	serine/threonine p
33	99.5	2.5	794	2	E59069	Z13 protein - mous
34	99.5	2.5	981	1	FW06M	gag-ab1 polyprotel
35	99	2.5	341	2	H71716	190 kd antigen pre
36	99	2.5	783	2	A31491	sex-determining re
37	99	2.5	970	2	S63059	hypothetical prote
38	98.5	2.5	353	2	T33782	hypothetical prote
39	98.5	2.5	963	2	A23381	type I site-specif
40	98.5	2.5	993	2	I48653	mouse developmenta
41	98.5	2.5	1050	2	G96582	exodeoxyribonuclea
42	98.5	2.5	1050	2	H72041	exodeoxyribonuclea
43	98.5	2.5	1050	2	C81624	exodeoxyribonuclea
44	98	2.4	526	2	T16124	hypothetical prote
45	98	2.4	820	2	S33794	hypothetical prote

ALIGNMENTS

RESULT 1

T42695

hypothetical protein DKFZp434N1928.1 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000

C:Accession: T42695

R:Bioecker, H.; Boecker, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, November 1999

A:Reference number: Z22230

A:Accession: T42695

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-564 <AAA>

A:Cross-references: EMBL:AL133097

A:Experimental source: adult testis; clone DKFZp434N1928

C:Genetics:

A:Note: DKFZp434N1928.1

Query Match 74.9%; Score 3005; DB 2; Length 564;

Best Local Similarity 99.8%; Pred. No. 8.5e-234;

Matches 563; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	190	HPFFFRTRACDILLOPDNLACPKPPKPRNLNISQSGDMQVDFDHPHNFGRFFFLYLYK	249
DB	1	HPFFFRTRACDILLOPDNLACPKPPKPRNLNISQSGDMQVDFDHPHNFGRFFFLYLYK	60
QY	250	LKHGEPKRTCKQKQOTTETTSCLQNVSPGDYIIELVDDTNTTKVMYALKPVHSPNA	309
DB	61	LKHGEPKRTCKQKQOTTETTSCLQNVSPGDYIIELVDDTNTTKVMYALKPVHSPNA	120
QY	310	GPIRAVAITVPLVVISAFATLFTVMCRKQOENYSHLDESESESTYTAALPRRLRPR	369
DB	121	GPIRAVAITVPLVVISAFATLFTVMCRKQOENYSHLDESESESTYTAALPRRLRPR	180
QY	370	PKVFLCYSSKDGONHNVQCFAYFLQDFCCCEVALDWFSLCREGQREWIQIHES	429
DB	181	PKVFLCYSSKDGONHNVQCFAYFLQDFCCCEVALDWFSLCREGQREWIQIHES	240
QY	430	QFIIVGCKGMKYFVDKKNYKKGGRSGSGKGLFLVAVSAIAEKLRQAKQSSAALS	489
DB	241	QFIIVGCKGMKYFVDKKNYKKGGRSGSGKGLFLVAVSAIAEKLRQAKQSSAALS	300
QY	490	IAVTFDYSCGDVPGVGLDLSYKRLMDNLPOLCSHLSDRDLQEPQGTGQSRNRYR	549
DB	301	IAVTFDYSCGDVPGVGLDLSYKRLMDNLPOLCSHLSDRDLQEPQGTGQSRNRYR	360
QY	550	SKSGRSLYIAICNNHQFIDDEPDWFEKQFVFPHPPPRYRREPVLKFDGLVNDVWCKP	609
DB	361	SKSGRSLYIAICNNHQFIDDEPDWFEKQFVFPHPPPRYRREPVLKFDGLVNDVWCKP	420
QY	610	GPESDFCLKYEAAVLCATGPADQSHQSGGLDQDGEARALDQSAALQPLLHTVWAGSP	669

C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Feb-2001

C/Accession: T00867; G84891

R/Roundsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL data library, March 1998

A/Description: Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence.

A/Reference number: 214207

A/Accession: T00867

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-2946 <ND>

A/Cross-references: EMBL:AC003680; NID:92979540; PID:92979554

A/Experimental source: cultivar Columbia

M.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.

euas, D.; Mierman, W.C.; White, O.; Eisen, J.A.; Salsberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: G84891

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-2946 <STO>

A/Cross-references: GB:AE002093; NID:92979554; PIDN:AAC06163.1; GSPDB:GN00139

C/Genetics:

A/Map position: 2

A/Introns: 652/1; 913/3; 1165/3; 1210/3; 1245/3; 1283/3; 1309/2; 1336/3; 1438/3; 1638/2;

2449/2; 2481/3; 2643/1; 2890/3; 2931/3

Query Match 2.9%; Score 117; DB 2; Length 2946;

Best Local Similarity 18.7%; Pred. No. 4.3;

Matches 164; Conservative 105; Mismatches 314; Indels 234; Gaps 40;

QY 2 APWQLQSVFETTVNACLSQSLVAAGSGRARGADTCGRWKAARPRCLVANGVGA 61

DB 393 ATWIVIESFADTNAATAAATAA---AKSGKTSMSAANAAS---ALAGEG---441

QY 62 SRSGLNIFKDYNTTLYNPGKHVADIAQNTISQYACHDOVAVTILNPGALGIEF 121

DB 442 ---TAMPRLFSLSADNMGIEAFHA---QF 467

QY 122 LAGFRVILEELKSEGR---QC---QQLIKDPKQLNSSFRTG 158

DB 468 L---VYESGSGKRSLSHTFAKPCQVYFGLSECKGLGKAESLRLYDGL 522

QY 159 MESOPFLNMFETDYFKVVPSPISKNESNTHPFF---RTRACDIL 202

DB 523 YESRPF---DPRISK---PLSFCCIGTNPPTNAGLQRRRCQCLF 563

QY 203 LQ---PDNLACKPFWKPNLINSORGSDMVSFDHAPNFGFRFFYLHYLKLKHEGPFKRT 260

DB 564 AEMGPVIFKEIPGPMARLASRGDVLPCFGNCA---GLPWLATNDVVRN---612

QY 261 CROSTTETS---CLLQNVSPGDYIELVDVDTTTRK---VHXYA---300

DB 613 KAESSILADIGGTHLLYHECLLSGRFCD---ASLSGAAGTLRPRAEVLQGVHATR 669

QY 301 LKPVESPA---GPIRAVAIV---PLVVISAFATLFTVM---334

DB 670 MPVSTWALAYGPMASLLPLATVSSVHKDSLPCGLNPLSLSTVTLAAPVRIMSVAIQ 729

QY 335 ---CRKQOE---NIYSHLDEESSESTVTAALPRRLRPRKPVLCYSSKDGON 383

DB 730 HPGNEELCTQGPETILARILSYLLESLSLDKRDGVEEL---VAAIVSLCOSK---IN 786

QY 384 HNVVQCFATLQDFGCEVALDMEFSLCREGOREWVIOKIHESOFIVVCSGKM---441

DB 787 HVLKVLQFRTLLD---LKW---SLCNYGLQKLLSLQDMVFVEATAMRDAEI 836

QY 442 ---YFDKKN---YKKGSGGSGKGFPLVAVSAIAEKLRQAKSSAA---485

DB 837 QLLDGCRCRYWIMISEKSDSTTFPLDGNTRQWGNELNALLIDELVIELLMGASLSLAD 896

QY 486 LSKFIATVFDYSCBEDYVPGILDISTKYRLMDNL---POLCSHLHSDHGLQD---PQOH 538

DB 897 DLARLLGFIIDSPQNOVARVLHMYRLVLPQNAARQAFVITSGIETLLVLLQRE 956

QY 539 TROGSRNRTFRSGKSGSLVAICNMHOFIDEEPWFQKVPFPPPLRYREPVLKRFDS 598

DB 957 AKGEDNVLANGRSGR---SSDPSKES---PYN---ESGSKQLDS 995

QY 599 GLVLNDV-MCKPGPESDFCLKVEAVLNGATG-PADSOHESQHGGLDQGEARPALDGSAA 656

DB 996 NPHDNEIGDFLCPDGN---SYEDDNVGSINVPSYRQKEHG---1035

QY 657 LQPLHRTVAGSPSONKRDGYTSSVPSSELSPLMEGLSTDQTFSTLSYESVSSSGL 716

DB 1036 ---STPVVCDSDSVSISNTERLS---AEIGGISLSISADSAR 1074

QY 717 GE---EEPPA---LPSKLLSSGSKADLGCBS 742

DB 1075 NNTVNDNSDVAVVGIIIRLIGALISSGHLTFDFDARS 1111

RESULT 7

F83781

transposase (08) / ABC transporter (ATP-binding protein) BH1054 [imported] - Bacillus

C/Species: Bacillus halodurans

C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C/Accession: F83781

R/Takami, H.; Nakasone, K.; Takaki, Y.; Mieno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H

Nucleic Acids Res. 28, 4317-4331, 2000

A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a

A/Reference number: A83650; MUID:20512582; PMID:11058132

A/Accession: F83781

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-901 <STO>

A/Cross-references: GB:AP001510; GB:BA000004; NID:910173440; PIDN:BA804773.1; GSPDB:G

A/Experimental source: strain C-125

C/Genetics:

A/Gene: BH1054

Query Match 2.9%; Score 116.5; DB 2; Length 901;

Best Local Similarity 19.6%; Pred. No. 0.82;

Matches 112; Conservative 76; Mismatches 169; Indels 215; Gaps 27;

QY 61 ASRNSGLNITFYDNCITLYNPGKHVADIAQNTISQY-ACHDOVAVTILNPGALGI 119

DB 333 ALKESGL---PLPKTLIADAGTSGESNTVMADELTFETFS---371

QY 120 EFLKGFVILEELKSEGR---QCQOL---ILKDPKQLNSSFRTGMSOPFLNKF 169

DB 372 ---BTRF---QEQKRSFAKKRHFYNNWCDETDVYWCNQRKVSPKRVTKRTDPY---GY 423

QY 170 ETDYEV---KVVPF-PSI---KNESNYHFFEFTRACDILLQPNLACKPFKPR 217

DB 424 ARDFKYTECEGCPFPPECTKARGNQVYINPV---EELAKQHOKLK 471

QY 218 NLNISOHG---SDMQVSFDHAPNFGFRFFYLHYLKLKHEGPFKRTKQEQTTET 269

DB 472 ---SEEGRTLYQKRTDYESVFGHVKNLGRFRRLHGRK---507

QY 270 TSCILQNVSPGDYIELVDVDTTTRKYVHVALKPVHSPWAGPIRAVAVTVPWLWIS-AFA 328

DB 508 ---ESVHELGLVALAHNR 524

QY 329 TLFVYCRKQKQENYSHLDRESSSTYTAALPRELRPRKPVLCYSSKDGONHNVV 388

DB 525 KRATYDRSRKEPNTNKHREN---RIKRF---SRETYL 558

QY 389 QCF---AYFLQDFGCEVALDMEFSLCREGOREWV---IOKIHESOFIVVCSGKM 441

DB 559 RCFWDSPPFIKSDGOYASFALFD---KLREGENNIEVLDLSKYRNQVY---KGIN 612

QY 442 YFDKKNYKKGSGGSGKGFPLVAVSAI---AEKLRQAKQSSAALS 488

Db 613 MEIERGEMVGLGPNAGKSTTSMISLLQPTSGDVLKGGTHKQSKAIRSILGVVQ 672
QY 489 FIATFDYSC-----GDVPGILDSTYRLMDNLPOLCSHLSRDBHGOEPCQTRQG 542
Db 673 EYAVYDUTARENLAFFKYGKGLKELKHEP-MESTLQV-----GLEE-----RON 718
QY 543 SRNTFRSKRSGLYVAICNNH-----FIDEEP 571
Db 719 DRVHTFSGMKRLNIAVALLHPELINDP 750

RESULT 8
149071

protein kinase - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C:Accession: I49071
R:Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.
Mech. Dev. 48, 153-164, 1994
A:Title: Identification of novel protein kinases expressed in the myocardium of the developing mouse
A:Reference number: I49071; MUID:95200798; PMID:7893599
A:Accession: I49071
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-938 <RES>
A:Cross-references: EMBL:U11493; NID:g595418; PIDN:AA67925.1; PID:g595419
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
C:Keywords: ATP; transmembrane protein
F:571-839/Domain: protein kinase homology <KIN>
F:579-587/Region: protein kinase ATP-binding motif
F:862-928/Domain: SAM homology <SAM>

Query Match 2.9%; Score 115.5; DB 2; Length 938;
Best Local Similarity 19.4%; Pred. No. 1;
Matches 160; Conservative 120; Mismatches 285; Indels 259; Gaps 45;

QY 9 SVFTVNAFL-NGSLAVA-----AGGSQR-----ARGADTCGRWMAAARPLC----- 52
Db 170 SLVIAPRACIANAVEVPLKLYCNGDGMVPGVACTCATGHEPAKESQCRACPPG 229
QY 53 VANEGVGA-----SRNSG-----LYNIFKYN-----CTTYLNPVGRHVIAD 93
Db 230 KAKQGGPCPCPNSTTSPASICTCHNNFTRADSDSADSACTTRSP-PRGVISN- 287
QY 94 NITISQACHDQVAVTILMS-PGALGIEFLKGRFVILELK-SBG-----RQCQQLIL 144
Db 288 -----NETSLILENSEPRDLGRDDLLYNVICKRGSSGAGPATCSCDDNVE 337
QY 145 KQKOLNSFKRTGMSQPLNKFDTYFVKVPPFPKINSEYHFFFTFTRACDLLQ 204
Db 338 FVPRQLGTERVHLS-----HLLAHTRTFEVQAVNGVSGKPLPRYAANVTNNQAA 392
QY 205 PONLACKPFWKPRNLNISOHSDOMQVSDPHAPNFGFFYLYLHKHEGPF-KRTCKQ 263
Db 393 PSEV-----PTLHSTSGSSITLWAPPERPNC-----VILDYEMKY-----FEKSAIAS 439
QY 264 EOTTETTSCLLQNSP-GDYILVDDTNTTKV-----MHYALKPVHSPWAGPTRA 316
Db 440 TVISONSVDLQGLQDARYVQV-----RARTVAGYQYTHPAEFFTSERGGAGQQLQ 494
QY 317 ITVPLVWISAF-----TLFTVMCRKKQENIYHLSDESSSESTYTAALPRERL 368
Db 495 EQPLTVGNSVAGFVFWVWVIALVCLRKQRH-----GPDARTTEKL-QQYIAP 543
QY 369 RPEVLCYSSKDGONNNVQCFAYFLQDFC-GCEVALDMEDESICREGREWYQIKH 427
Db 544 GMYIYDPTIEDPN-----EAVREFAKEIDVSKVIEVIGAGEFGEVCR-----589
QY 428 ESQFIIVCSKGMKYFVDKKNYKKGGRSGKGLFLVAVSAI-----AEKLRQAKQSSS 483
Db 590 -----GRKLPGRRVFF-VAINTLAVGTERRQDFLSEA 623

QY 484 AALSKFTAVFYDSCDVPDGIILDS-----TKYR-----LMDNLPOLCSHLSRDBHGLQ 533
Db 624 SNMQCF-----DHPNIRLEGGVYKSRPVMILTEFENC-ALOSFLRLND----- 667
QY 534 EPGQHT-----RQSSRRNY-FRSKSGRLYV-----AIC-----NMHQFIDE 569
Db 668 --GQFTVQLVGLRGTAAGMYLSEMYTVHRLAARNILVNSLVCKVSKDPSGLSRFLED 725
QY 570 EPDNFERQF-----VPEH-----PPPLATREPVLEKDS-----GLYLDNMCKPGPE 612
Db 726 DPS-----DPTYSYSSLOGKIPINWTAPEIAR-----KDSASDVWSYGVWNEVMS----- 773
QY 613 SDFCLKEAAVVLGATGADSGHESQHGGLDQGEARPALDGSAAALQPLHTVKAQSPDM 672
Db 774 -----YGEQTYWNSQDDINAVEQDYRLPPPMDCPTALHQLMASCWVRDLRL 822
QY 673 PRDGGIYD-----SSVPSSELSLPLMBGLSTDDT 701
Db 823 PKFSQIYNTLKLIRNAASLKVATASAPSG-MSQPLLDRTVPDYT 865

RESULT 9
S37627

protein-tyrosine kinase (EC 2.7.1.112), receptor-type - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 03-Aug-1995 #text_change 04-Feb-2000
C:Accession: S37627
R:Boehme, B.; Holtrich, U.; Wolf, G.; Luzius, H.; Grzeschik, K.; Ru
Oncogene 8, 2857-2862, 1993
A:Title: PCR mediated detection of a new human receptor-tyrosine-kinase, HEK 2.
A:Reference number: S37627; MUID:93390963; PMID:8397371
A:Accession: S37627
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-998 <BOE>
A:Cross-references: EMBL:X75208; NID:g406867; PIDN:CAA53021.1; PID:g406868
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein
F:631-839/Domain: protein kinase homology <KIN>
F:639-647/Region: protein kinase ATP-binding motif
F:922-988/Domain: SAM homology <SAM>

Query Match 2.9%; Score 115; DB 2; Length 998;
Best Local Similarity 19.0%; Pred. No. 1.3;
Matches 158; Conservative 122; Mismatches 301; Indels 250; Gaps 42;

QY 35 GADTCGRWMAAARPLC-----VANEGVGA-----SRNSG-----LYNIFK 73
Db 267 GACTCATGHEPAKESQCRPPGSKAKQGGPCPCPNSTTSPASICTCHNNFYR 326
QY 74 YDN-----CTTYLNPVGRHVIADQNTITISQACHDQVAVTILMS-PGALGIEFLKGR 126
Db 327 ADSDSADSACTTVPSP-PRGVISN-----NETSLILENSEPRDLGVRDOLLN 374
QY 127 VILEELKSEG-----RQCQQLILKQPLKOLNSFKRTGMSQPLNKFDTYFVKVPP 181
Db 375 VICKKCHGAGSASCRDNDNVEFVPRQLGLSEPRVHTS-----HLLAHTRTFEVQAVN 429
QY 182 SIKNESYHFFFTFTRACDLLQLQDNLACKPFWKPRNLNISOHSDOMQVSDPHAPN 241
Db 430 GVSCKSPPLPRYAANVTNNQAAPEV-----PTLHSSSGSSITLWAPPERPNC- 481
QY 242 RFFYLYLHKHEGPF-KRTCKQEDOTTTTSCLLQNSP-GDYILVDDTNTTKRVHY 299
Db 482 --VILDYEMKY-----FEKSGIASVTYSQNSVQLDGLRDPARYVQV-----RARTVAGY 531
QY 300 A--LKPVE-----SPWAGPTRAIVAVTLPVWISAFATL-----FTVMCRKKQENIYS 345
Db 532 QOYSPRAFEFTTSERGGAGQQLQPLVGSATAGLVFVAVVAVVIAVCLRKQRH----- 587
QY 346 HLDESSSESTYTAALPRERLPRPKVFLCTSSKDGONNNVQCFAYFLQDFC-GCEVA 404
Db 588 -----GSDSEYTEKL-QQYIAPGMYIYDPTIEDPN-----EAVREFAKEIDVSKVIEV 638

QY 405 LDWEDFSLCRGOREWVIOKIHESOFIIVVCSKGMKYFVDKKNKHKGGSGRGKGLF 464
Db 639 IGAGEGCEVR-----GRKQGRREVTF 661
QY 465 LVAVSAI-----AKLROAKOSSAALSKEFLAVFYDSCBEDVPGILDLS---TYVR---513
Db 662 -VAIKLVGVYERQORDFLEASIMGQF-----DIPNIRLEGVYIKSRPMI 709
QY 514 ---LMDNLPLQASHLSRDHGLQEPQHT-----ROGSRNRY-PRSKSGR 554
Db 710 LTFEMENC-ALDSFLRLND-----GOFTVQLVGLRGIAAGMYLSMENVYHDLAAR 762
QY 555 SLTV---AIC-----NMHQFIDEPPDFWFEKQFVFPHP-----PLRYREP---VLKFFD 597
Db 763 NILVNSMLVKYSDFCGLSFLLEDPS-----DPTYSILSKGIPIRTWPAEATAYRFT 816
QY 598 S-----GLVLDVWVCAPGPESDFCLKVAIVLGATGAPDSQHSQGGGLDQGEARPA 650
Db 817 SASDWSYIGVMEVNS-----YGERPTWMSNQDVINAVEZDYRLPPP 860
QY 651 LDGSAALQPLHVTYKAGSPDNPRDSGIYDS-----SVPSSELSLPLMEGL 696
Db 861 MDCPTALHQLMDVVRDLNRLRPFQSLVNTLDKLIRNAASLKVIASQAQSGMSQPLDRT 920
QY 697 STDTSTSSITSSVSSGLGEERPPALPSKLLSSGSCADLCGRSYDEL 747
Db 921 VEDITFTTGVMDLAIK-MGRYK-----ESFVSAGFADFVLVAQMTAEDL 965

RESULT 10
T17212
hypothetical protein DKFp434p211.1 - human (fragments)
C:Species: Homo sapiens (man)
C:Date: 15-Oct-1999, #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T17212
R:Poustka, A.; Klein, M.; Meves, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A:Reference number: Z18723
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-489-535 <PDB>
A:Cross-references: EMBL:AL117401
A:Experimental source: adult testis; clone DKFp434p211
A:Note: the cDNA sequence contains a -1 frameshift near codon 488
C:Genetics:
A:Note: DKFp434p211.1

Query Match 2.7%; Score 110; DB 2; Length 535;
Best Local Similarity 23.5%; Pred. No. 1.3;
Matches 70; Conservative 49; Mismatches 108; Indels 78; Gaps 17;

QY 474 KLRQAKOSS-SAALSKEFLAVFYDSCBEDVPGI-----LDLSTYRLMDNLQ 520
Db 103 RYNTQTSWTSCTNRNAISSSTYGGPLGLRRRGPASSHCQLTSSKTSYSDRPQ 162
QY 521 LCSHLHSRDHGLQEPQHTROGSRNRYFRSKSRLYVAICNMHOFIDEPPDFWFEKQF 578
Db 163 AVSGHGTQCEKAADIAPGQTLT--LRNDSSTSEASRP-----STHKE---PLLPERRG 210
QY 579 VPFH-PPPL-----RYREPVLKFFDSGLVNDVM---CKPGPSDFCLKVEA 622
Db 211 EPLMLPPPLELGYRTVVDLRETAAPQINSALQVDEKALSDCRPSRSH---TLSSL 267
QY 623 VLGATG-PADSOHESQHGGLDQGEARPALDGSAAALQPLHVTYKAGSPDNPRD-578
Db 268 ATGASGLPAPVSKAPS-----MDAQOETHKSQDCGLDLOPLASA--AGVSTAPMSGKKHRP 321
QY 676 SG-TYDSSVPSSELSLPLMEGLSTDTQTSSTLSTSVSSSSGLGEERPPALPSKLLSSG 732
Db 322 PGFLFSSDP-----LPATSSDSQDSQAQVTSLI-----PAFFPAASNDAG 361

RESULT 11
I49239
vesicle transport protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I49239
R:Wellam, J.F.; McIntosh, S.; James, D.E.
J. Biol. Chem. 270, 5857-5863, 1995
A:Title: Molecular identification of two novel Munc-18 isoforms expressed in non-neur
A:Reference number: I49238; PMID:95197608; PMID:7890715
A:Accession: I49239
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-392 <RES>
A:Cross-references: EMBL:U19521; NID:9642027; PIDN:AAA69913.1; PID:9642028
C:Genetics:
A:Gene: munc-18c

Query Match 2.7%; Score 110; DB 2; Length 592;
Best Local Similarity 18.5%; Pred. No. 1.5;
Matches 93; Conservative 64; Mismatches 157; Indels 189; Gaps 22;

QY 321 LVVISAFAATLFTVCRKQKQ-----ENIYSHLDESSSESTYTAALPRRLPRPK 371
Db 34 IMLEDEFTYKLLSSCCCTTOLLEGIIVTENTYKREPVROMKALYP-----ISFTPK 86
QY 372 VFLEYSSKDGQNHNVVOCFAIFLQDFC-----GCE-----402
Db 87 SVDCFLRDFGSKSEKYYKAAIYFTDFCDPSLNFNIKASCSIRCKEINISFIPQESQ 146
QY 403 -VALDLWEDFSLC-----REGOREWVIOKIHESOFIIVVC-----SKGMKY 442
Db 147 VTYLDVDPDAFYCYSPDSNASRKEVVMEMAEQ--IVTVCATLDENPGVYIKSKPLDNA 204
QY 443 -----FVDRK--NYK--HGGGSGSGKGLFLV-----AVSAIAEKLRQAKOSSAALS 487
Db 205 SKLAQLVKKLEDDYKIDKGLIKGTQSLQAIIDRGDPDPVSTVLHEL-----252
QY 488 KFIATVFD-----YSCGEG-DVPGIL-----DLSTKYR-----LMDNLPLQASHLH 526
Db 253 TFOAMAYDLLPIENDTYKNTDCKEKEAVLEDDDLVWVRVHRHIAVVLEIIPKMKETS 312
QY 527 SRDGLQEPQHTROGSRNRYFRSKSRLYVAICNMHOFIDEPPDFWFEKQFVFPHPPL 586
Db 313 STK-----KATGKTSLSALTQLMKKMPHFRKQISKQVY-----HL 348
QY 587 RYREPVLKFF-----DSGLVNDVMCKPGPSDFCLKYE 620
Db 349 NLAEDCHNKFNLNTEKCKTEQDLALGTDAEQVRKDSMLVLLPVLL--NKNHNDCKIR 406
QY 621 AAVLGATGPADSOHESQHGGLDQGEARPALDGSAAALQPLHVTYKAGSPDNPRD-SGIY 679
Db 407 AVLLIFIGINTTEEN-----LDRLHNKVIDEDSDMIRNWSHLG 446
QY 680 DSSVPSSELSLPLMEGLSTDTQ 701
Db 447 VPIVPPSQQAAPLRKDRSAEET 468

RESULT 12
T13960
beige protein homolog - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T13960
R:Mori, M.; Nishikawa, T.; Higuchi, K.; Nishimura, M.
submitted to the EMBL Data Library, November 1998
A:Description: Deletion in the beige gene of the beige rat due to recombination betwe
A:Reference number: Z17037
A:Accession: T13960
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Accession: 1-3788 <MOR>
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-3788 <DIE>
 A:Cross-references: EMBL:Y17034; NID:G3413809; PIDN:CAA76598.1; PID:G3413810
 A:Experimental source: strain DA; spleen
 C:Genetics:
 A:Gene: beige

Query Match 2.7%; Score 108.5; DB 2; Length 3788;
 Best Local Similarity 19.4%; Pred. No. 31;
 Matches 144; Conservative 98; Mismatches 267; Indels 235; Gaps 38;

QY 20 GSOLAVAGSGRGADTCGWRKAAARPLCVANEGVGPASRNSGLYNTFKYDNCVT 79
 DB 651 GETLOGYLCGAGPSGLPSYRF-----QGILP-----SSGEFLMKWDALEA 695
 QY 80 YLMPGVKIVADAQNTISYACH--DOVAVTILSPGCAIEFLKGRVILEELKSEG- 136
 DB 696 YQNFIFQF--DLRLHTQIASHCILQKGNVIVQ-----KLYNIFNPVLQGV 743
 QY 137 ---RQCQILKDKPKLNSFKTKMESQPLMKFET--DYFVKVP-----EP 181
 DB 744 ELVHCCQLSI-----TSACTHSSQLKQYLQVLOIYKTLPIILKSRVIRDLFL 795
 QY 182 STAN-----ESNY-----HFF--FFTRACDLQPDMLACKPPKPNLNISQHSMDQ 229
 DB 796 SCGVNHIILYLDGIRSHSLKAFETLIVSGKQKAAVGV---DGLDIQOELSL 852
 QY 230 VSFDAHNFGRFFLYLKLKHEGPFKRTCKQQTETTSCLLQNVSPGDYIIELVD 289
 DB 853 V-----GPSLKH-----QOASTDSCSLRK-----FYASLRT 880
 QY 290 TWTTRKMHYALKPVHSPWAGPIRAVAITVPLVISAATLFTVCKRKOENIYSHLDE 349
 DB 881 DPKKKTVO-----DAHNTINFLCVAF-----LCVSKADSRESAN- 920
 QY 350 ESSESTY--TAALPRELRAPKVFCLYSSKDGQNHNVY---QCFAYFLADFCGEV 403
 DB 921 ESEDTSYDTSVAPSLSHMLPLSL-----ENVVLPSPCLHE-----958
 QY 404 ALDNEFSLCREGQEWV--IOKIHESOFI-----LVVCSKGMKYFYDKNKKYKGGRG 457
 DB 959 ADIN--SMCR-----WYILNVSFQKQFHLGGFQVCHL-LIFHIQKLFRTSHEDG 1009
 QY 458 SKGELF-----LVAVSAETAKLROKSSAALKSFIAVFDYSCGDPVPGILD-----507
 DB 1010 ROEGMSYNNKQGLRISOPEMILKEDVSSSTAPEGFLKRSADRVSELSQMLPTSAE 1069
 QY 508 --LSTK-----YRLMDNLPOLCSH-----LHSRDBGLQEPQHTROG 542
 DB 1070 QILATKSPGEAKTFMNOESETCLOSIRLLESLLAICLSARASQKMELELPQ-----1124
 QY 543 SRRTFRSKRSYLYAICNHFQIDEEP-----DWFQKVPFPPPLPKYREP 591
 DB 1125 -----SLSLENLICELRDLHSQSVAETELAKPLFALIRVALGNHSDADLPDGT 1174
 QY 592 VLEKFDGLVNDVCKPSPGSCFLKVEAAVILGATG-----PADSOHESQHGGLDQCE 646
 DB 1175 VTEKSHPS--EVLSPQGFSEAEEDSQCSKLLGEEGYEADSESNEDEGETODGV 1231
 QY 647 ARPALDG--SAALQP--LLETVRAG 667
 DB 1232 ELPEAEFGSGSIVPNNLLESLLTHG 1255

RESULT 13

T42730
 Basoon protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
 R:Accession: T42730
 R:Dieck, S.; Sanmarti-Villa, L.; Langnaese, K.; Richter, K.; Kandler, S.; Soyke, A.; Weiz, J. Cell Biol. 142, 499-509, 1998
 A:Title: Basoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized
 A:Reference number: 22249; MUID:98345363; PMID:9679147

A:Accession: T42730
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-3942 <DIE>
 A:Cross-references: EMBL:Y17034; NID:G3413809; PIDN:CAA76598.1; PID:G3413810
 A:Experimental source: strain 129 SVJ
 C:Genetics:
 A:Map position: 9f1
 A:Introns: 72/2; 208/3; 505/3; 675/3; 2889/3; 3582/1; 3851/3; 3886/1; 3930/1
 A:Note: basoon
 C:Function:
 A:Description: may be involved in cytomatrix organization at the site of neurotransmission
 A:Note: component of the presynaptic cytoskeleton
 C:Keywords: coiled coil; zinc finger

Query Match 2.7%; Score 107.5; DB 2; Length 3942;
 Best Local Similarity 19.1%; Pred. No. 39;
 Matches 58; Conservative 29; Mismatches 99; Indels 117; Gaps 11;
 QY 516 DNLPOLCSHLSRDHGLQEPQHTROGSRNYPFRSKRSYLYAIC-----NMHQFIDEE 570
 DB 3535 DYCPOFCS-----SHSKPDVQEHVKGDPRAHAYKREGYMLDDSHCVSDSEAYHLGQEE 3589
 QY 571 PDWFKQVFFHPPLRYRE-----PVLEKF-----DSGLVLDNYMCKPG 610
 DB 3590 TDWTDK---PRDARSDFRHHGGHTVSSSKQKPARSHYHDYDEPPEGLWPHD---DSG 3643
 QY 611 PESDFCLKVEAAVLGATGPAQSQESQHG-----GLDQDG-----EARP- 649
 DB 3644 PGRH-----TSAKERHSHSDGRHSGRHAGEEPGRRAAPHARDMGREARPH 3691
 QY 650 -----ALDGSAAALQPLLTIV 664
 DB 3692 PQASPAPAMOKQPGYPPSADYSQSRAPSAHYHASESKSGRQARTGPSALQPKADTQ 3751
 QY 665 KAGSPDMRDSGIYDSSVSPSELPLMGLSTQDTSTSLTESVSSSGSGEPEPAL 724
 DB 3752 AQPMQGRQAAPGQSQSPSSRQT---PSGTASRQPTQOQOQOQOQOGLGQQAPOA 3808
 QY 725 PSK 727
 DB 3809 PSQ 3811

RESULT 14

T30851
 Lysosomal trafficking regulator, long splice form - mouse
 N:Alternate names: beige protein homolog
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 24-Nov-1999
 R:Accession: T30851
 R:Barbosa, M.D.F.S.; Tchernev, V.T.; Kingsmore, S.F.
 submitted to the EMBL Data Library, September 1996
 A:Description: Two bg or not two bg? Longest isoform of mouse Lyst (beige) gene.
 A:Reference number: Z20903
 A:Accession: T30851
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-3788 <BAR>
 A:Cross-references: EMBL:U70015; NID:G1813541; PID:G1813542; PIDN:AAC53011.1
 A:Experimental source: strain C57BL/6J
 C:Genetics:
 A:Gene: Lyst
 A:Map position: 1
 C:Keywords: alternative splicing

Query Match 2.7%; Score 107; DB 2; Length 3788;
 Best Local Similarity 19.5%; Pred. No. 40;
 Matches 156; Conservative 104; Mismatches 288; Indels 254; Gaps 44;
 QY 20 GSOLAVAGSGRGADTCGWRKAAARPLCVANEGVGPASRNSGLYNTFKYDNCVT 79
 DB 651 GETLOGYLCGAGTSLGPSYRF-----QGILP-----SSGEFLMKWDALEA 695

QY 80 YLNPVGHVIAQNTISYACH--DQAVATILSPGALGIEFLKGRVILEELKSEG- 136
DB 696 YQSEVQE--DRLENIQIANHICNLQGNVYQW-----KLNIYFNPVLQGV 743
QY 137 ---RCCOOLILKPKLNSSFKRCMESOPFLNKKFET--DYFVKVVP-----FP 181
DB 744 ELVHCQOLISPS-----ACHRCSQLKQYLPOEVLOIYKILPVLKLSRVIRDEL 795
QY 182 SIRN-----HFF--FPRTRACDILLOPNLACKPFPKPRNLINISQSGDMQ 229
DB 796 SCNGVHIILANTLQIISHSLAKAFETILVSLAGEQKDAALVDV---DELQIQELPSLS 852
QY 230 VSDPHAPNFGPFPFHYLKLKHEGPKRKTCKOBTETTSCLLQNSPGDYIIELVDD 289
DB 853 V-----GPSLHK---QQASSDSCSLRK-----FYASLREP 880
QY 290 TINTRKVMYALPVHSPWAGPIRAVAITVPLVVISAPATLVWCRKKQENIYSHLDE 349
DB 881 DPKRATIH---QDVH-----INTINFLCVAF-----LCVSKEDS---DR 916
QY 350 ESSESITTAALPRERLPRKVFICYSSKDGQENNVV---QCFAFLQDFCQCEVAL 405
DB 917 ESANESEDTSGVDSPPSEPLSHMLPCLSLD-----VYLPSPCLHH-----AA 960
QY 406 DLNEDSLCREGOREWV--IOLIHESOFI---IVVCSKGMKYFDKKNYKKGGRSG 459
DB 961 DIW---SMCR-----WITLANSVFOKQHRLGQVQCHE-LIFMLIQKLFHSHTEDQGR 1011
QY 460 KGEFL---IVAVSAIAELKRAKQSSAALSKFIYVFDYCEGDPVQIL--DLSTK 511
DB 1012 QGMSRNEQELIRIS-----YPELTLKGVSSATAPDLGLF 1048
QY 512 YRLMDN-----LPOLCSLHSLRQGLQEPQOHTGSRNRYFRSKSGSLYVAICN 562
DB 1049 RKSADSVRGFQSPQVLPYSAQIVATE---SVFGE-----RKAFNSQOSETSLQIRL 1098
QY 563 MEQFIDEEDPWEKOFVFPHPPLRYEPVIEKFDGSLVINDVCK----- 608
DB 1099 LESILO-----ICLSARACQOMLELPQSGLSVENILRELHLSQSKVAETE 1148
QY 609 -PGPESDFCLKVEAAVIGA--TGPADS-----QHSQEGGLDQGEARPALDGSAAALQPLH 662
DB 1149 LAKPLFDALLRVALGNHSLDGLPGDAVTEKSHPEELLSQPGDFSEAEQSCSLKL 1208
QY 663 TVKAGSPDM---PRDSGIYDSSVPSSLSLPLMEGLSDQOTETSLTESVSSSGLGE- 718
DB 1209 GEEGTEASENPDVNTQDGV---ELN-PEAEGFS-GSIVSNLLENLTH-----GEI 1259
QY 719 --EPPALPSKLLSSGCKADL 738
DB 1260 IYPEICMGLNGLISAKKALDV 1281

RESULT 15

D86477

Protein F1504.27 [Imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: D86477

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.B.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shlan, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; PMID:21016719; PMID:11130712

A:Accession: D86477

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-638 <STO>

A:Cross-references: GB:AE005172; NID:g8778345; PIDN:AAF79353.1; GSPDB:GN00141

C:Genetics:

A:Gene: F1504.27

A:Map position: 1

Query Match

Best Local Similarity 19.4%; Pred. No. 3.1;

Matches 94; Conservative 63; Mismatches 175; Indels 153; Gaps 24;

QY 94 NITISQYACHQVAVTILSPGALGIEFLKGRVILEELKSEGROCOOLILKPKLNSS 153
DB 275 DIKYGOYSLQDCFFVVS-----KCATHEWVNDGKELWEIETEDTISP 322
QY 154 FKRTCHESOPFLNKKFETDYFVKVVPF---SIKNSNTHFFPFRTRACDILLOPNLAC 210
DB 323 FRNLG-----DGFIRKFKHRLKLNHDCGARTKOCAC---IYP--IVS 364
QY 211 KPFWPRNLINISQHG--SDMQVSFDHAPNFGREFYLYLKLKHEGP--FKRTCKRQBT 266
DB 365 HQFTCKKCNYSLHEVCAGLSRKLDHALHN-----HTLILSPSPGKFCSCACSREST 416
QY 267 TETTSCLLQNSPGDYIIELVDDTNTTRKVMYALPVHSPWAGPIRAVAITVPLVISA 326
DB 417 GFSYIC--SNKGCODFVLV-----RCISVLYFFIHRGHEH-----PIFISTS 457
QY 327 FAYLFTVMCRKKQENIYSHLDEESE--SSTYTAALPREE--RLRPRKVLFCYSSKDG 381
DB 458 YNSKDEILLKCKKRCGLAHLOCTLCEFTWCYSALIPDEIHYKFDKHLPLTLSCGESAD- 516
QY 382 ONEMNVOCFAFLQDFCQCEVALDWEDFSLCRGQREWIQKIHESQFIIVVCSKGMK 441
DB 517 ----NWTCEV-----CEKQLDPKWFYTCNK-----CCITIH-----LGLIFGSS 553
QY 442 YFVDMKNKTHGGGSGKGLFLVAVSAIAELKRAKQSSAALSKFIYVFDYCEGDP 501
DB 554 VFM-----KPG-----SIFRDIYTKVQ 570
QY 502 VFGILDSTKRLMDNLPLCPSLHSLRQGLQEPQOHTGSRNRYFRSKSGSLY-V 558
DB 571 V-----FRNNSNTQLCYCNKNCYGL-----IFTEGYRRNATYYNHNSTRH 616
QY 559 AICNM 563
DB 617 IFCSL 621

Search completed: May 19, 2003, 09:25:43

Job time : 38.7988 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 19, 2003, 09:08:53 Search-time: 15:2893 Seconds
(without alignments)
2042.709 Million cell updates/sec

Title: US-09-912-157-2

Perfect score: 4013

Sequence: 1 MAPWLQCSVEFTVNAQLG.....CRADIGCRSYTDELHNAVPL753

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	310	7.7	866	1	IL17R_HUMAN	Q96F46 homo sapien
2	306	7.6	864	1	IL17R_MOUSE	Q60943 mus musculu
3	135.5	3.4	502	1	IL17S_HUMAN	Q9NRM6 homo sapien
4	126.5	3.2	718	1	YSO2_CAEEL	Q10128 caenorhabdi
5	115	2.9	998	1	EPB3_HUMAN	P54753 homo sapien
6	110.5	2.8	499	1	IL17S_MOUSE	Q9J1P3 mus musculu
7	110	2.7	592	1	STB3_MOUSE	Q60770 mus musculu
8	104	2.6	1462	1	PTP6_DROME	P16620 drosophila
9	103.5	2.6	663	1	RGF2_HUMAN	P47736 homo sapien
10	102	2.5	859	1	ABR_HUMAN	Q12979 homo sapien
11	101	2.5	1275	1	GNRP_HUMAN	Q13972 homo sapien
12	100.5	2.5	974	1	RUG6_HUMAN	Q43182 homo sapien
13	99.5	2.5	794	1	ZFY2_MOUSE	Q60821 mus musculu
14	99	2.5	783	1	ZFY2_MOUSE	P20662 mus musculu
15	99	2.5	970	1	PSD1_YEAST	P53550 saccharomyc
16	98.5	2.5	993	1	EPB3_MOUSE	P54754 mus musculu
17	98.5	2.5	1050	1	EX5B_CHLPN	Q92797 chlamydia p
18	98	2.4	820	1	CTNB_TRIGR	P35223 tripneustes
19	97.5	2.4	1845	1	Z236_HUMAN	Q9U136 homo sapien
20	97	2.4	984	1	EPB1_CHICK	Q07494 gallus gall
21	97	2.4	984	1	EPB1_CHICK	P09759 rattus norv
22	96.5	2.4	746	1	ABL_MLVAB	P00521 abelson mur
23	96.5	2.4	902	1	EPBB_XENLA	Q91736 xenopus lae
24	96	2.4	424	1	HT31_ARATH	P45984 homo sapien
25	96	2.4	660	1	HT31_ARATH	Q04996 arabidopsis
26	96	2.4	1114	1	E2K3_MOUSE	Q922b5 mus musculu
27	95	2.4	828	1	CAN_DROME	Q11002 drosophila
28	95	2.4	933	1	PRGR_HUMAN	P06401 homo sapien
29	95	2.4	1036	1	AXO1_CHICK	P26885 gallus gall
30	94.5	2.4	351	1	HM14_CAEEL	P20271 caenorhabdi
31	94.5	2.4	770	1	GIT1_RAT	Q92272 rattus norv
32	94.5	2.4	841	1	I163_MCMVS	Q69154 murine cyto
33	94.5	2.4	1011	1	M3K6_HUMAN	Q95382 homo sapien

34	94	2.3	984	1	EPB1_HUMAN	P54762 homo sapien
35	94	2.3	2044	1	SIF2_DROME	P91620 drosophila
36	94	2.3	2064	1	SIF1_DROME	P91621 drosophila
37	94	2.3	3224	1	RBP2_HUMAN	P43792 homo sapien
38	93.5	2.3	806	1	RMLL_CHICK	Q04982 gallus gall
39	93.5	2.3	807	1	RMLL_COTJA	P34908 coturnix co
40	93.5	2.3	901	1	AL80_MOUSE	Q61548 mus musculu
41	93.5	2.3	915	1	AL80_RAT	Q05140 rattus norv
42	93	2.3	429	1	EPC_RAT	P01855 rattus norv
43	92.5	2.3	347	1	SH33_MOUSE	Q62421 mus musculu
44	92.5	2.3	548	1	IDD_MOUSE	P98154 mus musculu
45	92.5	2.3	684	1	FBL1_CHICK	O73775 gallus gall

ALIGNMENTS

RESULT 1
IL17R_HUMAN
ID IL17R_HUMAN STANDARD; PRT; 866 AA.
AC Q96F46; Q43844;
DT 15-JUN-2002 (Rel: 41, Created)
DT 15-JUN-2002 (Rel: 41, Last sequence update)
DE Interleukin-17 receptor precursor (IL-17 receptor).
GN IL17R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=98035683; PubMed=9367539;
RA Yao Z., Spriggs M.K., Derry J.M.J., Strockbine L., Park L.S.,
RA VandenBos T., Zappone J., Painter S.L., Armitage R.J.;
RT "Molecular characterization of the human interleukin (IL)-17
receptor";
RL Cytokine 9:794-800(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=uterus;
RA Strausberg R.;

Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for IL17. Binds its ligand with low affinity,
CC suggesting that additional components are involved in IL17-induced
CC signaling.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- PTM: Glycosylated.

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EMBL; U58917; AAB99730.1;
DR EMBL; BC011624; AAH11624.1;
DR Genew; HGNC:5985; IL17R.
DR MIN; 605461;
KW Receptor; Transmembrane; Signal; Glycoprotein.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 866 INTERLEUKIN-17 RECEPTOR.
FT DOMAIN 32 320 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 321 341 POTENTIAL.
FT DOMAIN 342 866 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 810 818 POLY-GLU.
FT CARBOHYD 49 49 N-LINKED (GLCNAC... (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC... (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC... (POTENTIAL).

FT CARBOHYD. 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL)
 FT CARBOHYD. 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL)
 FT CARBOHYD. 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL)
 FT CONFLICT. 367 367 V -> A (IN REF. 1)
 FT CONFLICT. 580 580 H -> R (IN REF. 1)
 SQ SEQUENCE. 866 AA; 96131 MW; 28330BED23090C9 CRC64;
 Query Match 7.7%; Score 310; DB 1; Length 866;
 Best Local Similarity 23.1%; Pred. No. 5.4e-16;
 Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;
 QY 69 NITFKYDNC--FTYLPVGRKVIADAGNIT-----ISQYACHDQ-----VAVTILAS 113
 DB 49 NCTVKMSTCLDSDWHP-----RNLTPSPKDLQQLGFAHTQDGLFVAHLEWT 99
 QY 114 -PGALGIEFLAGFRVILEELKSGRCQQLILKDPKQNSFKRTGMSQPPFLNKFETD 172
 DB 100 LQTDASILIEGAEUSVLQATNERLCVR--FEFLSKRHHRRWRTFSHFV-VDQGE 156
 QY 173 YFVKV--VFPPSIKSNYHPFFTRACDLQLQDNLACK---PFMKPRNL----- 219
 DB 157 YEVTHLEKPIPDGDPNHOQKNPLVPCDEHAKMYTTPCMSGSLMDP-NITVETLEAH 215
 QY 220 -----NISQHSQMOVSDFAHPNFGFRFFLYHKLHKGPFKTKCKOBOTTEFT 270
 DB 216 QLVSTLWNESTHYQILTSFPMENHSCFEHM-HIPAPPEFHORSNVILTANLK 274
 QY 271 SCLQWNSGDIYIELVDIT--NTRKVMHYALKPVSPWAGPIRAVAITVPLWISAF 327
 DB 275 GCRHQVOIQPFSSCLNDCLRHSATVSCPEMDTPEPIPYMPLWTFITGISILLG 334
 QY 328 ATFTVNCRRKQENIYSHLDESESTYTAALPRERLRPP-----KVFCTSSKDGQN 383
 DB 335 SVILLIVCMTRLAGPS-----EKYSOOTKTYDGLPVADLIPPLAPKRWIISA-DHPL 390
 QY 384 HNNVOCFAFLQDCGEVALDWEPSLCREGRENV-----IQKHESOFIIVCSKG 439
 DB 391 YDVVLKFAQLTACGTEVALDLEQALISEAGVTWVGROKQWESNKIIVLCISRG 450
 QY 440 MYTFVDKKNYKHGG-----RSGKGELFVAVSAIAEKLQAKQSSAALSKEFIA 491
 DB 451 TR-----AKWALLSGAPVRLCRDGHGKPVGLDFTAMNNILPDFKR-----PACFGTYV 501
 QY 492 VIF-DYSCGDPVGLDLSKYRLMDNLPCLSHLSRDBGLQEPQRTGQ-----SRNRYF 548
 DB 502 CYSEVSCDGVDPDLGAAPYPLMDREFEV--YFRIQDLEMPQGRHVRVGLSGDNYL 559
 QY 549 RSKSGSLVACNKHQFIDEEPWF-----KQVFPHPPLRYREPVLEKFDGSL 600
 DB 560 RSPGRLAALDRFDQVHCDFPWFECENLYSADQDAPSLDEEV-FEELPLP-OTGI 617
 QY 601 VLADVCKPGPESDFCLKVAEALVAGTAPDSOHE-----SOHGG 640
 DB 618 VKRAPLVRE-PSQACLAIDLPGVEGGAVALKLEPHLPQCPAPQPLETLVLAEGA 676
 QY 641 LDQGGARPAIDGSA--ALQ-----PLHTVKAGSPMDPSGGIYDSSVPSSELSLP 691
 DB 677 LVAVEPGPLADGAARVALAAGEACPLIGSPGAG-----RNSVLF--LPVDPEDSP 727
 QY 692 LMEGLSTQDTSETSSLESVSSSGIGEEPPALPSKLLSSGCKADLQAC 740
 DB 728 L--GSSTPMASPDLLPEDVR-----EHLGLMLSLFEQSLSCQAQGC 768

RESULT 2

ID 117R_MOUSE STANDARD: PRT: 864 AA.
 AC Q60943;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-17 receptor precursor (IL-17 receptor).
 GN IL17R.

OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID-10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-rhymic lymphoma;
 RX MEDLINE-96111968; PubMed-8777726;
 RA Yao Z., Fanslow W.C., Seldin M.F., Rousseau A.M., Painter S.I.,
 RA Comeau M.R., Cohen J.I., Spriggs M.R.;
 RT 'Herpesvirus Saimiri encodes a new cytokine, IL-17, which binds to a
 novel cytokine receptor'.
 RL Immunity 3:811-821(1995).
 CC -!- FUNCTION: Receptor for IL17. Binds its ligand with low affinity,
 CC suggesting that additional components are involved in IL17-induced
 CC signaling (By similarity).
 CC -!- SUBCELLULAR LOCATION: type I membrane protein (By similarity).
 CC
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 CC
 CC EMBL: U31993; AAC53357.1;
 DR MGI: 107399; IL17.
 KW Receptor; Transmembrane; Signal; Glycoprotein.
 FT SIGNAL 1 31 POTENTIAL
 FT CHAIN 32 864 INTERLEUKIN-17 RECEPTOR.
 FT DOMAIN 32 322 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 323 343 POTENTIAL.
 FT DOMAIN 344 864 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 809 814 POLY-GLU.
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 864 AA; 97807 MW; 343FD51AA67DA31 CRC64;
 Query Match 7.6%; Score 306; DB 1; Length 864;
 Best Local Similarity 22.5%; Pred. No. 1.1e-15;
 Matches 189; Conservative 128; Mismatches 319; Indels 203; Gaps 43;
 QY 40 GWRM-----KAAAPRL-----CVAHEGYGVPASRNSGLYNTFYKDYNCYTYLNPVK 86
 DB 17 GWLLLLNLVAPGRAPRLDLPAPVCAQEGLSCKVKNSTCLDSDSWHPKNTLPPSPKRI 76
 QY 87 RVIADAQNTISQYACHDQAVT-ILWS-PGALGIEFLKGRVILEELKSGRCQCO--- 141
 DB 77 YI-----NLSYSTQHGELVPVILHVEWTLQDASILEGAEISVLAQNTNERLCVKFOF 131
 QY 142 --LILKDPKOLNSFKRTGMSQPPFLNKFETDYFVKVYPPSPKSNESYHPFFTRAC 199
 DB 132 LSNLQHRKRWRFSG-----SHFVVDPGQEVTVHLPKPIPDGDPNHSKIIIVPOC 185
 QY 200 D-----LLIQDNLACKPWPKNLNI-----SOH-----GSDMQV 230
 DB 186 EDSKMRNTSCVSSGSLMDP-NITVETLQTHLRVDFTLWNESTPYQVLESSESNES 244
 QY 231 SFD-----HAPHNFGFRFFLYHKLKHE-----GPKRKTCKQQTTFETSCLL 274
 DB 245 CFDVVKQIFAPRQBEFFQRANVTFTLSKEFWCHHHVQVQPF-FSSCLND-----CLR 296
 QY 275 QNVSPGDIYIELVDITNTRKVMHYALKPV--HSP-WA-GPIRAVAITVPLWISAFATL 330
 DB 297 HAVTVPCPVI-----SWT-----VPKPVADYIPLWYGLITLAI-----LLVGSIVL 341
 QY 331 FTVMCKKQENIYSHLDESESTYTAALPRERLRPPKRVKFLCYSSKDGQNHNNVQC 390

Db 342 IICMTWRLSGAQEKHGDDSKINGILPVADLPPLRER-KVILVISA-DHPLVREVLK 399
 QY 391 FAYFLQDCGEVALDWEFSICREGQREWIQR-----IHESFIIVCSKGMKTFYDK 446
 Db 400 FAQFITTACGTEVALDILEQVISEVGMVTSROKQWESNKIILCSRG-----TO 454
 QY 447 KNYKKG-----GRSGKGELFLVAVSAIAEKLQAKSSAALSKEFIAYFDY 496
 Db 455 AKKAILGWAEPAYOLACDHWKPGDLFTAAANMLPDKR-----PACGRTVVCYFSG 509
 QY 497 SC-EGDVGILDLSTKYRLNDNLPLCLSHLSRDRGLOEQC---HTQGRSRNYFERSG 553
 Db 510 IGSEEDVDLENIISRIPIADREFEV---YFRIDLEMEFGRMHVRLELTDNLQSPSG 567
 QY 554 RSLVAICNMHQTIDEEPWFKEQFYFHP-----PPLR---YREPVLEKFDGLVNDVM 606
 Db 568 RQLKAVLRUFQEWQTCQPDWFERENICLADGDLPSLDEEVEDPILPP-GGCIKQKQL 626
 QY 607 CRPGPESDFCLKVAALVGLATGADSOHESORGLDOD-----GEAR 648
 Db 627 VRELPSDGLVDVCV-----SEESRMKIDPOLMPQRELVAITLQSNVLAEGV 677
 QY 649 PALGSAALQPLITVYKAGSPDMP---RDS-----GIYDSV---PSSLSLPL----- 692
 Db 678 PA---AHVPELHPDGSAAQPLMTEDSEACPLLGVRNSILCLPVDSDDLPLGSTM 734
 QY 693 -----MEGLSDYDTETSLSITESVSSSGIGEEPPALPSKILLSGCKADLCGRSYDE 746
 Db 735 MSPDRHQDAREQLESIMLSVLQSLGQPLESNR-PEVLE-----GCTSEEE 784

RESULT 3
 IL17B_HUMAN
 ID IL17B_HUMAN STANDARD; PRT; 502 AA.
 AC Q9NRM6; Q9BP20; Q9NR4; Q9NR5;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Interleukin-17B receptor precursor (IL-17B receptor) (IL-17 receptor homolog-1) (IL-17R1) (IL17R1) (Cytokine receptor CR14).
 GN IL17B OR EV127
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RA Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A., Copeland N.G., Shaugnessy J.D. Jr.;
 RT "Ev127 encodes a novel membrane protein with homology to the IL17 receptor."
 RL Oncogene 19:2098-2109(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF N-TERMINUS.
 RC TISSUE=Lung;
 RX MEDLINE=20317118; PubMed=10749887;
 RA Shi Y., Ullrich S.J., Zhang J., Connolly K., Grzegorzewski K.J., Barber M.C., Wang W., Wathen K., Hodge V., Fisher C.L., Olsen H., Ruben S.M., Knyazev I., Cho Y.H., Kao V., Wilkinson K.A., Carrell J.A., Emer R.;
 RT "A novel cytokine receptor-ligand pair. Identification, molecular characterization, and in vivo immunomodulatory activity."
 RL J. Biol. Chem. 275:19167-19176(2000).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Zhang W., Cao X;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Cervix;
 RA Strausberg R.;

RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RX PubMed=11058597;
 RA Lee J., Ho W.H., Maruoka M., Corpuz R.T., Baldwin D.T., Foster J.S., Goddard A.D., Yansura D.G., Vandlen R.L., Wood W.I., Gurney A.L.;
 RT "IL-17E, a novel proinflammatory ligand for the IL-17 receptor homolog IL-17R1."
 RL J. Biol. Chem. 276:1660-1664(2001).
 CC -1- FUNCTION: Receptor for the proinflammatory cytokines IL17B and IL17E. May play a role in controlling the growth and/or differentiation of hematopoietic cells.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1); Secreted (isoform 2).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here), and 2; are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Expressed in several endocrine tissues, mostly in fetal and adult liver, kidney, pancreas, testis, colon, brain and small intestine; not detected in peripheral blood leukocytes, lymphoid organs, and most cell lines.
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 DR EMBL; AF208110; AAF6051.1;
 DR EMBL; AF208111; AAF6052.1;
 DR EMBL; AF212365; AAF7876.1;
 DR EMBL; AF250309; AAK37428.1;
 DR EMBL; AF250380; AAH00980.1;
 DR Genbank; HGNC:18015; IL17BR.
 DR MIN; 605458;
 KW Receptor; Transmembrane; Signal; Glycoprotein; Alternative splicing.
 FT SIGNAL 1 17
 FT CHAIN 18 502 INTERLEUKIN-17B RECEPTOR
 FT DOMAIN 18 292 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 293 313 POTENTIAL.
 FT DONAIN 314 502 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 67 67 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 103 103 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 283 283 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARSPPLIC 250 288 LTPYFPCGSDCIHKGTVLGRGVFPFLDNKSKPG
 FT > VKFSELWGGHRRHFLHSLLRSLSSLLNALLPAUT
 FT S (IN ISOFORM 2).
 FT MISSING (IN ISOFORM 2).
 FT L -> I (IN REF. 1).
 FT LFPLA -> SSPCL (IN REF. 2).
 FT MISSING (IN REF. 2).
 FT L -> F (IN REF. 1).
 FT SEQUENCE 502 AA; 55884 MW; CDB87586FAAE49CC CRC64;
 Query Match 3.4%; Score 135.5; DB 1; Length 502;
 Best Local Similarity 20.1%; Pred. No. 0.0078;
 Matches 76; Conservative 49; Mismatches 141; Indels 113; Gaps 14;
 QY 218 NLNLSQSGSDMQVSF-----DHAPHNFGFRFFVYHKLKHEGPFPRKTC----- 261
 Db 143 NANNEDGPKSNVNFSPGCLDH-----IMTKY-----KKCVKAGSLMDPN 183
 QY 262 -----KQQTTE---TTSCLQNVSPGDIYIELVDYDNTNTRKVMHYALPVSPWAGPIR 313
 Db 184 ITACKNEETVEVNFITPL-----GNRYNALIQHSTI-----IGFSQVFPEPKKQT 231
 QY 314 AVAITPLVVISAFATL-----FTVMCRKQKQENIYSHLDESSSESS 355
 Db 232 RASVIVPTGDSBGATVQLTPYFPTCGSDCIHKGTVLVC---PQTGVFPFLDNKSKPG 288

356 TITAA-----PRELR-----PRKVFCTSSKDGQNHNN 386
 Db 289 GNPILLISLVATVWVAGYILWVHERIKKTSFTVTLPLPKVLVWVFPSEICFHH-- 346
 QY 387 VVOCFAFLDPCGCEVALDWFDSICRGOREVIOKIHESFIIVVCSKGYFVK 446
 Db 347 TICITFEFLONCESEVILEKWKKIAENGPPQWLATYKRAKQVFFLLSDVNSVCDG 406
 QY 447 KTKKGGGSGGGEFLVAVSAIAEKLROAKOSSAALSFKTAVTFDSCGDVPGIL 506
 Db 407 TCKSGSPSENQ-DLFFPLAFNLCSDLR-----SQHLKHYVWVYFREIDTKDDYNAL 460
 QY 507 DLSIKYRLMDNLPOLCSHL 525
 Db 461 SVCPRYHLAKDATAFCAEL 479

RESULT 4
 ID YS02 CAEL STANDARD; PRT; 718 AA.
 AC Q10128;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Hypothetical 81.6 kDa protein F56D1.2 in chromosome II precursor.
 GN F56D1.2
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodermidae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol W2;
 RA Chisoe S., Wilson R.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
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 or send an email to license@isb-sib.ch).
 CC EMBL; U39997; AAA81100.1;
 DR WormPep; F56D1.2; CE01970.
 KW Hypothetical protein; Transmembrane; Signal.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 718 HYPOTHETICAL PROTEIN F56D1.2.
 FT TRANSMEM 373 393 POTENTIAL.
 SQ SEQUENCE 718 AA; 81622 MW; 4289E056288417AA CRC64;

Query Match 3.24; Score 126.5; DB 1; Length 718;
 Best Local Similarity 21.18; Pred. No. 0.064;
 Matches 82; Conservative 64; Mismatches 149; Indels 94; Gaps 19;
 QY 363 REELRPRP-----KVFATYSSKDGQNHNNVQCFAYFLQFCGCEVALDWFDS 412
 Db 398 RDKVRSREVRNIALTEFFKVMIVTAD-DNDLHDCVKLVLENLRCASCDPVDFLEKLIT 456
 QY 413 LCRGORENVIOKIHESQFIIVVCSKGYFVDKKNYKHGGGSGKGEFLVAVSAIA 472
 Db 457 ABOIVPSRWLVQISSLAKFIIVVSDCAEKILDTSETHOLVQARFADLFGPMENI- 515
 QY 473 EKLROAKOSSAALSFKTAVTFDSCGDPV---GILDSTKYRLMDNLPOLCSHLRSR 529
 Db 516--IRDATNFPKARKVAVRENTS--PVPVPMALNLPF-FILPEQFAQLTAFLNVE 570
 QY 530 HGLOEPGQHTGSGSRNVPFSKGRSLY---VAICMHOQIDEEPWFQKQFVP----- 580
 Db 571 H-----TERANNVTQIRISQAQIHEWNLCSGMSFFVRPNWLETRWPKPDLEAA 619

QY 581 FHPPLATYREPVLKEDSGIIVLVCKPSPESDFCLKVEAVLGGATGADSGHESORGG 640
 Db 620 LH---LKRQSPVIVPIOT-----EED---RIAASIKYINLVPPQALVDS--- 657
 QY 641 LDQGEARPALDGSAMALQPLHETVTRAGSPSON--PRSGIYDSSVSPSELSLPLMEGLST 698
 Db 658 -DED-----DVLQPP--FASHONQPLILPPECG-----PDS-SD 690
 QY 699 DQETSSLTSSVSSSGGEEPPALPSK 727
 Db 691 SESDSSSESESDNEG---EDPKTIIVK 716

RESULT 5
 ID EPB3 HUMAN STANDARD; PRT; 998 AA.
 AC P54753;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ephrin type-B receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein
 DE kinase receptor HEK-2).
 GN EPB3 OR ETK2 OR HEK2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RC MEDLINE=93330963; PubMed=8397371;
 RA Boehme B., Holtrich U., Wolf G., Luzius H., Grzeschik K.-H.,
 RA Streibhardt K., Ruebsamen-Waigmann H.;
 RT PCR mediated detection of a new human receptor-tyrosine-kinase, HEK
 RT 2.;
 RL Oncogene 8:2857-2862(1993).
 CC 1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. BINDS TO
 CC EPHRIN-B1 AND -B2.
 CC 2- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 CC tyrosine phosphate.
 CC 3- SUBCELLULAR LOCATION: Type I membrane protein.
 CC 4- TISSUE SPECIFICITY: UBIQUITOUS.
 CC 5- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC 6- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC 7- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 CC RECEPTOR SUBFAMILY.

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 CC EMBL; X75208; CAA53021.1;
 CC HSSP; P29323; I84F.
 CC Genew; HGNC:3394; EPB3.
 CC MIM; 601839;
 CC InterPro; IPR001090; Ephrin_receptor.
 CC InterPro; IPR000719; Euk_pkinase.
 CC InterPro; IPR003961; FN_III.
 CC InterPro; IPR003962; FN_III_repeat.
 CC InterPro; IPR001660; SAM.
 CC InterPro; IPR001245; Tyr_pkinase.
 CC InterPro; IPR001426; YKase_receptor.
 CC Pfam; PF00041; fn3; 2.
 CC Pfam; PF00069; pkinase; 1.
 CC Pfam; PF00536; SAM; 1.
 CC Pfam; PF01404; EPH_LBD; 1.
 CC PRINTS; PR00014; FNTYPEIII.
 CC PRINTS; PR00109; TYRKINASE.
 CC ProDom; PD000001; Euk_pkinase; 1.

Query Match 2.9%; Score 115; DB 1; Length 998;
Best Local Similarity 19.0%; Pred. No. 0.78;
Matches 158; Conservative 122; Mismatches 301; Indels 250; Gaps 42;

35	QY	GADTCGRKAKAAARPLC-----VANEGVGPA-----SRNSG-----LYNIFK 73
267	Db	GACTCATGHEPAAKASCPCPGPGYAKAQEGPCFLCPNPSRTTSPAASICTCHNNPFR 326
74	QY	YDN-----CITYLNPVGHVIADQAQNTISQYACHDQAVAVILWS-PGALGTFLKGR 126
327	Db	ADSDSANDSACTVESP-PRGYSLN-----NETSLILENSEPRDLGVDRDILLN 374
127	QY	VILEELKSEG-----RCQQLILKDPQOLANSFKFTGMESQFLMKFETDYFKVVPVP 181
375	Db	VICKCHGAGAGASACSDONVEFFVPGLGSLSEPRVTS-----HLAARTYTFEYOAVN 429
182	QY	SKINESNHPFFPTRACDILLQPNLACKPFWKPRRLNISQBGSDMOWSFDAHPNFCF 241
430	Db	GVSGKSLPPRYAAVNITTTNQAAPEV-----PTLRHSSGSGSLTSLWAPERPNG- 481
242	QY	RFTYLYKIKHEGP-KRKTCEQOETTTSCILLQNVSP-GOYIELVDOTNTRVMHY 299
482	Db	-VILDYEMKY-----FKRSGEIASTVTSOMNSVQLGRDPARYVQV-----BARTVAGY 531
300	QY	A--LKPVE-----SPWAGPRAVAIVTVPWLWISAFATL-----FTVMCKKQOENIYS 345
532	Db	QYTSRPAEFETTSERGGAQIQEQPLPLVGSATAGLVFVVAVVVIAIVCLKQRE- 587
346	QY	HLDERSSSSYTTAALPRELPRKVPCLYCKSDQONHNWVQCFAFYIQDFC-GCEVA 404
588	Db	-----GSDSYTEKL-QYLIAPGMKVYIDPFYEDPN--EAVREFAKEIDVSCVRIEY 638
405	QY	LQIWEDFSLCQREGRENVQIKIHESQFIIVVCSKMGKFPVDKNKYKKGQSGRGSGKELF 464
639	Db	IGAGEFGVCR-----GRKQPGRGREVF 661
465	QY	LYAVSAI-----AEKLQAKQSSAALSKFIAVDFYSCBQDVPGLDLS--TKYR----- 513
662	Db	-NAIKTLKVYTERQRERDPLFSAASINGF-----DHPNIIIRLEGVWTKSPVMI 709

514 QY ---LADNLPOLZSHLSHDGLOBPQOHT-----RQSRRT-PRSKGR 554
710 DDB LTFEMNC-ALDSFLRLND-----GQFTVIQVGMAGTIAAGKYLSEKYNVHRDLAAR 762
555 QY ---SLIV---AIC---NMHQFIDEEPWFQKQVPPHP-----PLRYREP---VLEKFD 597
763 DDB NILVNSLNCKVSDRGLSRFLEDDPS-----DPTTSSLGKIPKWTAPAEIAIRKFT 816
598 QY S-----GLVLNDVCKPGPESDFCLKVEANVLGATCPADSOHQHGGLODGEARPA 650
817 DDB SASDWSYGIWMEVMS-----YGERPYWGMNQDVINAVSQDTRLPP 860
651 QY LDGSAMLOPILHTVKAGSPMDPRDSGIYDS-----SVPSSELSLPLMEGL 696
861 DDB MDCPTALHGLQJDCWVRDNLRFKFSQYVNTLKLIRNAASLKVYASQSGNSQPLDRT 920
697 QY STQDTSTSLTSSVSSSGGLGEEPPALPSKILLSCGCKADLCGRSYTDEL 747
921 DDB VPDYTFVTVGMDLAIK-MGRYK-----ESFVSAGFASFDVAQTAEDL 965

RESULT 6

IL17S MOUSE

IL17S_MOUSE STANDARD; PRT: 499 AA.

Q9JIP3; Q9JIP2;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Interleukin-17B receptor precursor (IL-17B receptor) (IL-17 receptor homolog 1) (IL-17R1) (IL17RH1) (IL-17R) (IL-17R or EV127).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
[1]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE=2073223; PubMed=10815801;
Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A., Copeland N.G., Shaughnessy J.D. Jr.,
"Ev127 encodes a novel membrane protein with homology to the IL17 receptor."
Oncogene 19:2098-2109(2000).
-1- FUNCTION: Receptor for the proinflammatory cytokines IL17B and IL17E. May play a role in controlling the growth and/or differentiation of hematopoietic cells.
-1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1); Secreted (isoform 2).
-1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.
-1- TISSUE SPECIFICITY: Liver and testis. Expressed at lower level in kidney and lung. Expressed in selected T-cell, B-cell and myeloid cell lines.
-1- MISCELLANEOUS: EV127 is a common site of retroviral integration in BXH2 murine myeloid leukemias, localized near the IL17BR gene. Proviral integrations result in increased expression of IL17BR on the cell surface.

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EMBL: AF208109; AAF86049.1;
EMBL: AF208109; AAF86050.1;
MGD: MGI:1355292; IL17br.
Receptor; Transmembrane; Signal; Glycoprotein; Alternative splicing.
SIGNATURE 1 17 BY SIMILARITY
CHAIN 18 499 INTERLEUKIN-17B RECEPTOR.

FT DOMAIN 18 286 EXTRACELLULAR (POTENTIAL)
 FT TRANSFEN 287 307 POTENTIAL
 FT DOMAIN 308 499 CYTOPLASMIC (POTENTIAL)
 FT CARBOHYD 67 67 N-LINKED (GLCNAC) (POTENTIAL)
 FT CARBOHYD 103 103 N-LINKED (GLCNAC) (POTENTIAL)
 FT CARBOHYD 156 156 N-LINKED (GLCNAC) (POTENTIAL)
 FT CARBOHYD 157 197 N-LINKED (GLCNAC) (POTENTIAL)
 FT VARSPLIC 163 218 LRVYKIKKCTGCTGSLNDPDIACKKKNWVNTNPL
 FT SAPPLOPPGGSDVILPPOPPLASLPHDFVKLT (IN
 FT ISOFORM 2)
 FT VARSPLIC 219 499 MISSING (IN ISOFORM 2)
 FT SQ SEQUENCE 499 AA: 55617 MW: C66440430E3C31F3 CRC64;

Query Match 2.8%; Score 110.5; DB 1; Length 499;
 Best Local Similarity 24.1%; Pred. No. 0.66;
 Matches 40; Conservative 27; Mismatches 82; Indels 17; Gaps 4;
 QY 355 STYTAALPRERLRPRKFLCYSSKQGNHNVQCFAYFLQDFGCGEVALDLWEFSLC 414
 DB 314 STKTSPISTMLPLIKLVVYPSEICFHH--TVCFRTDFLQNYCRSEVILEKWKKKKA 371
 QY 415 REGOREWIKTHESQFTIVVCSKMKRYFYDKNTKHKGGGSGKGLFLVAVSAIAEK 474
 DB 372 EMGPVQMLTQKQAKVFLPSDVTPLDSCAGHNSGARSNSQ--DLFPLAFNLFCS 430
 QY 475 LROAKSSAALSRELIANYDYSCGVDPCILDLSLTKYLMNLPQ 520
 DB 431 F-----SSQTHLKLIVYL-----GGADLGDYNAISVCPQ 462

RESULT 7
 STB3_MOUSE
 ID STB3_MOUSE STANDARD; PRT: 592 AA.
 AC Q60770;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Syntaxin binding protein 3 (UNC-18 homolog 3) (UNC-18C) (M0NC-18-3).
 GN STXB3 OR UNC18C.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95197608; PubMed=7890715;
 RA Tallam J.T., McIntosh S., James D.E.;
 RT "Molecular identification of two novel Munc-18 isoforms expressed in
 RL J. Biol. Chem. 270:5857-5863(1995)."
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN-BALB/c; TISSUE=Brain;
 RC MEDLINE=96421662; PubMed=8824310;
 RA Gengyo-Ando K., Kitayama H., Mukaida M., Ikawa Y.;
 RT "A murine neural-specific homolog corrects cholinergic defects in
 CC Cnora1b-deficient mice." J. Neurosci. 16:6693-6702(1996).
 CC J. Neurosci. 16:6693-6702(1996).
 CC -1- TISSUE SPECIFICITY: OBVIOUSLY EXPRESSED.
 CC -1- SIMILARITY: BELONGS TO THE STXB3/UNC-18/SEC1 FAMILY.
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 CC or send an email to license@sib-sib.ch).
 CC EMBL: U19521; AAA69913.1;
 CC EMBL: D30798; BAA19478.1;
 CC MGD: MGI:107362; Stxbp3.

DR InterPro: IPR001619; Sec1-like.
 DR Pfam: PF00995; Sec1-like.
 KW Protein transport.
 SQ SEQUENCE 592 AA: 67942 MW: 7874B71DE107871A CRC64;
 Query Match 2.7%; Score 110.5; DB 1; Length 592;
 Best Local Similarity 18.5%; Pred. No. 0.92; Indels 188; Gaps 22;
 Matches 93; Conservative 64; Mismatches 157; Indels 188; Gaps 22;
 QY 321 LVVTSAFATLTVNCRKKQ-----ENTYSHLEESSESTYTAALPRERLRPRK 371
 DB 34 IMLEDEFTKLLSCCKNTDLLEGITVIENTYKREPVOMKALYF-----ISPTPK 86
 QY 372 VFICYSSKQGNHNVQCFAYFLQDFC-----GCE----- 402
 DB 87 SVDCFLRDFGSKSEKKYKAAIYFTDFCPDSLNNKIKASCSTIRCKEINISFIPQESQ 146
 QY 403 -VALDIEDFSLC-----REGOREWIKTHESQFTIVV-----SKMKY----- 442
 DB 147 VTLVDPAFTYCYSPDPSNASRKYVMEAMAO--IVTVCATLDENPGVYKSKPLDNA 204
 QY 443 -----FVDKK---NFK--HKGGRSGSGKGLFLV-----AVSAIAEKLRQAKSSAALS 487
 DB 205 SKLAOLVEKKLEDDYKIDKGLIKGTQSOLAIIDRGDFPVSTVLHEL----- 252
 QY 488 KEIANYFD-----YSCG-DVPGIL-----DLSTKYR-----LADNLPOLCSHLH 526
 DB 253 TFOAMAYDLLPIENDYTKYTKDCKEAVLEDDDLVYVVRHRIAVVLEIPKLAKEIS 312
 QY 527 SDHGLOPEGOHTROGSRNRYFRSKSLYVAINKHQFIDEPDWFEKQFVPPHPP 586
 DB 313 STK-----KATEGKTSLSALTQLMKMKPHRKQISKQVY-----HL 348
 QY 587 RYREPVLKFF-----DSGLVNDVMCKPGPESDFCLKVE 620
 DB 349 NLAEQCNKKFKLNEKLECKTEQDLALGDAEQVCKDSMLVLLPVL--NKNENDCKIR 406
 QY 621 AAVLGATGPADQSIESHQGLQDGEARPDGSAALQPLHTVYKAGSPSDPRD-SGII 679
 DB 407 AVLLYIFGINTTEEN-----LDRLHNHYKTEDSDMIRNWSHLG 446
 QY 680 DSSVPSESLSLPMEGLSTQDT 701
 DB 447 VPVPPSOAKPLKDRSAEET 468

RESULT 8
 PTP6_DROME
 ID PTP6_DROME STANDARD; PRT: 1462 AA.
 AC P16620;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protein-tyrosine phosphatase DPTP precursor (EC 3.1.3.48) (Protein-
 DE tyrosine-phosphate phosphohydrolase).
 GN PTP6SD OR DPTP.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90046860; PubMed=2554325;
 RA Struelli M., Krueger N.X., Tsai A.Y.M., Saito H.;
 RT "A family of receptor-linked protein tyrosine phosphatases in humans
 CC and Drosophila."
 CC Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).
 CC -1- FUNCTION: IT IS POSSIBLE THAT DPTP IS A CELL ADHESION RECEPTOR.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O -> protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

QY 136 RVILEELKSGROCOOL-ILKD---PKQLNSFKRTGME---SQPFLMKPFEDYFVK 176
 DB 243 QVTFSLAEAEVVOOLHVLVNFELRPLRMAASKEPITHDDVSSIFLNS--ETINFLH 300
 QY 177 VVPFSPKSNESVHPFFPFRACDILLQPNLACKPMPKRNLTISO---HGSMDVOVS 231
 DB 301 QIFTQGLKARISWPLVLAIDLILP-----MLNYQEFVNHQYSQI- 346
 QY 232 FDHAPHNGFRFFLYLHKHSGPPKRTKQBOETTFSCLLQNVSGDYIIEVD--- 288
 DB 347 LAHQKQRDRDKLKHYEAKPD-----C-EETLETFYTFMQIP-RYILTLHDVLA 397
 QY 289 ---DNTTRKVMYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVNCRKQOENIYS 345
 DB 398 HYPEHVERNSLOYA-----KSKLEELSR 421
 QY 346 HLDSESESTYTAALPRELRPRKVPCLYSSKQGNHNVVOCEAYFLQDFQCEVAL 405
 DB 422 IMHDEVSEYENIRKNLAIERM-----IIE-----GCEILL 451
 QY 406 DLWEDF-----SLCRGQREWVQIKIHESQFIYVVCSEGM 440
 DB 452 DTSQTFVROGSLQVPMSEKGIKTRGLSGLSLEKEGECQFLSKH-----LIICTRGS 506
 QY 441 ---KVFYDKNY-----KKGKG-----RGSKGGELETA 467
 DB 507 OGKLELTKNGVISLICTLLEPSTEEAKGSGQDIDHDFKIGVPEKSPPTVILVA 566
 QY 468 VSAIAELKRAQSSAALSKEFIAYFYDSCBVDGVLGDLSTKYKLMNDLPQCSHLHS 527
 DB 567 SS-----ROKAANTSDISQCD---NIRCNGLAMNAFEENSKV---TVPQMI- 608
 QY 528 RDHGLQPGQHTQSGRRNYFYSKSGSLY 557
 DB 609 -----KRTREGTREEM-SRSDASLY 628

RESULT 12
 ID RG66_HUMAN STANDARD; PRT; 974 AA.
 AC Q43182; Q43437; Q9P1B3; Q9UK81; Q9UK82;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Rho-GTPase-activating protein 6 (Rho-type GTPase-activating protein
 DE RhoGAP2-1).
 GN ARGAP6 OR RHOAP6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., REVISIONS, FUNCTION, SUBCELLULAR LOCATION, AND
 RP ALTERNATIVE SPLICING.
 RC TISSUE-Fetal kidney;
 RX MEDLINE=40184286; PubMed=10699171;
 RA Prakash S.K., Paylor R., Jenna S., Lamarche-Vane N., Armstrong D.B.,
 RA Xu B., Mancini M.A., Zoghbi H.Y.;
 RT *Functional analysis of ARGAP6, a novel GTPase-activating protein for
 RT RhoA*.
 RN Hum. Mol. Genet. 9:477-488(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=98086484; PubMed=9417914;
 RA Schaefer L., Prakash S.K., Zoghbi H.Y.;
 RT *Cloning and characterization of a novel rho-type GTPase-activating
 RT protein gene (ARGAP6) from the critical region for microphthalmia
 RT with linear skin defects*.
 RL Genomics 46:268-277(1997).
 CC -1- FUNCTION: GTPASE ACTIVATOR FOR THE RHO-TYPE GTPASES BY CONVERTING
 CC THEM TO AN INACTIVE GDP-BOUND STATE. COULD REGULATE THE
 CC INTERACTIONS OF SIGNALING MOLECULES WITH THE ACTIN CYTOSKELETON.
 CC PROMOTES CONTINUOUS ELONGATION OF CYTOPLASMIC PROCESSES DURING

CELL MOTILITY AND SIMULTANEOUS RETRACTION OF THE CELL BODY
 CHANGING THE CELL MORPHOLOGY.
 -1- SUBCELLULAR LOCATION: Cytoplasmic.
 -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: 1, 2, 3 (SHOWN HERE), 4 AND 5;
 -1- ARE PRODUCED BY ALTERNATIVE SPLICING
 -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN KIDNEY, HEART AND SKELETAL
 MUSCLE FOLLOWED BY RETINA, LYMPHOBLAST, PLACENTA, LONG, BRAIN,
 PANCREAS AND LIVER.
 -1- DISEASE: DEFECTS IN ARGAP6 MAY BE A CAUSE OF MICROPHthalmia WITH
 LINEAR SKIN DEFECTS (MLS), A DOMINANT MALE-LETHAL DISORDER
 CHARACTERIZED BY EYE, SKIN AND CENTRAL NERVOUS SYSTEM (CNS)
 MALFORMATIONS.
 -1- SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.
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 or send an email to license@sib-sib.ch).
 ENBL: AF117067; AAF43261.1;
 ENBL: AF177663; AAD53166.1;
 ENBL: AF177665; AAD55087.1;
 ENBL: AF012272; AAC98539.2;
 ENBL: AF022212; AAC98540.2;
 HSP: Q07960; IRGP.
 Gene: HGNC:676; ARGAP6.
 MIM: 300118;
 MIM: 309801;
 InterPro: IPR000198; RhoGAP.
 Pfam: PF00620; RhoGAP; 1.
 SMART: SM00324; RhoGAP; 1.
 Alternative splicing: GTPase activation; SH3-binding.
 SITE 342 352
 DOMAIN 411 564
 FT VARSPLIC 1 203
 FT VARSPLIC 196 196
 FT VARSPLIC 637 658
 FT VARSPLIC 659 974
 FT VARSPLIC 726 765
 FT VARSPLIC 766 974
 FT CONFLICT 231 231
 FT SEQUENCE 974 AA; 105973 MW; 7FD63AE78720DB25 CRC64;
 Query Match 2.5%; Score 100.5; DB 1; Length 974;
 Best Local Similarity 18.68; Pred. No. 9.9;
 Matches 178; Conservative 99; Mismatches 294; Indels 385; Gaps 46;
 QY 27 AGGSGRARGAUTCGRMKA-----AARPLCVANGVGPASRN----- 64
 DB 51 AGAEGSARGA-TAG-RLYSPSLPAESLGRPLASSRSGPPPPRATRLPPPGPLCSFSFSTP 108
 QY 65 -----SGLYNTTFKYDCTTLPVGV-----KHVIADQANITISQYACHQDVAVILWS 113
 DB 109 PQEKPSG-----SPHFD-----YEVPLGRGGLKSKMADLPVLAGPASSRSASSILCSSG 160
 QY 114 PGALGIEFLKGRVILEELKSGROCOOLILKOPKOLNSFFRTGMSQPLMKPFEDY 173
 DB 161 GPGNGI-----FASPREWLQKQFQSPD-----SRGHPIVVMKSGDP 199
 QY 174 F-----VKYVFPFSIKNESNYH-----PFFETRACDILLQ-----PDNLACPFVK 215
 DB 200 TWSNMSGRSVRLRSVPDIQSLSELERARLQEVPTQLQDCDLSCQITIPKDGRRK-K 256
 QY 216 PRMLNISQSGSDMQVSPFDHAPHNGFRFFYL-----HYELKHE-----G 254
 DB 257 SLRKKLSDLSGKKNKDEKFIQAFGMPLSVIANDRAYKADQLQDRQKADSDVASLL 316

QY 255 PFRKTCQE-----OTETTSCLQNVSG-----DYIELVDV 289
 Db 317 PFGKRNKELSSNSLSSTETPN---ESTSPNTPPPARRRGMVSVDITLDON 373
 QY 290 TNRKRVH-----YALKVPHSPNAGPIRAVAITVPLVVISAPATL- 330
 Db 374 QSLLEALQLSLPAAQSKKEKARDKLSLNDIYR-----QVPLVDSCQHLE 422
 QY 331 -----FTVCKKQOENIYSHLDE-----SSSESTYTAALPRELRPRKVEL- 374
 Db 423 AKGLQTVGFRVSGSKRVRQLREDFORDIVSLSEHSVDVAALKKEFLRMDPPLT 482
 QY 375 -CYAS-----KQGNHNVQCFATFLQDFGCEVALQWE-----DFSICRG 417
 Db 483 RELITAFINTLLPEPQGLTQLLIYLLPP-CNCDTLRLLOFLSVARHADNDISKDG 541
 QY 418 Q-----REWVIO-----KIHESQFIIVVCSKGMKYFVDK 446
 Db 542 QEVTKGNTSLNATIFGNLLKOKSKDEFSVQSARAEESTALLAVVQKMI----- 595
 QY 447 KTKKGGGRSGKGLFLVAVNAEKL-----ROAKOSSAAL----- 486
 Db 596 ENVE-----ALFVPPDLQNEVLISLETDPDVPDYLLRRKASQSSPDMLQSE 644
 QY 487 -----SKFIATVFDYSCGD-----VFGILD 507
 Db 645 VFSVSGRHSSTGSKASSGDISPYDNNSPVLRSLLAMQEDAAPGSEKLYRVPGQM 704
 QY 508 L-----STYKRLMDLPLQCSHL-----HSR-DHGLQPGQFTROGSRNYS 550
 Db 705 LVGLHSSKRSRSPGRLKDLSEPPDINGTWSTLKSQKPGM---TGSQDIFES 761
 QY 551 KGRSLIVAINCMHQFIDEPPWFKEQFVFFHPPLRYREPVLEKFDGSLVNDVMCKRP 610
 Db 762 S-----SLRAGPCSLSG-NLSPNRPWQSGP-----AELDS-----792
 QY 611 PESDFCLVEAAVLGATGPADSQSHQSGHGLDQGEARPDALDGAALQPLHVVKAGSPS 670
 Db 793 -DTQAGARTQA-----APA-----TEGRAHPAVSRACSTPHVYVAGKAERT 834
 QY 671 DMPRD-----SGIYSSVPSSELSPLMEGLSTDQFTSTLSTESVSSSGGEEPP 722
 Db 835 ARSEQTLTSGAHLDS-ESELDVAGLSRATPQCOR-----PHGSGRDKRPP 881

RESULT 13

Z151_MOUSE STANDARD; PRT: 794 AA.
 AC Q60821; Q60699;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Zinc finger protein 151 (Polymavirus late initiator promoter binding protein) (fp-1) (Zinc finger protein z13).
 GN ZNF151 OR ZFP100.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid-10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rapp L., Carmichael G.G.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CBA; TISSUE-Kidney;
 RA MEDLINE-96003919; PubMed-7575457;
 RA Schulz T.C., Hopwood B., Rathjen P.D., Wells J.R.E.;
 RT An unusual arrangement of 13 zinc fingers in the vertebrate gene
 RT z13.;
 RL Biochem. J. 311:219-224(1995).
 CC -1- FUNCTION: MAY FUNCTION AS A HOUSEKEEPING DNA-BINDING PROTEIN THAT

CC REGULATES THE EXPRESSION OF SPECIFIC GENES.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -1- TISSUE SPECIFICITY: FOUND IN ALL THE EMBRYONIC AND ADULT TISSUES EXAMINED.
 CC -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
 CC -1- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
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 CC EMBL; U22396; AAA64848.1;
 CC EMBL; U14556; AAA85493.1;
 CC BSSP; P08046; IAH.
 CC MGP; MGI-107410; Zfp100.
 CC InterPro; IPR000210; BTB_POZ.
 CC InterPro; IPR000822; Znf_C2H2.
 CC Pfam; PF00096; zf-C2H2; 13.
 CC Pfam; PF00631; BTB; 1.
 CC PRINTS; PR00048; ZINC_FINGER.
 CC ProDom; PD000003; Znf_C2H2; 1.
 CC SMART; SM00225; Zfp_C2H2; 13.
 CC SMART; SM00355; Znf_C2H2; 13.
 CC PROSITE; PSS0097; BTB; 1.
 CC PROSITE; PS00028; ZINC_FINGER_C2H2_1; 13.
 CC PROSITE; PS00157; ZINC_FINGER_C2H2_2; 13.
 CC Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
 KW Nuclear protein; Repeat.
 FT DOMAIN 1 104 BTB.
 FT ZN_FING 297 730 ZINC_FINGERS.
 FT ZN_FING 297 319 C2H2-TYPE.
 FT ZN_FING 325 347 C2H2-TYPE.
 FT ZN_FING 353 375 C2H2-TYPE.
 FT ZN_FING 381 403 C2H2-TYPE.
 FT ZN_FING 409 431 C2H2-TYPE.
 FT ZN_FING 437 459 C2H2-TYPE.
 FT ZN_FING 465 487 C2H2-TYPE.
 FT ZN_FING 493 515 C2H2-TYPE.
 FT ZN_FING 519 543 C2H2-TYPE.
 FT ZN_FING 549 571 C2H2-TYPE.
 FT ZN_FING 577 599 C2H2-TYPE.
 FT ZN_FING 605 628 C2H2-TYPE.
 FT ZN_FING 708 730 C2H2-TYPE.
 FT CONFLICT 507 507 G -> A (IN REF. 2).
 FT CONFLICT 573 573 N -> K (IN REF. 2).
 SQ SEQUENCE 794 AA; 86664 MW; FFF8E56DEBFFED CRC64;
 Query Match 2.5%; Score 99.5; DB 1; Length 794;
 Best Local Similarity 20.6%; Pred. No. 8.9;
 Matches 71; Conservative 41; Mismatches 146; Indels 87; Gaps 15;

QY 399 CGCEVALDLEDWEDSLCREGQRENVQIKIHESQFIIVVCSKGMK-YFVCKKQOENIYSHLDE-----SSSESTYTAALPRELRPRKVEL- 457
 Db 24 CDTFFVD-GVDF-----KAKKA-VLACSETFKMLFDVDRDVLVDISNA 67
 QY 458 SKGGEFLVAVSAIAEKLROAKOSS-----AALSKFIATVFDYSCGDVPGILDST 510
 Db 68 AGLAQ-----VLEFMTAKLSLSPENVDDVLAVASFQMQ-----DVT 106
 QY 511 KYRLMDNLPLQCSHL-HSRDHGLQPGQH-----TROGSRNRYFKSKRSLY 557
 Db 107 ACHYLKSLAEPSTTGESADASAVEGGDKRAKDAKAATMLSRIGQARSSSTGPGRELK 166
 QY 558 VAICNMHQFIDEPPWFKEQFVFFHPPLRYREPVLEKFDGSLVNDVMCKRPGSPDCL 617
 Db 167 EERGGQAESASSGAQTEKADAPREPP-----VELKPDPTSSNA- 206
 QY 618 KYEAVLIGATGPADSQSHQSGHGLDQGEARPDALDGAALQPLHVVKAGSPDPRDSG 677

DB 207 AAEALSSBDEMEVEPASKG--EDQEEGAGPATVKEGMB-LONGEPPEENESA 263
 QY 678 YDSSVPSLSLP---LAEGLSDTSTSLATESVSSSSGLGEE 719
 DB 264 GTDS--GQELGEGNLSGYGDRSKAYGSIHKCEDGKE 305

RESULT 14

ID ZFY2_MOUSE STANDARD: PRT: 783 AA.
 AC P20662;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Zinc finger Y-chromosomal protein 2.
 GN ZFY2.OR.ZFY-2.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89168416; PubMed=2493989;
 RA Mardon G., Page D.C.;
 RT "The sex-determining region of the mouse Y chromosome encodes a
 RT protein with a highly acidic domain and 13 zinc fingers";
 RL Cell 56:765-770(1989).
 CC -1- FUNCTION: PROBABLE TRANSCRIPTIONAL ACTIVATOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC
 CC FINGER PROTEINS. ZFY/ZFY SUBFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EXBL; M24401; AAA56845.1;
 DR PIR: A31491; A31491.
 DR HSP: P08048; 5ZNF.
 DR MGD: MGI:99213; ZFY2.
 DR InterPro: IPR000822; Znf_C2H2.
 DR Pfam: PF00096; Zf-C2H2; 13.
 DR PRINTS: P000048; ZINC_FINGER.
 DR PRODOM: PD000003; Znf_C2H2; 1.
 DR SMART: SM00355; ZNF_C2H2; 13.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 7.
 DR PROSITE: PS00157; ZINC_FINGER_C2H2_2; 10.
 KW Transcription regulation; Activator; zinc-finger; Metal-binding;
 KW DNA-binding; repeat; Nuclear protein.
 FT DOMAIN 372 382 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 403 777 ZINC FINGERS.
 FT ZN_FING 403 425 C2H2-TYPE.
 FT ZN_FING 434 456 C2H2-TYPE.
 FT ZN_FING 466 488 C2H2-TYPE.
 FT ZN_FING 497 520 C2H2-TYPE.
 FT ZN_FING 526 548 C2H2-TYPE.
 FT ZN_FING 554 577 C2H2-TYPE.
 FT ZN_FING 583 605 C2H2-TYPE.
 FT ZN_FING 611 634 C2H2-TYPE.
 FT ZN_FING 640 662 C2H2-TYPE.
 FT ZN_FING 668 691 C2H2-TYPE.
 FT ZN_FING 697 719 C2H2-TYPE.
 FT ZN_FING 725 748 C2H2-TYPE.
 FT ZN_FING 754 777 C2H2-TYPE.
 SQ SEQUENCE 783 AA; 88856 MW; 1722D1C23F019DF8 CRC64;

Query Match 2.5%; Score 99; DB 1; Length 783;
 Best Local Similarity 19.2%; Fred. No. 9.6;

Matches: 117; Conservative: 74; Mismatches: 207; Indels: 210; Gaps: 34;
 QY 71 TPKINDCTYILNPYGVKRVIAADQNIITISOTACHDOVAVTILWSPALGIEFLAGFVRVILE 130
 DB 339 TAATDNNSDEI-----EVQNTASAWLHDESG-----GLD-----RVPKQ 374
 QY 131 ELKS-----EGRCQQILKDPKQLNSFKYMGESOP--FLAMFETDYFVKKVPPFSIK 184
 DB 375 KSKKKRPESQYQSAIFVAPDQOT-----LRVYPCFKCGKFKYKRLK-----RHIK 423
 QY 185 NESNYHPFFFRACDILLOPDLACKPFWKPRNLNLSQBGSDMQVSDFAHPNFGRFF 244
 DB 424 N-----HPEVLANKKY-----HCTEDYSTNKKIS----- 448
 QY 245 YLHYKLKHEGPFKRTCKQSQOTTTSCILLONVSPQDIILVDDTNTTKVMYALKPV 304
 DB 449 LHNHESHE-----KLTIKTEKTECDDC--KKNLSHA-----GTLCYTKHTE----- 490
 QY 305 HSPWAGPIRAVAITVPLVVI---SAFATLPT-----VMCKKKQENIYSHLDESSSY 357
 DB 491 -----KGVNKTCKKFCDIETAEQTLNHLHLLVHKKK-----EPHICGEGCGFRH 537
 QY 358 TAALPRE-RLRPRPKVFLC-----YSSKQGN-----HNVVQCFAVFLQFCGCEVALDLWE 409
 DB 538 PSALAKHRIHVTEGKPYECQCYCEKSDSNLTKHSHKSEIPLK-----CDICL-----L 590
 QY 410 DESLCREGREWVI---OKIHESOFIIVVCGKGMKYFYVDKKNYKHKGGRGSGKGLFLV 466
 DB 591 TFSDTKEAQOAHVLRHQRTHQ-----CS-----HCNKKSSNSDLKRHIISV 633
 QY 467 AVSAETAKLRQAKOS--SSAALSKEIATVFDYS-----CEGDVPG-----ILDLSK 511
 DB 634 HYKAPKHCDCMCKGPFHPSLAKKVAHSHKSKKQCHQCHCDENSPDFLLSHLSHLSNPK 693
 QY 512 YRLMNLPLQSLHSLHSDHGLQEPQHTQSGRRNFRSKRSLSLYAICNMHQFIDEP 571
 DB 694 -----NVFPCKRCKK-----EPQOQCELOTHMKTSSRYQ--CEYCEYSTKA 737
 QY 572 DNFEKOFVFPFPPPLRPREVLEKFDLSGLVINDVMCKPGPESDFCLAYEAALVGLGTPAD 631
 DB 738 SGFKRKRVISIHTKYPKR-----CDFCKK-----GFRPPSE 768
 QY 632 -SOHESQH 638
 DB 769 KNOHMRH 776

RESULT 15

ID PSUI_YEAST STANDARD: PRT: 970 AA.
 AC P53550;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE mRNA decapping protein 2 (PSUI protein).
 GN DCP2 OR PSUI-OR INL18C OR N1917.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D273-10B;
 RA Tzagoloff A.A.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97245296; PubMed=9090055;
 RA de Antoni A., D'Angelo M., Del Pero F., Sartorello F., Pandolfo D.,
 RA Pallavicini A., Lanfranchi G., Valle G.;
 RT "The DNA sequence of cosmid 14-13b from chromosome XIV of
 RT Saccharomyces cerevisiae reveals an unusually high number of
 RT overlapping open reading frames.";

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OM protein - protein search, using sw model

Run on: May 19, 2003, 09:14:29 ; Search time 59.0725 Seconds
 (without alignments)
 2626.495 Million cell updates/sec

Title: US-09-912-157-2
 Perfect score: 4013
 Sequence: 1 MAPWLQCSVEFTVNAQLG.....CKADLCGRSTDELAHVAPL 753

Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPTREMBL_21:
 1: sp_archaea:
 2: sp_bacteria:
 3: sp_fungi:
 4: sp_human:
 5: sp_invertebrate:
 6: sp_mammal:
 7: sp_mhc:
 8: sp_organelle:
 9: sp_phage:
 10: sp_plant:
 11: sp_rodent:
 12: sp_virus:
 13: sp_vertebrate:
 14: sp_unclassified:
 15: sp_rvirus:
 16: sp_bacteriap:
 17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3005	74.9	564	Q9UFA0	Q9UFA0 homo sapien
2	2616.5	65.2	582	Q8R5J8	Q8R5J8 mus musculus
3	1961	48.9	745	Q8QJ39	Q8QJ39 brachydanio
4	1952	48.6	745	Q8QJ36	Q8QJ36 brachydanio
5	170.5	4.2	846	Q9NA64	Q9NA64 caenorhabdi
6	117.5	2.9	562	Q99755	Q99755 homo sapien
7	117	2.9	757	Q13399	Q13399 ustilago ma
8	117	2.9	917	Q81789	Q81789 arabidopsis
9	117	2.9	2946	Q64634	Q64634 bacillus ha
10	116.5	2.9	901	Q9KE04	Q9KE04 arabidopsis
11	115.5	2.9	938	Q11606	Q11606 mus musculus
12	115.5	2.9	549	Q99754	Q99754 homo sapien
13	111.5	2.8	348	Q9H460	Q9H460 homo sapien
14	111.5	2.8	370	Q96KN9	Q96KN9 homo sapien
15	110	2.7	428	Q9NTU6	Q9NTU6 homo sapien
16	108.5	2.7	3788	Q942X9	Q942X9 rattus norv

17	108	2.7	903	5	Q95WA7	Q95WA7 bulla gould
18	108	2.7	1058	10	Q9AY10	Q9AY10 oryza sativ
19	108	2.7	11962	11	Q9WUF3	Q9WUF3 mus musculu
20	107.5	2.7	3942	11	Q88737	Q88737 mus musculu
21	107	2.7	1322	11	Q9QZP6	Q9QZP6 mus musculu
22	107	2.7	1545	11	Q8VBS6	Q8VBS6 mus musculu
23	107	2.7	3788	11	P97412	P97412 mus musculu
24	106.5	2.7	3638	10	Q9LQF8	Q9LQF8 arabidopsis
25	106.5	2.7	1907	4	Q15017	Q15017 homo sapien
26	106	2.6	549	5	Q19655	Q19655 caenorhabdi
27	106	2.6	593	11	Q99PV2	Q99PV2 rattus norv
28	106	2.6	1448	16	Q8VWJ8	Q8VWJ8 anabaena sp
29	106	2.6	1516	4	Q9CDJ2	Q9CDJ2 homo sapien
30	105	2.6	901	5	Q24573	Q24573 drosophila
31	105	2.6	1545	5	Q9BHW7	Q9BHW7 leishmania
32	105	2.6	1571	11	Q54978	Q54978 mus musculu
33	105	2.6	2031	5	Q9N9I8	Q9N9I8 leishmania
34	104.5	2.6	707	4	Q96SK7	Q96SK7 homo sapien
35	104.5	2.6	806	5	Q9VQK5	Q9VQK5 drosophila
36	104.5	2.6	924	10	Q9ZVD5	Q9ZVD5 arabidopsis
37	103.5	2.6	625	10	Q9FMD7	Q9FMD7 arabidopsis
38	103.5	2.6	1289	11	Q9WTR2	Q9WTR2 mus musculu
39	103.5	2.6	1308	2	Q9L8Z1	Q9L8Z1 enterococcu
40	103	2.6	1158	5	Q967X9	Q967X9 tribolium-c
41	103	2.6	1428	5	Q9VU03	Q9VU03 drosophila
42	102	2.5	1654	5	Q9VC36	Q9VC36 drosophila
43	102	2.5	4169	4	Q8TCU4	Q8TCU4 homo sapien
44	101.5	2.5	341	6	Q9N0B3	Q9N0B3 macaca fasc
45	101.5	2.5	1639	3	Q9P7Q7	Q9P7Q7 schizosacch

ALIGNMENTS

RESULT 1
 Q9UFA0 PRELIMINARY; PRT; 564 AA.
 AC Q9UFA0;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE Hypothetical 63.1 kDa protein (fragment).
 GN DRFP2434N1928.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiuidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RA Bloeker H., Boecher M., Brandt P., Mewes H.W., Gassenhuber J.,
 RA Wiemann S.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL133097; CAB61408.1;
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 564 AA; 63134 MW; 6B3AA5BD4523E88C CRC64;

Query Match 74.98; Score 3005; DB 4; Length 564;
 Best Local Similarity 99.8%; Pred. No. 1.2e-266;
 Matches 563; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	190	HPFFETRADCLLQPNLACKPFWKPRNLNLSQHGSDMQVSDRAPHNFGFFFLHYK 249
DB	1	HPFFETRADCLLQPNLACKPFWKPRNLNLSQHGSDMQVSDRAPHNFGFFFLHYK 60
QY	250	LKHEGPFKTKCKQQTETFTSCLLQNVSPGDYIIELVDVTNTRKVMHYALKPVSPWA 309
DB	61	LKHEGPFKTKCKQQTETFTSCLLQNVSPGDYIIELVDVTNTRKVMHYALKPVSPWA 120
QY	310	GPTRAVATVPILVVISAFATFTVMCRKKQOENIYSHLDEESSESYTALPRELRPR 369
DB	121	GPTRAVATVPILVVISAFATFTVMCRKKQOENIYSHLDEESSESYTALPRELRPR 180

QY 370 PRVFLCYSSKDGQNNHNVQCFAYFLQDPCGCEVALDMEFSLCREGQRENVIOKIHES 429
 DB 181 PRVFLCYSSKDGQNNHNVQCFAYFLQDPCGCEVALDMEFSLCREGQRENVIOKIHES 240
 QY 430 QPILVYCSKGMKYFVDKNTKHKGGGSGGZELFLVAVSAIAEKLRQAKQSSAALSKF 489
 DB 241 QPILVYCSKGMKYFVDKNTKHKGGGSGGZELFLVAVSAIAEKLRQAKQSSAALSKF 300
 QY 490 IAVFDYSCBGDVPGLDLSLTKYRLMDNLPOLCSHLSRDRGLQEPQHTROGSRNFR 549
 DB 301 IAVFDYSCBGDVPGLDLSLTKYRLMDNLPOLCSHLSRDRGLQEPQHTROGSRNFR 360
 QY 550 SSKGSLVYALCNHOFIDEEPDMFEKQFVFPFPPPLRYREPVLKFGSGLVNDVNCRP 609
 DB 361 SSKGSLVYALCNHOFIDEEPDMFEKQFVFPFPPPLRYREPVLKFGSGLVNDVNCRP 420
 QY 610 GPESDFCLKVEAVLGNATGPADSOHESQHGGLDQGEARPALDGSAAALQPLHTYKAGSP 669
 DB 421 GPESDFCLKVEAVLGNATGPADSOHESQHGGLDQGEARPALDGSAAALQPLHTYKAGSP 480
 QY 670 SDMPRDSGYDSSVPSSELSPLMEGLSTDDTETSSILTESVSSSGLGEPEPPALPSKLL 729
 DB 481 SDMPRDSGYDSSVPSSELSPLMEGLSTDDTETSSILTESVSSSGLGEPEPPALPSKLL 540
 QY 730 SSGCKADIGCRSYTDELHAPVL 753
 DB 541 SSGCKADIGCRSYTDELHAPVL 564

RESULT 2

QY 8R5J8 PRELIMINARY; PRT; 582 AA.
 AC 08R5J8;
 DT 01-JUN-2002 (TREMREL 21, Created)
 DT 01-JUN-2002 (TREMREL 21, Last sequence update)
 DE Similar expression to FGF protein (fragment).
 GN SEF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21824237; PubMed-11802165;
 RA Furthner M., Lin W., Aug S.L., Thisse B., Thisse C.;
 RT "Seif is a feedback-induced antagonist of Ras/MAPK-mediated FGF
 signalling.";
 RL Nat. Cell Biol. 4:170-174(2002).
 DR EMBL; AF424804; AAL79530.1;
 FT NON_TER 1
 SQ SEQUENCE 582 AA; 65263 MW; 5666382981C4268E CRC64;

Query Match 65.28; Score 2616.5; DB 11; Length 582;
 Best Local Similarity 84.6%; Pred. No. 5.6e-231;
 Matches 496; Conservative 34; Mismatches 49; Indels 7; Gaps 4;
 QY 171 TDYFVKVVPFPPSKNESNTHPFFTRACDILLQPDNLACKPFWKPRNLNISOHSDMOV 230
 DB 1 TDYFVKVVPFPPSKNESNTHPFFTRACDILLQPDNLACKPFWKPRNLNISOHSDMHV 60
 QY 231 SFDHAPNFGFRFYLKHLKHEGPFKTKQKQOTTTSCLLQNVSPGDYIELVDOT 290
 DB 61 SFDHAPNFGFRFYLKHLKHEGPFKTKQKQOTTTSCLLQNVSPGDYIELVDOT 120
 QY 291 NTRKAYHIALKPVHSPWAGPIRAVAITVPLWISAFATLFTVCKKQENIYSHLEE 350
 DB 121 NTRKAAQYVYKVSQSPWAGPIRAVAITVPLWISAFATLFTVCKKQENIYSHLEE 180
 QY 351 SSESSTYALPRELPRPRKFLCYSSKDGQNNHNVQCFAYFLQDPCGCEVALDMEF 410
 DB 181 SPESSTYALPRELPRPRKFLCYSSKDGQNNHNVQCFAYFLQDPCGCEVALDMEF 240

QY 411 FSLCREGQRENVIOKIHESQFIIYVCSKGMKYFVDKNTKHKGGGSGGZELFLVAVSA 470
 DB 241 FSLCREGQRENVIOKIHESQFIIYVCSKGMKYFVDKNTKHKGGGSGGZELFLVAVSA 300
 QY 471 IAEKLRQAKQSSAALSKFIAVFDYSCBGDVPGLDLSLTKYRLMDNLPOLCSHLSRDR 530
 DB 301 IAEKLRQAKQSSAALSKFIAVFDYSCBGDVPGLDLSLTKYRLMDNLPOLCSHLSRDR 357
 QY 531 GLQEP-QQHTROGSRNFRSKGSLVYALCNHOFIDEEPDMFEKQFVFPFPPPLRYR 589
 DB 358 GEQEVLGQHPGHSSRRNFRSKGSLVYALCNHOFIDEEPDMFEKQFVFPFPPPLRYR 417
 QY 590 EPVLKFGSGLVNDVNCRPESDFCLKVEAVLGNATGPADSOH-ESQHGGLDQGEA 647
 DB 418 EPVLKFGSGLVNDVNCRPESDFCLKVEAVLGNATGPADSOH-ESQHGGLDQGEA 477
 QY 648 RPALDGSAAALQPLHTYKAGSPSDMPRDSGYDSSVPSSELSPLMEGLSTDDTETSSLT 707
 DB 478 QPSCDSAPALQPLHTYKAGSPSEMPRDSGYDSSVPSSELSPLMEGLSPDQETSSLT 537
 QY 708 ESYSSSGLGEPEPPALPSKLLSGCKADIGCRSYTDELHAPVL 753
 DB 538 ESYSSSGLGEPEPPALPSKLLSGVSR-ERGCNHSYDELQALAPL 582

RESULT 3

QY 8R5J9 PRELIMINARY; PRT; 745 AA.
 AC 08R5J9;
 DT 01-JUN-2002 (TREMREL 21, Created)
 DT 01-JUN-2002 (TREMREL 21, Last sequence update)
 DE Seif.
 GN SEF.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21824236; PubMed-11802164;
 RA Tsang M., Friesel R., Kudoh T., Dawid I.;
 RT "Identification of Seif, a novel modulator of FGF signalling.";
 RL Nat. Cell Biol. 4:165-169(2002).
 DR EMBL; AF364103; AAL76112.1;
 SQ SEQUENCE 745 AA; 83431 MW; 56FE1F0B9D98DB4 CRC64;

Query Match 48.9%; Score 1961; DB 13; Length 745;
 Best Local Similarity 51.4%; Pred. No. 1.1e-170;
 Matches 390; Conservative 114; Mismatches 197; Indels 58; Gaps 10;

QY 1 MAPWLQCSVFTTVACNLGSQLAVAGSGRARGADTCGRWKAAARPRLCVANEVGP 60
 DB 7 LAHFFVASCFLCYTASYNG-----GKRGNSDKCSYK-----QGTQT 43
 QY 61 ASRNSGL--YNTTFYDNCITVLPVGVKHVIAQNTISQYACHQVAVTILWSPGALG 118
 DB 44 SMDGARKLVTFYDNCISVNWPLGKHAIHEVNITFSLSCDSQAVVWMAFPLG 103
 QY 119 IETLKFVILELSESGRQCOQLILDKPOLNSSPFKTGMSQFLANKETDTFVKVV 178
 DB 104 IETVGFVILELSESGRQCOQLILDKPOLNSSPFKTGMSQFLANKETDTFVKVV 163
 QY 179 PFTSINKESNTHPFFTRACDILLQPDNLACKPFWKPRNLNISOHSDMOVSDHAPN 238
 DB 164 PFTFLNDSFPFPLRNSCEVLLGPDNLVCKPFWKPRNLNISOHSDMHV 223
 QY 239 FGRFFFLYKHLKHEGPFKTKQKQOTTTSCLLQNVSPGDYIELVDOTNTRKWH 298
 DB 224 FGSIIYLYKLRQEGPFLKCRKPEQNGPKTTCLVQDVTGTYAIELRDSNTRQQT 283

299	QY	TALKPVHSWPAGIPRAVAITVPLVWISAFATLFTVCKKQKQENITSHLSESESESYTT	359
299	DB		
284	DB	THYSQVHSWPAGIPRAVAITVPLVWISAFATLFTVCKKQKQENITSHLSESESSOT	343
284	DB		
359	QY	AALPRERLARPRKPVFLCYTSKDGQNMNVVOCFAIFLDQCGCEVALDLWDFSLCREGQ	418
359	DB		
344	DB	TALSADRPWPRKPICTCYSSRDGAKELAVYQSFATFLDQCGCEVSLDWHELEICKEQ	403
344	DB		
419	QY	RENVIQKIHESQIFIVCSGKMYFDKKNYKHGGC-----GSGKGELFLVA	467
419	DB		
404	DB	KSWLRKIDAEAFITVCSGLGAKHFYKKRHKRGKATKKNRKPASDSSSSSRDLFIYA	463
404	DB		
468	QY	VSATAEKLRQAKQSSAALKSFITATFYDSCBGDVPGLDLSTKRYLMDNLPOLCSHLHS	527
468	DB		
464	DB	SATISEKLEKVRKSS-DLSRFNLSVDFYDSHETDVPSTLSAPKFLMDQLPOLFARLHS	522
464	DB		
528	QY	RDEGLQBPQCHTQGRSRNRTFRSKGSRSLYATVACNHOFTDREDPVPEKOPVPPHPPPLR	587
528	DB		
523	DB	ROLSLTDREPPQPNVSKRNTFCSKSGSLYATVIMHOHVTPQDPLKEKLM---PPPLP	579
523	DB		
588	QY	YREPVLEKFDGVLNDVWCKCPGSDPCLKVEAVT-----CATGPADQSHESQHG	640
588	DB		
580	DB	NKRTPEKVDGSLVNEVKLKHGSESCPPVRSNVILPOTPOGVGVSLSHREDLGEGS	638
580	DB		
641	QY	LDQDGEARPALDGSAAALQPLHFTVKAQSPDNPRDGSITDSSVPSSELSPLAMEGLSTQ	700
641	DB		
639	DB	SSOD-----AGSCRPFVLEVDGSSGPPMPDPSGIVDSSVPSSELSPLMDGLSPDH	689
639	DB		
701	QY	TETSSITSESVSSSGIGEEPAPLPSKLLSSSS--CKADL	738
701	DB		
690	DB	ADNSSLADSVSSSGLDGEPPNAVSLCHTAFTCKADL	728
690	DB		
RESULT 4			
Q80R06	ID	Q80H06 PRELIMINARY; PRG: 745 AA.	
AC	AC	Q80R06;	
01-JUN-2002	DT	(TRENBLrel. 21, Created)	
01-JUN-2002	DT	(TRENBLrel. 21, Last sequence update)	
01-JUN-2002	DT	(TRENBLrel. 21, Last annotation update)	
DE	DE	GFV signalling antagonist Sef.	
GN	GN	SEF	
OS	OS	Brachydanio rerio (Zebrafish) (Zebra danio).	
OC	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	
OX	OX	Cyprinidae; Danio.	
NCBI	NCBI	Taxid:7955;	
SEQUENCE FROM N.A.	SEQUENCE FROM N.A.		
MEDLINE:21824237; Pubmed:11802165;	SEQUENCE FROM N.A.		
Furthauer M., Lin W., Ang S.L., Thisse B., Thisse C.	SEQUENCE FROM N.A.		
*Sef is a feedback-induced antagonist of Ras/MAPK-mediated FGF	SEQUENCE FROM N.A.		
signalling*.	SEQUENCE FROM N.A.		
Nat. Cell Biol. 4:170-174(2002).	SEQUENCE FROM N.A.		
SEQUENCE FROM N.A.	SEQUENCE FROM N.A.		
Furthauer M., Lin W., Siew-Lan A., Thisse B., Thisse C.	SEQUENCE FROM N.A.		
Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.	SEQUENCE FROM N.A.		
EMBL; AF401232; AAL78817.1;	SEQUENCE FROM N.A.		
SEQUENCE 745 AA; 783437 MW; 759B9DECC08AA652; CRC64;	SEQUENCE FROM N.A.		

[illegible][illegible]

Best Local Similarity 21.46; Pred. No. 2.5e-06;
Matches 141; Conservative 82; Mismatches 225; Indels 211; Gaps 37;

QY 99 QYACHQVAVTILMSGALGTEFLKGRVILEELKSGRQCOOLIKDKPKOLNLSFRKTG 158
DB 294 QY-CFEYEVRLDSS--GIVMLOSALIYKDELRYE-----LINGRVQGEF-----338
QY 159 WESOPFLANKFEDIDFVKVVPFPPSINKESNYHFFFTTRACOLLQONLAC-PPFWKPR 217
DB 339 --NFTDILOLULIPVIPESAHQ-----GRC-LCYTNGCSCLAADKPKV 382
QY 218 NLNISQSDMVQSFHDHAPHNFGFRFFLYLKLKHEGPRFKTKQEQTTTSCLLQNV 277
DB 383 KLT-----RIKPPATSN-----QTEESDCKAEKKEDYTW-----415
QY 278 SPGDYIIELVDDNTTRKVMH-YALKPVHSPWAGPIRAVAVPLVVISAPATL--FTVM 334
DB 416 -----WHYIA-----ITGGALIAILFISVCAGLCKTKF 445
QY 335 CRKQENYSHLDEESSESTYTAALPRERLPRKVLICYSSKDGQNHNVVOCFAIF 394
DB 446 NKKKASNT--HLLNENPAFS-HSGSPL-ILKQISVLIYV-SHDSQAHEAAVLAPAE 500
QY 395 LQPCGCEVALDWEFSLCREGOREVIOKIHESQFIIVCGSKGMYFVDKKNYKHGG 454
DB 501 LRDVFNLANVLDWDEDI-ENRAEYINSIVRANKYIIINSIG-ATF--RTVFRQR--555
QY 455 GRGSGGELFLVAVSAIAEKLRQAKQSSAALSFKFIADVYSCBGV--PGIIDLSTKY 512
DB 556 -----EPAIERITGRND-----VIFDMQCELALQHPCVISCFYS 591
QY 513 -----RLMD-NLPOLCSHLGRDGLQEPQHTROGSRNRYFSKGRSLVAVI 560
DB 592 TNPRTVFFPPIRLQVSIIP---NSLMTMTALTQEPARPEQLAGNQVFAR---LQAAI 644
QY 561 CNMHQFIDEPPWFEK-----QVFPFHPPLRYR-----589
DB 645 SRKNTIESDPQWFETHVATRVSELEAHNIVPL-PPSELVKVEDAFQOMETLPI 703
QY 590 EPLVLEK-----DSGLVNDVCKPSPEDFCLKVEAAVLGATGADSOHES 636
DB 704 DELAKFAARLDLEVEDSDVLEEDVKAQCP-----IHVEPTEVLEPAEPEWEE 758
QY 637 QHGGLDQDGBARPALDGSAA-----LOPLL-HTVKAQSPMDPRDSDGSDS-VPSSLS 689
DB 759 AEED-EDEDDVDVSGQTARIEELQRLIVH-----KDNHDSGNLDSAYVSGSDFS 809

RESULT 6
Q99755 ID Q99755 PRELIMINARY; PRT; 562 AA.
AC AC Q99755;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 68 kDa type I phosphatidylinositol-4-phosphate 5-kinase alpha (EC 2.7.1.68).
DE 2.7.1.68).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97115834; PubMed=955136;
RX Lojens J.C., Anderson R.A.;
RT "type I phosphatidylinositol-4-phosphate 5-kinases are distinct
RT members of this novel lipid kinase family."
RL J. Biol. Chem. 271:32937-32943(1996).
DR EXEL; U78576; AAC50911.1;
DR InterPro: IPR002498; PIP5K.
DR Pfam: PF01504; PIP5K; 1.
DR SMART; SM00330; PIP5K; 1.
KW Kinase; Transferase.

SQ SEQUENCE 562 AA; 62633 MW; ABF7988EB73506A0 CRC64;
Query Match 2.94; Score 117.5; DB 4; Length 562;
Best Local Similarity 18.18; Pred. No. 0.098;
Matches 133; Conservative 105; Mismatches 239; Indels 257; Gaps 35;
QY 53 VANEGVGPASNSGLNITFKYDNCIT-----YLPVKGKVIADANITISQYACHQV 106
DB 1 MASASGSPSS-SVGFSDFPVPSCITLSAASGAIKRPWASEVLEARDSDYISL-----53
QY 107 AVTILMSGALGIEFLK-GFRVILEELKSGRQCOOLIKDKPKOLNLSFRKTGMSOPFL 165
DB 54 -----PVASGMPKIKIGHSVDSGETTYKTTSSALKGAKIOLGTHTVGSLSTKPR 106
QY 166 NKKFETDIFVKVVPFSS-----IKNESNYHFFFTTRACOLLQONLACPKFKNRLNI 221
DB 107 DVMQDFTVIESIIFPSEGSNLTFAHYINDFRKTYA-----143
QY 222 SQGSDMVQSFHDHAPHNFGFR--FFY-----LHYKLKHGPPFKRT 260
DB 144 -----PVAFRYFRELFGIRPDYILCSSEPLIELACSSGASGLFY-VSSDDEFIKT 195
QY 261 CKOBTETTSCLLQNVSPGDYIIELVDDNTTRKVMHYPVHSPWAGPIRAVAVTP 320
DB 196 VQKKEAE-----FLOKLLPGTYM-----NLQN-----P 219
QY 321 LVVISAFATLTVWCRKKQ-----OENYSHLDEESSESTYTAALPRERLPRP 370
DB 220 RTLLPKFTGLCYOAGGKNIRIVVMNMLPRSPVMIHIDKLGSTYKRRASOKEREKPLP 279
QY 371 KVELCYSSKDGQNHNVVQCFAYFLQDF-CGCEVALDWEFSLCREGOREVIOQ---KI 426
DB 280 -----TFKD-----LQFLQIDPGLFLDADMTN--ALCKTLQDCLVLOSFKI 320
QY 427 HESQFIYV-----CSKGMFYVDKKNYKHGGSGSGGELFLVAVSAIAEKLR 476
DB 321 MOYSLMSIHNIDBAQREPLSSTOYSDTR-----RPAPKALYSTAMESIOGEAR 372
QY 477 Q-----AKQSSAALSFKFIADVYSCBGVFGIIDLSTKYRLMDNLPOLC 522
DB 373 RGCTMETDQHMGPAPARNKSGERLLAYI-----GIIDILQSYRFVKLEHSH 419
QY 523 SHL-HSRDH-GLOEPQHTROGSRNRYFSKGRSLYVAICNMHOFIDEPPDFFKQFVP 580
DB 420 KALVHEDGTVSVHRRPGFYAERFOR-----PMCN-----TVFKK--IP 454
QY 581 FHPPLRTREPVLEKFGSLVNDVCKPSPEDFCLKVEAAVLGATGADSOHESQHG 640
DB 455 LKPSPSK-----KFRSG---SFSRRAGSGNSCITYQPSVSG-----EHAQ---494
QY 641 LQDQGEARPALDGSAAOLPILHTVKAQSPMDPRDSDGSDS-----SSVPSLSLPLMEGL 696
DB 495 -----VTTAEVPEGVH-----LGRDVLPTQTPPLEISEGSPIDPSFS-PLV-GE 539
QY 697 STDQTTSSLTESV 710
DB 540 TLQMLTTTSTLEKL 553

RESULT 7
O13399 ID O13399 PRELIMINARY; PRT; 757 AA.
AC O13399;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Telomere-associated recQ-like helicase (Fragment).
GN UTASRECO.
OS Ustilago maydis (Smut fungus).
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=5270;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN-C-125 / JCM 9153;
RX MEDLINE-20512582; PubMed-11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirano C., Nakamura Y., Ogasawara N., Kohara S.,
RA Horikoshi K.;
RT Complete genome sequence of the alkaliphilic bacterium Bacillus
halodurans and genomic sequence comparison with Bacillus subtilis.;
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
(ABC TRANSPORTERS).
DR EMBL; AP001510; BAB04773.1;
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR002559; ABC_transporter_1.
DR Pfam; PF00005; ABC_tran; 1.
DR Pfam; PF01609; Transposase_1; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transport; Complete proteome.
SQ SEQUENCE 901 AA; 104585 MW; E519406E650B2CBB CRC64;

Query Match 2.9%; Score 116.5; DB 16; Length 901;
Best Local Similarity 19.6%; Pred. No. 0.25;
Matches 112; Conservative 76; Mismatches 169; Indels 215; Gaps 27;

QY 61 ASRNSGLYNTFYDCTTLNPGVGHVIAQAQNTTISQY-ACHQDVAVTILWSPGALGI 119
DB 333 ALKESGL-----PLPKTLIADAGVGSNTVAMADELFTLPS----- 371

QY 120 EFLAGFVILEELKSGR-----QCOQL-ILKDPQLASSFKATGMSQFPLMKP 169
DB 372 ---HTFR-DEQAKSPAKRFPYINWRCDETDDVYMCNPKVYFKATKTDPT---GY 423

QY 170 ETDTEV-----KVPPF-PSI-----KNESNTHPEFFTRACDLIQLDNLACKPFMKPR 217
DB 424 ARDFKYECSCGCEGPECTKARGNQVHNPVY-----EELKAKQHOKLK 471

QY 218 MLNISQIG-----SDMOVSDHAPHNFCGFEFFLYHLKHEGPFKTKCKQPTTET 269
DB 472 ---SEGRTLQKRTDYESVGVKQNLGFRLLHGR----- 507

QY 270 TSCLLQNSPDYIIELVDVTTNRYNMYALKPVHSPWAGPIRAVAITVPLDWIS-AFA 328
DB 508 -----ESVHIELGLVALAHLNR 524

QY 329 TLTVMCKKQQENIYSHLDESSSTYTAALPRELRPRPKVFLCYSSKDGQNMNVV 388
DB 525 KRAVDRESKEPTNQHKNR-----RIKRF-----SRFVL 558

QY 389 QCF---NYFLQPCGCEVALDWEFSLCREGQEWY-----IKNHESOFITVWCSGKM 441
DB 559 RCFWSPFFTKDGKQYASFALED--KLREBGGEMIEVLDISKYTRNQVY---KGIN 612

QY 442 IFVDKKNYKKGGRSGGELFLVAVSAI-----AEKLRQAKSSSAALSK 488
DB 613 MFEIEGEMVLLGPNAGASTTISMISSLIQPTSGDVLVKGSIHQSKAINSLGVQVP 672

QY 489 FIATFYSC-----GVPGILDSTKYELMDNLPQLCSHLHSRDLGLOPQGHTRQG 542
DB 673 EIAYVHDLTARENLAFPGKIYGLRGEELKHE-NESTIQLV-----GLEE-----RQN 718

QY 543 SRNRYFSKSGRLVVAICNMQH-----FIDEEP 571
DB 719 DRVETSGGMKRLNIAVALLHEPELLIMDEP 750

RESULT 11
Q06069 PRELIMINARY; PRT; 938 AA.
AC Q06069
DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Protein kinase (Fragment).
DE EPHB3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-95200798; PubMed-7893599;
RA Ruiz J.C., Conlon F.L., Robertson E.J.;
RT Identification of novel protein kinases expressed in the myocardium
of the developing mouse heart.;
RL Mech. Dev. 48:153-164(1994).
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN
TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
RECEPTOR SUBFAMILY.
DR EMBL; U11493; AA67925.1;
DR HSP; P29323; IBAF.
DR MGD; MGI:104770; Ephb3.
DR InterPro; IPR001090; Ephrin_receptor.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003962; FcR1L_repeat.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR001660; SAM.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR001426; Kinase_receptorV.
DR Pfam; PF01404; EPH_1bd; 1.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00069; kinase; 1.
DR Pfam; PF00336; SAM; 1.
DR PRINTS; PR00014; FNTYPR11.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD001495; Ephrin_receptor; 1.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00454; SAM; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
KW Glycoprotein; Kinase; Phosphorylation; Receptor; Repeat;
KW Transmembrane; Tyrosine-protein kinase.
FT NON_TER 1
SQ SEQUENCE 938 AA; 103997 MW; 8D128CA46F19E73F CRC64;

Query Match 2.9%; Score 115.5; DB 11; Length 938;
Best Local Similarity 19.4%; Pred. No. 0.33;
Matches 160; Conservative 120; Mismatches 285; Indels 259; Gaps 45;

QY 9 SVFFTVNACI-NGSOLAVA---AGGSGR---ARGADTCGWRKAAARPLC----- 52
DB 170 SLVIAPACIANAVNEVTPLLKCYNGDGEWHPVACTCATGHEPAKESOCRAPPGSY 229

QY 53 VANEVGVA-----SRNSG-----LYNITFYDN-----CTYILNPVGRHVIADAQ 93
DB 230 KAKQGGCPCLPCPPNSRTTSPAASTCTCHNNFYRADSDADSACTTTRSP-PRGVISNV- 287

QY 94 NITISYACHDOVAVTILWS-PGALGTEFLKGFVRVILELK-SEG-----RCCQQLIL 144
DB 288 -----NETSILIEWSEPRDLGGDDLLYNVICKKRCGSSGAGGATCRDNDVZ 337

QY 145 KDPQLNSSFRTGMSQFPLNMFETDYFVYVVPFSPKSNESNHYFFFRTRACDLILQ 204
DB 338 FVPRQLGLTERVHIS-----HLLAHTYTFEVAQVNGVSGKSPLPPTAAVAVNTTNOAA 392

QY 205 PDNLACKPFWKPRNLNISOHSDMOVSFDHAPHNFGFRFFLYHLKHEGPF-KRKTCKO 263

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Db 393 PSEV-----PTLHSTSGSLTSLNAPPERNG-----VILDYENK-----PEKSAIAS 439
QY 264 EOTTETISCLQWSP-GDYIIELVDVDTTRKV-----MAYALKPVHSPWAGPTRA 316
Db 440 TVTSKNSVOLDGLOPARVVOV-----RARTVAGYQYTHPAEFFETSERGSAQQLQ 494
QY 317 IYVPLVLSAVA-----TLTVCKRKQENIYSLDESSESTYTAALPRELRP 368
Db 495 EQLPLVGSNVAGFVFWVVVVVIALVCLRKORH-----GPDAXTEKL-QOYIAP 543
QY 369 RPKFVLYSSKDGQNHNVQCFAYFLQDFC-GCEVALDWEDFSLCREQREWVQKIH 427
Db 544 GKVYIDPFTVEDPN-EAVREFAKBIDVSCVKEEVIGAGEFGEVCR-----589
QY 428 ESQFIIVCSGMYFYVDKKNYKHGSGRGSGKGLFVWYSAL-----AEKLRQAKOSS 483
Db 590-----GRLLPGRREV-VAKTLKVGTYTERQDRFLSA 623
QY 484 ALSRFIAYFYDCEGDVPGILDLS-----TKYR-----LADMLPOLCSHLSRDRGLQ 533
Db 624 SNGQF-----DHPNIIRLEGVYTKSRPYMILTEFMENC-ALDSFLRLND-----667
QY 534 EPGQRT-----ROGSRNRY-FRSKSGRLTY-----AIC-----NMHQFIDE 569
Db 668 --GQFTVQLVGLMLGTAAGMYLSEMYVVRDLAARNILVNSLVCKVSDGFLSRLFD 725
QY 570 EPDWEKOF-----VPEH-----PPPLRYREPVLKFS-----GLVLDVCKPGE 612
Db 726 DRS--DPTTSSLGKPIRWTAPEIAYR-----KFSADVWSYGVVWVNS-----773
QY 613 SDFCLKVAEVLGATGAPDSQESQHGGLDQGEAPALDGSAAALOPLLHTVKGSPSDM 672
Db 774 -----YGEQPTWMSNODINAVEQDYRLPPPMDCPTALHOLMASCWVRDLNR 822
QY 673 PROSGIYD-----SSVPSSELSPLMEGLSTDQT 701
Db 823 PRFSQIVNTLKLIRNAASLKVTASAPSG-MSQPLIDTVPDYT 865

RESULT 12
ID Q99754 PRELIMINARY; PRT; 549 AA.
AC Q99754;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE 68 Kda type I phosphatidylinositol-4-phosphate 5-kinase alpha (BC 2.7.1.68).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97115634; PubMed=8955136;
RA Lofjens J.C.; Anderson R.A.;
RT "Type I phosphatidylinositol-4-phosphate 5-kinases are distinct members of this novel lipid kinase family.";
RL J. Biol. Chem. 271:32937-32943(1996).
DR EMBL; 078575; AAC50910.1;
DR InterPro; IPR002498; PIP5K.
DR Pfam; PF01504; PIP5K; 1.
DR SMART; SM00330; PIP5K; 1.
DR Kinase; Transferase.
SQ SEQUENCE 549 AA; 61186 MW; 7CD48BEF175564A0 CRC64;

Query Watch 2.88; Score 112.5; DB 4; Length 549;
Best Local Similarity 18.18; Pred. No. 0.27;
Matches 121; Conservative 96; Mismatches 213; Indels 237; Gaps 32;

QY 114 PGALGIEFLK-GFRVILEELKSGROCOOLILKDPKLNSSFKRTGMSQFLNMFFTD 172
Db 41 PYASGPIKIGHRSVDSGETTYKNTSSALKGAIGIYTHVGSLSLTPRDRVLMQDF 100

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QY 173 YFVWVFPFS-----IKNESNYHFFPFRACDILLQPDNLACPFKPRNLNISQSGDM 228
Db 101 TVVESIFFPESGSLNPAHYNDFFKTYA-----LHYKLHSGPFRKVCQBOFTT 130
QY 229 QVSDHAPHNFGFR--FFY-----LHYKLHSGPFRKVCQBOFTT 267
Db 131 PVAFIRFELGIRPDYILSICSEPLIELSSGASSLFT-VSSDDEFIITKVHKKAE 189
QY 268 ETTSCILQNSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPTRAIVTPLYVISAF 327
Db 190 -----FLQKLLPGTYM-----NLNQN-----PRTLLPKF 213
QY 338 ATLTVWCKRKQ-----QENIYSLDESSESTYTAALPRELRPCKVFLCYS 377
Db 214 YGLTCVQAGGNIRIVVNNLLPRSVYMHYKLYDLKGYTKERRASQKEREKPLP-----T 267
QY 378 SROGQNHNVQCFAYFLQDFC-GCEVALDWEDFSLCREQREWVQ-----KHESQFI 433
Db 268 FKD-----LDLQIDIPDGLFLDADYN--ALCKTLQRDCLVQSFKIMDYSLIM 314
QY 434 VV-----CSKGMKYFYVDKKNYKHGSGRGSGKGLFVWYSALAEKLRQ-----477
Db 315 SIHNIDHAQREPLSSTQTSVDTR-----RPAPKALYSTAMESIQCEARRGTMET 366
QY 478 -----AKOSSAALSFIAYFYDSCGDVPGILDSTKYRLMDNLPOLCSHLSR 528
Db 367 DDHMGGIPARNSGERLLTY-----GIIDILQSTFRVKKLEHSHKALVHDG 413
QY 529 DH-GLOPGQGTROGSRNRYFRSKSGRLTYVAICNMQFIIDEPDWEKOFYVFFPPLR 587
Db 414 DTVSVHBPFGYABRFOR-----FMCN-----TVFKR--IPLAFSPSK 448
QY 588 YREPVLKFPDGLVNDVCKPESDFCLKVEAAVLGATGAPDSQESQHGGLDQGEA 647
Db 449 -----KFRSG--SFSFRAGSGNSCIYQFSVSG-----EHAQ-----481
QY 648 RPAIDGSAALOPLLHTVKGSPSDMPROSGIYD-----SSVPSSELSPLMEGLSTDQTET 703
Db 482 -----VTTKAEYEPGVH--LGRPDVLPOTPPLEISEGSPIDPFSFS-PLV-GETLQMLTT 533
QY 704 SSLTESV 710
Db 534 STTLEKL 540

RESULT 13
Q9H460
ID Q9H460 PRELIMINARY; PRT; 348 AA.
AC Q9H460;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE BA425A6.2 (Similar to connexin). (Fragment).
GN BA425A6.2
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Heath P.;
RA Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AL121749; CAC10186.1;
DR InterPro; IPR000500; Connexin.
DR Pfam; PF00029; connexin; 1.
DR PRINTS; PR00206; CONNEXIN.
DR SMART; SM00037; CNX; 1.
DR PROSITE; PS00407; CONNEXINS_1; 1.
DR PROSITE; PS00408; CONNEXINS_2; 1.
FT NON TER 1
SQ SEQUENCE 348 AA; 37805 MW; 07EB6478067F8995 CRC64;

```

Query Match 2.8%; Score 111.5; DB 4; Length 348;
 Best Local Similarity 28.9%; Pred. No. 0.17;
 Matches 43; Conservative 25; Mismatches 56; Indels 25; Gaps 8;

QY 600 LVLNDVMC-----KPGPESDFCLKVEAAVLGATGPADQSQHSQHGGLDQGEARPAL 651
 DB 189 LGLADLVCSLRRRRRRPGPTSPSIRKQS---GASGHAERRTDEGGREEG--APAP 243
 QY 652 DGSALQPLHTVKGSPDMRDSGYDSSVP---SSELSPLMEGLSTDTQTSSLTE 708
 DB 244 PGARA-----GGGAGSPRTSRVSG--HTKIPDESEVTSSASEKLGR-QPRGRPHRE 295
 QY 709 SVSSSSGLG-EEEPALPSKLLSSGCKA 736
 DB 296 AAQDPRGSGSEQPSAAPSRLAAPPSCSS 324

RESULT 14
 Q96KN9 PRELIMINARY; PRT; 370 AA.

AC Q96KN9;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Connexin40.1.
 GN CX40.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Eiberger J., Soehl G., Willecke K.;
 RT "Structural and functional diversity of connexin genes in the mouse
 RT and human genome";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ14564; CAC93846.1; -;
 DR InterPro; IPR000500; Connexin.
 DR Pfam; PF00049; connexin.1.
 DR PROSITE; PS00407; CONNEXINS.1; UNKNOWN.1.
 DR PROSITE; PS00408; CONNEXINS.2; UNKNOWN.1.
 SQ SEQUENCE 370 AA; 40140 MW; CD49F31743A7F7C2 CRC64;

Query Match 2.8%; Score 111.5; DB 4; Length 370;
 Best Local Similarity 28.9%; Pred. No. 0.18;
 Matches 43; Conservative 25; Mismatches 56; Indels 25; Gaps 8;

QY 600 LVLNDVMC-----KPGPESDFCLKVEAAVLGATGPADQSQHSQHGGLDQGEARPAL 651
 DB 211 LGLADLVCSLRRRRRRPGPTSPSIRKQS---GASGHAERRTDEGGREEG--APAP 265
 QY 652 DGSALQPLHTVKGSPDMRDSGYDSSVP---SSELSPLMEGLSTDTQTSSLTE 708
 DB 266 PGARA-----GGGAGSPRTSRVSG--HTKIPDESEVTSSASEKLGR-QPRGRPHRE 317
 QY 709 SVSSSSGLG-EEEPALPSKLLSSGCKA 736
 DB 318 AAQDPRGSGSEQPSAAPSRLAAPPSCSS 346

RESULT 15
 Q9NTU6 PRELIMINARY; PRT; 428 AA.

AC Q9NTU6;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Hypothetical 45.4 kDa protein.
 GN DKFP434P21.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;

[1]
 RN SEQUENCE FROM N.A.
 RP TISSUE-TESTIS;
 RX MEDLINE-11144917; PubMed-11230166;
 RA Wiemann S., Weill B., Wellenreuther R., Gassenhuber J., Glasel S.,
 RA Ansgore W., Boecker M., Bloecher H., Bauersachs S., Blum H.,
 RA Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,
 RA Meves H.W., Ottenwaelder B., Obermaier B., Tampe J., Neubner D.,
 RA Wambutt R., Korn B., Klein M., Poustka A.;
 RT "Towards a Catalog of Human Genes and Proteins: Sequencing and
 RT Analysis of 500 Novel Complete Protein Coding Human cDNAs";
 RL Genome Res. 11:422-435(2001).
 DR EMBL; AL117401; CAB55902.2;
 KW Hypothetical protein.
 SQ SEQUENCE 428 AA; 45443 MW; FA75BACIA3FDB3EE CRC64;

Query Match 2.7%; Score 110; DB 4; Length 428;
 Best Local Similarity 23.5%; Pred. No. 0.31;
 Matches 70; Conservative 42; Mismatches 108; Indels 78; Gaps 17;

QY 474 KLRQKQSS--SAALSKEFIAYFYDYSCEGDVPGI-----LDLSTKYLMDNLPQ 520
 DB 103 RYNTSOTSWTSCTNRNAISSYSTGLGLKRRRGPASSHCQLTSSSTVSEDRPQ 162
 QY 521 LCSHLHSRDHGLOE--PCQFTRQSGRRNFRKSGRSLYVAICNMHQFIDEPPDFEKFQ 578
 DB 163 AVSSGHTQCEKAADIAPGOTLT--LRNDSSTSEASRP-----STKPF---PLLPFRRG 210
 QY 579 VPEH-PPPL-----RYREPVLKFKDGLVLDVYM---CKPGPESDFCLKVEAA 622
 DB 211 EPLMLPPPLEGYRTVVDLDREKEAARINSALQVEDKAIISDCRPSRSH---TLSSL 267
 QY 623 VLGATG-PADQSQHSQHGGLDQGEARPALDGSAAIQLHTVKGSPSDMP-----RD 675
 DB 268 ATGASGLPAVSKAPS-----MDAQQETHKSDCLGLDPLASA--AGVPTAPMSGKKHRP 321
 QY 676 SG-TYDSSVSPSELSPLMEGLSTDTQTSTSTESVSSSGLEGEPPALPSKLLSSG 732
 DB 322 PGPLESSSDP-----LPATSSDSQSDSAQTSTLI-----PAPFPAASNDAG 361

Search completed: May 19, 2003, 09:24:05
 Job time : 64.0724 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 19, 2003, 09:07:58 ; Search time 20.9109 Seconds
(without alignments)
1771.498 Million cell updates/sec

Title: US-09-912-157-2_COPY_36_313
Perfect score: 1515
Sequence: 1 ADTCGRMKAAARPLCVAN.....RKVMETALPVESWAGPIR 278

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
A_Geneseq_101002.*	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. Is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1515	100.0	753	23	ABB07626 Human cytokine rec
2	1509	99.6	753	23	ABB07627 Human cytokine rec
3	1427	94.2	554	23	AAU91330 Human novel secret
4	1427	94.2	739	23	ABB07628 Human cytokine rec
5	1423	93.9	738	22	AAU09904 Human Interleukin
6	1423	93.9	738	22	AAU09953 Human Interleukin
7	1423	93.9	738	22	AAU09954 Human Interleukin
8	1423	93.9	738	22	AAU09955 Human Interleukin
9	1423	93.9	738	22	AAU09956 Human Interleukin
10	1423	93.9	738	22	AAU09957 Human Interleukin

11	1416	93.5	738	22	AAU09951 Human Interleukin
12	1416	93.5	738	22	AAU09952 Human Interleukin
13	1389	91.7	728	22	AAU04958 Human Interleukin
14	1386	91.5	739	22	AAU10602 Human Interleukin
15	1343.5	88.7	738	23	AAU11355 Human DNA cytokin
16	1334	88.1	296	22	AAU10601 5' portion of Huma
17	1290.5	85.2	739	23	ABB07630 Murine cytokine re
18	97	6.4	999	21	AAG33684 Arabidopsis thalia
19	97	6.4	1008	21	AAG33685 Arabidopsis thalia
20	97	6.4	1065	21	AAG33683 Arabidopsis thalia
21	92	6.1	1428	22	ABB65364 Drosophila melanog
22	89.5	5.9	368	19	AAW41360 tyb polypeptide
23	88	5.8	1173	23	ABB93479 Herbicidally activ
24	85.5	5.6	343	16	AAU73164 Coprinus cinereus
25	85.5	5.6	654	22	AAU78776 Human protein SEQ
26	85	5.6	313	21	AAU79996 Rat immunoglobulin
27	85	5.6	340	21	AAU03643 Bacillus KSM-P358
28	85	5.6	953	23	AAU51466 Coprinus cinereus
29	85	5.6	980	23	AAU51467 C. albicans RNA gu
30	84.5	5.6	343	16	AAU73145 Coprinus cinereus
31	84	5.5	333	21	AAU35508 RNA quanylyltransf
32	84	5.5	333	21	AAU32211 Coprinus cinereus
33	83.5	5.5	343	16	AAU73147 Coprinus cinereus
34	82.5	5.4	343	16	AAU73167 Coprinus cinereus
35	82.5	5.4	343	16	AAU73150 Coprinus cinereus
36	82.5	5.4	343	16	AAU73127 Human zcytor19 pro
37	82.5	5.4	520	23	ABB01643 Drosophila melanog
38	82.5	5.4	1276	22	ABB60848 Feline zona pelluc
39	82	5.4	716	15	AAU52000 Feline zona pelluc
40	82	5.4	716	20	AAU42473 Feline zona pelluc
41	82	5.4	716	20	AAU81810 Feline zona pelluc
42	82	5.4	716	21	AAU82208 Feline zona pelluc
43	82	5.4	716	21	AAU52173 Feline oocyte zona
44	82	5.4	716	21	AAU52173 Feline zona pelluc
45	82	5.4	716	21	AAU52977 Feline zona pelluc

ALIGNMENTS

RESULT 1
ABB07626
ID ABB07626 standard; Protein; 753 AA.
XX AC ABB07626;
XX AC 20-MAY-2002 (first entry)
DT XX Human cytokine receptor, zcytor18 amino acid sequence.
DE XX Cytokine receptor; zcytor18; cell proliferation; antiproliferative; human;
KW XX pulmonary alveolar proteinosis; familial periodic fever; antitumor;
KW XX erythroleukemia; chromosome 3p14.3; gene therapy.
XX OS Homo sapiens.
XX XX
PN WO200208259-A2.
XX PD 31-JAN-2002.
XX PF 23-JUL-2001; 2001WO-US23253.
XX PR 26-JUL-2000; 2000US-220747P.
XX PA (ZYMO) ZYMOGENETICS INC.
XX PI Presnell SR, Kuestner RE, Gao Z;
XX DR WPI; 2002-217048/27.
XX DR N-PSDB; ABA95031, ABA95032.
XX PT New cytokine receptor polypeptide designated zcytor18, useful for
inhibiting cell proliferation associated with psoriasis or tumor

PT growth, and modulating immune system by binding to endogenous zcytor18
 PT ligand
 PS Claim 1; Page 2; 119pp; English.
 XX
 XX The invention relates to an isolated cytokine receptor polypeptide
 CC designated zcytor18. The zcytor18 polypeptides can be expressed by
 CC standard recombinant methodology. The polypeptides can be used to inhibit
 CC cell proliferation associated with psoriasis or tumor growth. The
 CC encoding nucleic acids are useful for providing zcytor18 in vivo by gene
 CC therapy techniques. zcytor18 oligonucleotide probes are useful for in
 CC vivo diagnosis, and the zcytor18 probes and primers can be used to detect
 CC and localize zcytor18 gene expression in tissue samples. The probes are
 CC also useful for detecting gross aberrations in chromosome 3 in which
 CC zcytor18 gene resides. The zcytor18 polynucleotides can also be used in
 CC linkage-based testing of pulmonary alveolar proteinosis, familial
 CC periodic fever and erythroleukemia, and erythroleukemia associated with
 CC polymorphisms of cytokine receptors. The present sequence represents a
 CC human zcytor18 amino acid sequence.
 XX
 SQ Sequence 753 AA;

Query Match 100.0%; Score 1515; DB 23; Length 753;
 Best Local Similarity 100.0%; Pred. No. 2, 2e-161;
 Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADTCGWRKAAARPRCLVANGVGPASRNSGLNITFKYDNCITTLNPGKRVIAQAQNI 60
 DB 36 ADTCGWRKAAARPRCLVANGVGPASRNSGLNITFKYDNCITTLNPGKRVIAQAQNI 95
 QY 61 TISQYACHDQAVTILWSPGALGIEFLKGRVILEELKSGRCQOOLILKDPKQLNSFK 120
 DB 96 TISQYACHDQAVTILWSPGALGIEFLKGRVILEELKSGRCQOOLILKDPKQLNSFK 155
 QY 121 RTGMSOPFLANKFETDYFVKVPPSPSIKNSNTHPFFTRACDLILQPDNLACKPFWK 180
 DB 156 RTGMSOPFLANKFETDYFVKVPPSPSIKNSNTHPFFTRACDLILQPDNLACKPFWK 215
 QY 181 PRNLNISQSGSDQVSDHAPNFGFRFFYLHYLKLHKGFFKTKCKQBTETTSCLIQ 240
 DB 216 PRNLNISQSGSDQVSDHAPNFGFRFFYLHYLKLHKGFFKTKCKQBTETTSCLIQ 275
 QY 241 NVSPGDYIIELVDVTNTTRKVMHYALKPVHSPWAGPIR 278
 DB 276 NVSPGDYIIELVDVTNTTRKVMHYALKPVHSPWAGPIR 313

RESULT 2
 ABB07627
 ID ABB07627 standard; Protein: 753 AA.
 XX
 XX ABB07627;
 XX
 XX 20-MAY-2002 (first entry)
 XX
 XX Human cytokine receptor, zcytor18 variant sequence.
 DE
 XX Cytokine receptor; zcytor18; cell proliferation; antipsoriatic; human;
 KW pulmonary alveolar proteinosis; familial periodic fever; antitumor;
 KW erythroleukemia; chromosome 3p14.3; gene therapy; variant.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 289 /label- T269M
 FT /note- "wild-type Thr is replaced with Met"
 FT Misc-difference 750 /label- V750A
 FT /note- "wild-type Val is replaced with Ala"
 XX
 XX WO200208259-A2.

PD 31-JAN-2002;
 XX 23-JUL-2001; 2001WO-US23253.
 XX 26-JUL-2000; 2000US-220747P.
 XX (ZIMO) ZYMOGENETICS INC.
 XX Presnell SR; Kuestner RE, Gao Z;
 WPI; 2002-217048/27.
 N-PSDB; ABA95033, ABA95034.
 New cytokine receptor polypeptide designated zcytor18, useful for
 inhibiting cell proliferation associated with psoriasis or tumor
 growth, and modulating immune system by binding to endogenous zcytor18
 ligand.
 XX
 PS Disclosure; Page 94-98; 119pp; English.
 XX
 CC The invention relates to an isolated cytokine receptor polypeptide
 CC designated zcytor18. The zcytor18 polypeptides can be expressed by
 CC standard recombinant methodology. The polypeptides can be used to inhibit
 CC cell proliferation associated with psoriasis or tumor growth. The
 CC encoding nucleic acids are useful for providing zcytor18 in vivo by gene
 CC therapy techniques. zcytor18 oligonucleotide probes are useful for in
 CC vivo diagnosis, and the zcytor18 probes and primers can be used to detect
 CC and localize zcytor18 gene expression in tissue samples. The probes are
 CC also useful for detecting gross aberrations in chromosome 3 in which
 CC zcytor18 gene resides. The zcytor18 polynucleotides can also be used in
 CC linkage-based testing of pulmonary alveolar proteinosis, familial
 CC periodic fever and erythroleukemia, and erythroleukemia associated with
 CC polymorphisms of cytokine receptors. The present sequence represents a
 CC human zcytor18 variant amino acid sequence.
 XX
 SQ Sequence 753 AA;

Query Match 99.6%; Score 1509; DB 23; Length 753;
 Best Local Similarity 99.6%; Pred. No. 1, 1e-160;
 Matches 277; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ADTCGWRKAAARPRCLVANGVGPASRNSGLNITFKYDNCITTLNPGKRVIAQAQNI 60
 DB 36 ADTCGWRKAAARPRCLVANGVGPASRNSGLNITFKYDNCITTLNPGKRVIAQAQNI 95
 QY 61 TISQYACHDQAVTILWSPGALGIEFLKGRVILEELKSGRCQOOLILKDPKQLNSFK 120
 DB 96 TISQYACHDQAVTILWSPGALGIEFLKGRVILEELKSGRCQOOLILKDPKQLNSFK 155
 QY 121 RTGMSOPFLANKFETDYFVKVPPSPSIKNSNTHPFFTRACDLILQPDNLACKPFWK 180
 DB 156 RTGMSOPFLANKFETDYFVKVPPSPSIKNSNTHPFFTRACDLILQPDNLACKPFWK 215
 QY 181 PRNLNISQSGSDQVSDHAPNFGFRFFYLHYLKLHKGFFKTKCKQBTETTSCLIQ 240
 DB 216 PRNLNISQSGSDQVSDHAPNFGFRFFYLHYLKLHKGFFKTKCKQBTETTSCLIQ 275
 QY 241 NVSPGDYIIELVDVTNTTRKVMHYALKPVHSPWAGPIR 278
 DB 276 NVSPGDYIIELVDVTNTTRKVMHYALKPVHSPWAGPIR 313

RESULT 3
 AAU91330
 ID AAU91330 standard; Protein: 554 AA.
 XX
 XX AAU91330;
 XX
 XX 18-JUN-2002 (first entry)
 XX
 XX Human novel secreted protein LP253.
 DE
 XX Human; secreted protein; cancer; autoimmune disease;
 KW

arthritis; osteoporosis; Alzheimer's disease; Parkinson's disease; meningitis; encephalitis; neoplasia; trauma; ischaemia; infarction; mania; stroke; cardiovascular disease; atherosclerosis; sepsis; anaemia; rheumatoid arthritis; hypothyroidism; allergic response; liver failure; multiple sclerosis; haemorrhage; paranoia; obsessive-compulsive disorder; autism; panic disorder; learning disability; feeding disorder; sleep pattern disorder; balance; perception; Th1-dependent insulinitis; adult respiratory distress syndrome; ARDS.

Homo sapiens.

WO200214358-A2.

21-FEB-2002.

30-JUL-2001; 2001WO-US21124.

11-AUG-2000; 2000US-224642P.

19-OCT-2000; 2000US-241779P.

(ELIL) LILLY & CO ELI.

Edmonds BT, Micanovic R, Ou W, Su EW, Tschang SR, Wang H;

WPI; 2002-304057/34.

N-PSDB; ABK62082.

Novel polypeptides and polynucleotides of secreted proteins useful for treating various diseases such as multiple sclerosis, cancer, autoimmune diseases, osteoporosis, Alzheimer's disease and Parkinson's disease.

Claim 9; Page 171-173; 235pp; English.

The invention relates to a novel human secreted polypeptide having sequence 90% identical to the polypeptide sequences of LP105, LP061, LP224, LP239(a), LP243(a), LP243(b), LP253, LP218, LP251(a), LP252, LP239(b), LP223(a), LP255(a), LP244, LP186, LP251(b), LP255(b), or LP223(b). Also included are the nucleic acids encoding the LP proteins (including complement, fragments encoding mature forms of the polypeptide or variant), a vector comprising the nucleic acid, a host cell comprising the vector, the preparation of the protein, an anti-LP antibody, antagonists of LP and anti-LP-encoding mRNA ribozymes. The secreted protein or its agonist is useful in the manufacture of a medicament for treating a mammal suffering from a disease (and in diagnosis), condition or disorder associated with aberrant levels of the secreted protein e.g. cancer, autoimmune diseases, arthritis, osteoporosis, Alzheimer's disease, Parkinson's disease, meningitis, encephalitis, neoplasia, trauma, ischaemia and infarction, mania, stroke, cardiovascular disease, atherosclerosis, rheumatoid arthritis, hypothyroidism, anaemia, sepsis, allergic responses, multiple sclerosis, liver failure, haemorrhages, paranoia, obsessive compulsive disorder, autism, panic disorder, learning disabilities, ALS (amyotrophic lateral sclerosis) psychoses, disorders in feeding, sleep patterns, balance, and perception. The secreted protein is further useful for identifying compounds that bind to the secreted protein. The present sequence represents a novel secreted protein of the invention.

Sequence 554 AA;

Query Match 94.2%; Score 1427; DB 23; Length 554;
Best Local Similarity 95.0%; Pred. No. 1.2e-151;
Matches 264; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 ADTCGWRKAAARPRCLVANEVGVGSPASRNSGLNITFKYDNCCTYILNPVKGKVIADAQNI 60

Db 36 ADTCGWR-----GVGSPASRNSGLNITFKYDNCCTYILNPVKGKVIADAQNI 81

QY 61 TISQYACHQDVANTILMSPGALGIEFLKGFVRVILEELKSGRQCQQLILKDPKQLNSFFK 120

Db 82 TISQYACHQDVANTILMSPGALGIEFLKGFVRVILEELKSGRQCQQLILKDPKQLNSFFK 141

QY 121 RTGMESQFLNMFETDYKVVPPSPKNSNTHPFFETTRACDILLQPDNLACKPFWK 180
Db 142 RTGMESQFLNMFETDYKVVPPSPKNSNTHPFFETTRACDILLQPDNLACKPFWK 201
QY 181 PRNLNLSQHSQSDMVSDHAPNFGFRFYLYHKLKHEGFFKRTCKQ80TTETTSCLIQ 240
Db 202 PRNLNLSQHSQSDMVSDHAPNFGFRFYLYHKLKHEGFFKRTCKQ80TTETTSCLIQ 261
QY 241 NVSPGDYIIELVDVTNTTKVMHYALKPVHSPWAGPIR 278
Db 262 NVSPGDYIIELVDVTNTTKVMHYALKPVHSPWAGPIR 299

RESULT 4

ABB07628
ID ABB07628 standard; Protein; 739 AA.

XX AC ABB07628;

XX DT 20-MAY-2002 (first entry)

XX DE Human cytokine receptor, Zcytor18 splice variant.

Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human; pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy; splice variant.

OS Homo sapiens.

PN WO200208259-A2.

XX PD 31

XX PF 23-JUL-2001; 2001WO-US23253.

XX PR 26-JUL-2000; 2000US-220747P.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Presnell SR, Kuestner RE, Gao Z;

XX WPI; 2002-217048/27.

XX DR N-PSDB; ABA95035, ABA95036.

New cytokine receptor polypeptide designated zcytor18, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytor18 ligand

Claim 1; Page 102-106; 119pp; English.

The invention relates to an isolated cytokine receptor polypeptide designated zcytor18. The zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumor growth. The encoding nucleic acids are useful for providing zcytor18 in vivo by gene therapy techniques. Zcytor18 oligonucleotide probes are useful for in vivo diagnosis, and the zcytor18 probes and primers can be used to detect and localize zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which zcytor18 gene resides. The zcytor18 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human zcytor18 splice variant.

XX Sequence 739 AA;

Query Match 94.2%; Score 1427; DB 23; Length 739;
Best Local Similarity 95.0%; Pred. No. 1.8e-151;
Matches 264; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 ADTCGWRKAAARPRCLVANEVGVGSPASRNSGLNITFKYDNCCTYILNPVKGKVIADAQNI 60

Db 36 ADTCGWR-----GVGPASRNSGLYNITFKYDNCNTTYLNPVGHVIAQAQNI 81
QY 61 TISQYACHDOAVATILNSPGALGIEFLKGFVRVILELSEKSGROCOOLILKDPKOLNSFK 120
Db 82 TISQYACHDOAVATILNSPGALGIEFLKGFVRVILELSEKSGROCOOLILKDPKOLNSFK 141
QY 121 RTGQESQPLNKKFTDTFVKKVPPSPKNSNYHFFPRACDLLOPDNCKPFWK 180
Db 142 RTGQESQPLNKKFTDTFVKKVPPSPKNSNYHFFPRACDLLOPDNCKPFWK 201
QY 181 PRLNLSQSGSDQMSQVDFDAPHNFGFFRYLHYKLKHEGPPKRTCKQEQTTTSCLLQ 240
Db 202 PRLNLSQSGSDQMSQVDFDAPHNFGFFRYLHYKLKHEGPPKRTCKQEQTTTSCLLQ 261
QY 241 NVSPGDIYIELVDNTNTRKVMHYALAPVHSPWAGPIR 278
Db 262 NVSPGDIYIELVDNTNTRKVMHYALAPVHSPWAGPIR 299

RESULT 5
AAU09904
ID AAU09904 standard; Protein: 738 AA.
AC AAU09904;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human Interleukin 17 (hIL-17) receptor like protein.
XX
KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
KW bone disease; vascular disorder; eye disorder; cancer; human.
XX
OS Homo sapiens.
XX WO200168859-A2.
XX
XX 20-SEP-2001.
XX
XX 15-MAR-2001; 2001WO-0508678.
XX
XX 16-MAR-2000; 2000US-189816P.
XX 28-NOV-2000; 2000US-0724460.
XX
XX (AMGE-) AMGEN INC.
XX
XX Jing S;
XX
XX WPI; 2001-611392/70.
XX N-PSDB; AAS15346.
XX
XX Nucleic acids encoding interleukin 17 receptor like polypeptides,
XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
XX diabetes, psoriasis and glaucoma.
XX
XX Claim 2; Page 157-154; 158pp; English.
XX
XX The invention describes novel nucleic acids encoding interleukin (IL) 17
XX receptor like polypeptides useful as vaccines and in gene therapy. These
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
XX osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and
XX ophthalmological activities. The IL-17 receptor like nucleic acids and
XX proteins may be used to prevent and treat diseases associated with
XX inappropriate IL-17 receptor like polypeptide (IL17rip) expression. These
XX include, for example immune disorders (e.g. inflammation, diabetes and
XX transplant rejection), infections (e.g. hepatitis and septicemia),

CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
CC breast cancer), reproductive disorders (e.g. infertility and
CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
CC DNA and its complements may also be used as diagnostic probes to detect and
CC quantitate the presence of similar nucleic acids in samples and identify
CC patients needing restorative therapy. The IL17rip may also be used as
CC antigens in the production of antibodies against the proteins and in
CC assays to identify modulators of expression and activity. The
CC anti-IL17rip antibodies and antagonists may also be used to down regulate
CC expression and activity. This is the amino acid sequence of the human
CC Interleukin 17 (IL-17) receptor like protein described in the method of
CC the invention.
XX
XX Sequence 738 AA;
XX
XX Query Match 93.9%; Score 1423; DB 22; Length 738;
XX Best Local Similarity 94.9%; Pred. No. 5.2e-151;
XX Matches: 263; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
XX
QY 2 DTGGRKMAARPLCVANEGVGPASRNSGLYNITFKYDNCNTTYLNPVGHVIAQAQNI 61
Db 37 DTGGR-----GVGPASRNSGLYNITFKYDNCNTTYLNPVGHVIAQAQNI 82
QY 62 ISOYACHDOAVATILNSPGALGIEFLKGFVRVILELSEKSGROCOOLILKDPKOLNSFK 121
Db 83 ISOYACHDOAVATILNSPGALGIEFLKGFVRVILELSEKSGROCOOLILKDPKOLNSFK 142
QY 122 TQWESQPLNKKFTDTFVKKVPPSPKNSNYHFFPRACDLLOPDNCKPFWK 181
Db 143 TQWESQPLNKKFTDTFVKKVPPSPKNSNYHFFPRACDLLOPDNCKPFWK 202
QY 182 RNLNLSQSGSDQMSQVDFDAPHNFGFFRYLHYKLKHEGPPKRTCKQEQTTTSCLLQ 241
Db 203 RNLNLSQSGSDQMSQVDFDAPHNFGFFRYLHYKLKHEGPPKRTCKQEQTTTSCLLQ 262
QY 242 VSPGDIYIELVDNTNTRKVMHYALAPVHSPWAGPIR 278
Db 263 VSPGDIYIELVDNTNTRKVMHYALAPVHSPWAGPIR 299

RESULT 6
AAU09953
ID AAU09953 standard; Protein: 738 AA.
XX
XX AAU09953;
XX
XX 14-FEB-2002 (first entry)
XX
XX Human Interleukin 17 (hIL-17) receptor like protein substitution #3.
XX
XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
XX anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
XX hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
XX anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
XX vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;
XX hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
XX bone disease; vascular disorder; eye disorder; cancer; human; mutant;
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Misc-difference 363 /label- Ser, Thr, Ala, Cys
XX WO200168859-A2.
XX

PD 20-SEP-2001.
 XX 15-MAR-2001; 2001WO-US08678.
 XX PF
 PR 16-MAR-2000; 2000US-189816P.
 PR 28-NOV-2000; 2000US-0724460.
 XX PA (AMGE-) AMGEN INC.
 XX JIng S;
 XX WPI; 2001-611392/70.
 XX Nucleic acids encoding interleukin 17 receptor like polypeptides,
 PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
 XX diabetes, psoriasis and glaucoma.
 XX Claim 20; Page -; 158pp; English.
 XX The invention describes novel nucleic acids encoding interleukin (IL) 17
 CC receptor like polypeptides useful as vaccines and in gene therapy. These
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, and
 CC osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and
 CC proteins may be used to prevent and treat diseases associated with
 CC inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
 CC include, for example immune disorders (e.g. inflammation, diabetes and
 CC transplant rejection), infections (e.g. hepatitis and septicemia),
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 CC (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
 CC breast cancer), reproductive disorders (e.g. infertility and
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 CC DNA and its complements may also be used as diagnostic probes to detect and
 CC quantify the presence of similar nucleic acids in samples and identify
 CC patients needing restorative therapy. The IL17rlp may also be used as
 CC antigens in the production of antibodies against the proteins and in
 CC assays to identify modulators of expression and activity. The
 CC anti-IL17rlp antibodies and antagonists may also be used to down regulate
 CC expression and activity.
 CC Note: This sequence is not given in the specification but is based on the
 CC human interleukin 17 (IL-17) receptor like protein sequence (AAU09904)
 CC and has been created according to information given in claim 20.
 XX SQ Sequence 738 aa;

Query Match 93.98; Score 1423; DB 22; Length 738;
 Best Local Similarity 94.99; Fred. No. 5.2e-151;
 Matches 263; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 2 DTGCMRKAAPRLCVANBVGCPASRNSGLNITFKYDNCCTVTLNPGKHVIADQAQNT 61
 DB |||||
 37 DTGCMR-----GVCPSRNSGLNITFKYDNCCTVTLNPGKHVIADQAQNT 82
 QY 62 ISQACHQDVAVTILWSPGALGTEFLKGFVILELKSQGCQOOLILKDPKQLNSFPR 121
 DB |||||
 83 ISQACHQDVAVTILWSPGALGTEFLKGFVILELKSQGCQOOLILKDPKQLNSFPR 142
 QY 122 TGMSQPLNKKMFETDYFKVVPFPPSIKNSNTHPFFTRACDLILQPNLACKPFWKP 181
 DB |||||
 143 TGMSQPLNKKMFETDYFKVVPFPPSIKNSNTHPFFTRACDLILQPNLACKPFWKP 202
 QY 182 RNLTISQGSQDMQVSFOHAPNPGFFETFLYKLKHEGPFKKTKQBOTTTSCILQN 241
 DB |||||
 203 RNLTISQGSQDMQVSFOHAPNPGFFETFLYKLKHEGPFKKTKQBOTTTSCILQN 262
 QY 242 VSPGYIIELVDDTNTTRKVMHYALPVPSPWAGPIR 278
 DB |||||

DB 263 VSPGYIIELVDDTNTTRKVMHYALPVPSPWAGPIR 299

RESULT 7

AAU09954

ID AAU09954 standard; Protein; 738 AA.

AC AAU09954;

XX 14-FEB-2002 (first entry)

DE Human interleukin 17 (hIL-17) receptor like protein substitution #4.

XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 KW mutin.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FH Misc-difference 374 /label= Val, Ile, Met, Leu, Phe, Ala, Nle

PT WO200168859-A2.

XX 20-SEP-2001.

XX 15-MAR-2001; 2001WO-US08678.

XX 16-MAR-2000; 2000US-189816P.

XX 28-NOV-2000; 2000US-0724460.

XX (AMGE-) AMGEN INC.

XX JIng S;

XX WPI; 2001-611392/70.

XX Nucleic acids encoding interleukin 17 receptor like polypeptides,
 PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
 PT diabetes, psoriasis and glaucoma.
 XX Claim 21; Page -; 158pp; English.

XX The invention describes novel nucleic acids encoding interleukin (IL) 17
 CC receptor like polypeptides useful as vaccines and in gene therapy. These
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, and
 CC osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and
 CC proteins may be used to prevent and treat diseases associated with
 CC inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
 CC include, for example immune disorders (e.g. inflammation, diabetes and
 CC transplant rejection), infections (e.g. hepatitis and septicemia),
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 CC (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
 CC breast cancer), reproductive disorders (e.g. infertility and
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 CC DNA and its complements may also be used as diagnostic probes to detect and
 CC quantify the presence of similar nucleic acids in samples and identify
 CC patients needing restorative therapy. The IL17rlp may also be used as
 CC antigens in the production of antibodies against the proteins and in

CC assays to identify modulators of expression and activity. The
 CC anti-IL17p antibodies and antagonists may also be used to down-regulate
 CC expression and activity.
 CC Note: This sequence is not given in the specification but is based on the
 CC human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)
 CC and has been created according to information given in claim 21.
 XX
 SQ Sequence 738 AA;

Query Match 93.9%; Score 1423; DB 22; Length 738;
 Best Local Similarity 94.9%; Pred. No. 5.2e-151;
 Matches 263; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
 2 DTCCGWRKAAARPRCLVANEVGPASRNSGLYNTTFYDNTYLPVGRVIAQAQNT 61
 DB 37 DTCCWR-----GVGPASRNSGLYNTTFYDNTYLPVGRVIAQAQNT 82
 62 ISQACHQVAVTILSPGALIEFLKGRVILEELSEKSGROCOQLILKDPQLNSFKR 121
 DB 83 ISQACHQVAVTILSPGALIEFLKGRVILEELSEKSGROCOQLILKDPQLNSFKR 142
 122 TGMESQFLANKFETDFYKVVPPFSIKNESNYHFFTRACDILLQDNLCKPFWKP 181
 DB 143 TGMESQFLANKFETDFYKVVPPFSIKNESNYHFFTRACDILLQDNLCKPFWKP 202
 182 RNLNISQSGSDMVSDHAPNFGFRFFLYHLKHEGPFKRTCKOQTETTSCILQN 241
 DB 203 RNLNISQSGSDMVSDHAPNFGFRFFLYHLKHEGPFKRTCKOQTETTSCILQN 262
 242 VSPGDYIIELVDVDTNTRKVMYALKPVHSPWAGPIR 278
 DB 263 VSPGDYIIELVDVDTNTRKVMYALKPVHSPWAGPIR 299

RESULT 8
 AAU09955
 ID AAU09955 standard; Protein: 738 AA.
 AC AAU09955;
 XX
 XX 14-FEB-2002 (first entry)
 XX Human Interleukin 17 (hIL-17) receptor like protein substitution #5.
 XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 KW mutin.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 385 /label= Cys, Ser, Ala
 FT
 XX WO200168859-A2.
 XX 20-SEP-2001.
 XX 15-MAR-2001; 2001WO-US08678.
 XX 16-MAR-2000; 2000US-189816P.
 XX 28-NOV-2000; 2000US-0724460.
 XX (AMGE-) AMGEN INC.
 XX
 XX JING S;
 XX

DR WPI: 2001-611392/70
 XX Nucleic acids encoding interleukin 17 receptor like polypeptides,
 PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
 PT diabetes, psoriasis and glaucoma.
 XX
 PS Claim 22; Page 1; 158pp; English.
 XX
 CC The invention describes novel nucleic acids encoding interleukin (IL) 17
 CC receptor like polypeptides useful as vaccines and in gene therapy. These
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 CC immunosuppressive, hepatic, anorectic, anabolic, anti-asthmatic, anti-parkinsonian,
 CC anti-convulsant, anti-convulsant, anti-asthmatic, dermatological, renal,
 CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and
 CC proteins may be used to prevent and treat diseases associated with
 CC inappropriate IL-17 receptor like polypeptide (IL17r) expression. These
 CC include, for example immune disorders (e.g. inflammation, diabetes and
 CC transplant rejection), infections (e.g. hepatitis and septicemia),
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
 CC breast cancer), reproductive disorders (e.g. infertility and
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 CC DNA and its complements may also be used as diagnostic probes to detect and
 CC quantitate the presence of similar nucleic acids in samples and identify
 CC patients needing restorative therapy. The IL17r may also be used as
 CC antigens in the production of antibodies against the proteins and in
 CC assays to identify modulators of expression and activity. The
 CC anti-IL17r antibodies and antagonists may also be used to down regulate
 CC expression and activity.
 CC Note: This sequence is not given in the specification but is based on the
 CC human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)
 CC and has been created according to information given in claim 22.
 XX

Sequence 738 AA;
 Query Match 93.9%; Score 1423; DB 22; Length 738;
 Best Local Similarity 94.9%; Pred. No. 5.2e-151;
 Matches 263; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
 2 DTCCGWRKAAARPRCLVANEVGPASRNSGLYNTTFYDNTYLPVGRVIAQAQNT 61
 DB 37 DTCCWR-----GVGPASRNSGLYNTTFYDNTYLPVGRVIAQAQNT 82
 62 ISQACHQVAVTILSPGALIEFLKGRVILEELSEKSGROCOQLILKDPQLNSFKR 131
 DB 83 ISQACHQVAVTILSPGALIEFLKGRVILEELSEKSGROCOQLILKDPQLNSFKR 142
 122 TGMESQFLANKFETDFYKVVPPFSIKNESNYHFFTRACDILLQDNLCKPFWKP 181
 DB 143 TGMESQFLANKFETDFYKVVPPFSIKNESNYHFFTRACDILLQDNLCKPFWKP 202
 182 RNLNISQSGSDMVSDHAPNFGFRFFLYHLKHEGPFKRTCKOQTETTSCILQN 241
 DB 203 RNLNISQSGSDMVSDHAPNFGFRFFLYHLKHEGPFKRTCKOQTETTSCILQN 262
 242 VSPGDYIIELVDVDTNTRKVMYALKPVHSPWAGPIR 278
 DB 263 VSPGDYIIELVDVDTNTRKVMYALKPVHSPWAGPIR 299
 RESULT 9
 AAU09956
 ID AAU09956 standard; Protein: 738 AA.
 XX
 XX AAU09956;
 XX
 XX 14-FEB-2002 (first entry)
 XX

DE Human Interleukin 17 (hIL-17) receptor like protein substitution #6.
 XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KW vascular; cytostatic; anti-leukemic; dermatological; renal; osteopathic;
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 XX mitein.
 OS Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 XX Misc-difference 515 /label= Asp, Glu
 FT W0200168859-A2.
 XX 20-SEP-2001.
 XX 15-MAR-2001; 2001WO-US08678.
 XX 16-MAR-2000; 2000US-189816P.
 XX 28-NOV-2000; 2000US-0724460.
 XX (AMGE-) AMGEN INC.
 XX Jing S;
 XX WPI; 2001-611392/70.
 XX Nucleic acids encoding interleukin 17 receptor like polypeptides,
 XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
 XX diabetes, psoriasis and glaucoma -
 XX Claim 23; Page -: 158pp; English.
 XX The invention describes novel nucleic acids encoding interleukin (IL) 17
 XX receptor like polypeptides useful as vaccines and in gene therapy. These
 XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
 XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 XX osteopathic, vascular, cytostatic, anti-leukemic, anti-infectivity and
 XX ophthalmological activities. The IL-17 receptor like nucleic acids and
 XX proteins may be used to prevent and treat diseases associated with
 XX inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
 XX include, for example immune disorders (e.g. inflammation, diabetes and
 XX transplant rejection), infections (e.g. hepatitis and septicemia),
 XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal
 XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 XX (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
 XX breast cancer), reproductive disorders (e.g. infertility and
 XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 XX DNA and its complements may also be used as diagnostic probes to detect and
 XX quantify the presence of similar nucleic acids in samples and identify
 XX patients needing restorative therapy. The IL17rlp may also be used as
 XX antigens in the production of antibodies against the proteins and in
 XX assays to identify modulators of expression and activity. The
 XX anti-IL17rlp antibodies and antagonists may also be used to down regulate
 XX expression and activity.
 XX Note: This sequence is not given in the specification but is based on the
 XX human Interleukin 17 (IL-17) receptor like protein sequence (AA009904)
 XX and has been created according to information given in claim 23.
 XX Sequence 738 AA;

Query Match 93.9%; Score 1423; DB 22; Length 738;
 Best Local Similarity 94.9%; Pred. No. 5.2e-151;

Matches 263; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
 QY 2 DTCCGHEKAAARPLCVANGSGPARRNSGLYNTFKYDNTTYLNPVKEHVIADQNIT 61
 DB 37 DTCCGWR-----GVGPARNSGLYNTFKYDNTTYLNPVKEHVIADQNIT 82
 QY 62 ISQVACHDOVAVTLSPGALGTEFLKGFVILEELSEKQCOOLILKDPKQLASSFKR 121
 DB 83 ISQVACHDOVAVTLSPGALGTEFLKGFVILEELSEKQCOOLILKDPKQLASSFKR 142
 QY 122 TGMESQPLAMKETDYFVKVYPPFSIKNESNYHFFETFRACDLLODNLACPFKWP 181
 DB 143 TGMESQPLAMKETDYFVKVYPPFSIKNESNYHFFETFRACDLLODNLACPFKWP 202
 QY 182 RLNIISQSGSDMQVSDHAPHNFGFRFFLYLHKHSGPFRRKTCOSQOTTTSCILQN 241
 DB 203 RLNIISQSGSDMQVSDHAPHNFGFRFFLYLHKHSGPFRRKTCOSQOTTTSCILQN 262
 QY 242 VSPGDYIIELVDDTNTTRKVMYALKPVHSPWAGPIR 278
 DB 263 VSPGDYIIELVDDTNTTRKVMYALKPVHSPWAGPIR 299
 RESULT 10
 AAU09957
 ID AAU09957 standard; Protein; 738 AA.
 XX AC AAU09957;
 XX 14-FEB-2002 (first entry)
 XX Human Interleukin 17 (hIL-17) receptor like protein substitution #7.
 XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 XX anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 XX hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 XX anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 XX vascular; cytostatic; anti-leukemic; anti-infectivity; ophthalmological;
 XX hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 XX bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 XX mitein.
 XX Homo sapiens.
 XX Synthetic.
 XX Key Location/Qualifiers
 XX Misc-difference 602 /label= Cys, Ala, Ser
 XX W0200168859-A2.
 XX 20-SEP-2001.
 XX 15-MAR-2001; 2001WO-US08678.
 XX 16-MAR-2000; 2000US-189816P.
 XX 28-NOV-2000; 2000US-0724460.
 XX (AMGE-) AMGEN INC.
 XX Jing S;
 XX WPI; 2001-611392/70.
 XX Nucleic acids encoding interleukin 17 receptor like polypeptides,
 XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
 XX diabetes, psoriasis and glaucoma -
 XX Claim 24; Page -: 158pp; English.
 XX The invention describes novel nucleic acids encoding interleukin (IL) 17
 XX receptor like polypeptides useful as vaccines and in gene therapy. These
 XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
 XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 XX osteopathic, vascular, cytostatic, anti-leukemic, anti-infectivity and
 XX ophthalmological activities. The IL-17 receptor like nucleic acids and
 XX proteins may be used to prevent and treat diseases associated with
 XX inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
 XX include, for example immune disorders (e.g. inflammation, diabetes and
 XX transplant rejection), infections (e.g. hepatitis and septicemia),
 XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal
 XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 XX (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
 XX breast cancer), reproductive disorders (e.g. infertility and
 XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 XX DNA and its complements may also be used as diagnostic probes to detect and
 XX quantify the presence of similar nucleic acids in samples and identify
 XX patients needing restorative therapy. The IL17rlp may also be used as
 XX antigens in the production of antibodies against the proteins and in
 XX assays to identify modulators of expression and activity. The
 XX anti-IL17rlp antibodies and antagonists may also be used to down regulate
 XX expression and activity.
 XX Note: This sequence is not given in the specification but is based on the
 XX human Interleukin 17 (IL-17) receptor like protein sequence (AA009904)
 XX and has been created according to information given in claim 23.
 XX Sequence 738 AA;

immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, osteopathic, vascular, cytostatic, anti-leukemic, anti-infectivity and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor-like polypeptide (IL17rlp) expression. These include, for example immune disorders (e.g. hepatitis and septicemia), transplant rejection), infections (e.g. hepatitis and diabetes) and weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis), asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcemia), vascular disorders (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also used as diagnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17rlp may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-IL17rlp antibodies and antagonists may also be used to down regulate expression and activity.

Note: This sequence is not given in the specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 24.

Sequence 738 AA;

```

Query Match      93.9%; Score 1423; DB 22; Length 738;
Best Local Similarity 94.9%; Pred. No. 5.2e-151;
Matches 263; Conservative 0; Mismatches 14; Gaps 1;

      QY      2  DTCGWRKAAAPRLCVANECVGPASNSGLYNITFKYDNCCTYTLNVPVGEHVLAADAQNT 61
      |||||
      DB      37 DTCGWR-----GVGPASNSGLYNITFKYDNCCTYTLNVPVGEHVLAADAQNT 82

      QY      62 ISOTACHDOVATILWSFGALGIEFLAGFVILEELKSEGRQCOOLILKDPKQLNSSFPR 121
      |||||
      DB      83 ISOTACHDOVATILWSFGALGIEFLAGFVILEELKSEGRQCOOLILKDPKQLNSSFPR 142

      QY      122 TGMESQPFLLNMKEETDYFVKVVPVPPSPKIKESNTHPFFETRACDLLQLQDPNLACKPFWKPR 181
      |||||
      DB      143 TGMESQPFLLNMKEETDYFVKVVPVPPSPKIKESNTHPFFETRACDLLQLQDPNLACKPFWKPR 202

      QY      182 RNLLNLSQHSQDMQVGFDAHPANFQFREFYLYHLKLKHEGFFPKTKCKQEQTTETTSCLLQ 241
      |||||
      DB      203 RNLLNLSQHSQDMQVGFDAHPANFQFREFYLYHLKLKHEGFFPKTKCKQEQTTETTSCLLQ 262

      QY      242 VSPGDYIILVDQDTNTRKVMHYALKKPVHSPWAGPIR 278
      |||||
      DB      263 VSPGDYIILVDQDTNTRKVMHYALKKPVHSPWAGPIR 299

```

RESULT 11

AAU09951
ID AAU09951 standard; Protein: 738 AA.

AC 09951:

14-FEB-2002 (first entry)

Human Interleukin 17 (hIL-17) receptor like protein substitution #1.

Interleukin 17: hIL-17 receptor like protein; immunomodulatory;
anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
hepatic; anabolic; anorectic; anti-Alzheimer's; anti-parkinsonian;
osteoclast; anti-asthmatic; dermatological; renal; osteopathic;
vasculature; anti-atherogenic; neuroprotective; anti-amyloid;
hepatitis; anorexia; cachexia; muscle; functional; myofascial;
bone disease; vascular disorder; eye disorder; cancer; human; mutant;
mouse.

OS	Homo sapiens.
OS	Synthetic.
XX	
XX	
EH	Key
FT	Location/Qualifiers
FT	Misc-difference 45
XX	/label= Gly, Pro or Ala
XX	
PN	WQ200168859-A2.

XX
PD 20-SEP-2001.

15-MAR-2001: 2001WO-US08678.

16-MAR-2000: 2000US-189816P.

PR 28-NOV-2000; 2000US-0724460.
XX

PA' (AMGE-) AMGEN INC.
XX

PI - Jing S;
YY

DR WPI; 2001-611392/70.

PT Nucleic acids encoding interleukin 17 receptor like polypeptides,
PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
PT diabetes, psoriasis and glaucoma -

PS Claim 18; Page -; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, osteopathic, vascular, cytostatic, IL-17-leukaemic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These include, for example immune disorders (e.g. inflammation and diabetes and transplant rejection), infections (e.g. hepatitis and septicemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also be used as diagnostic probes to detect and quantify the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17rlp may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-IL17rlp antibodies and antagonists may also be used to down regulate expression and activity.

Note: This sequence is not given in the specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AA009904) and has been created according to information given in claim 18.

XX
Sequence 738 AA.

Query Match 93.5% Score 1416: DB 22: Length 738:

Best Local Similarity	94.6%	Pred: No. 3.2e-150;	
Matches 262:	Conservative	0: Mismatches	1: Indels
		14: Gaps	1:

05 2 DTCCGTRMKAABBPBLCVANEVCVCPASPNSCIYNITFEKYDNCTTYI.NPVGKHYIADAONIT 61

[illegible]

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

Db 143 TGESQPLNMFETDYKVVPPSPKSNTHPPFTRACDILLOPNLACKPWP 202
 QY 162 RNLTISQSGDMQVSDHAPNFCGFFLYLHYLKEGFFKTKCKQBTETTSCLQN 241
 Db 203 RNLTISQSGDMQVSDHAPNFCGFFLYLHYLKEGFFKTKCKQBTETTSCLQN 262
 QY 242 VSPGDYIIELVDYDNTTKVNYALKPVHSPWAGPIR 278
 Db 263 VSPGDYIIELVDYDNTTKVNYALKPVHSPWAGPIR 299

RESULT 12
 AAU09952
 ID AAU09952 standard; Protein; 738 AA.
 AC AAU09952;
 DT 14-FEB-2002 (first entry)
 XX Human Interleukin 17 (hIL-17) receptor like protein substitution #2.
 XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 KW anti-inflammation; anti-diabetic; immunosuppressive; anti-microbial;
 KW hepatic; anabolic; anorectic; anti-Alzheimer's; anti-parkinsonian;
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 KW mutin.
 XX Homo sapiens.
 OS Synthetic.
 XX Key
 FH Location/Qualifiers
 FT Misc-difference 227
 FT /label- Phe, Leu, Val, Ile, Ala, Tyr
 XX WO200168859-A2.
 XX 20-SEP-2001.
 XX 15-MAR-2001; 2001WO-US08678.
 XX 16-MAR-2000; 2000US-189816P.
 XX 28-NOV-2000; 2000US-0724460.
 XX (AMGE-) AMGEN INC.
 XX Jing S;
 XX WPI; 2001-611392/70.
 XX Nucleic acids encoding interleukin 17 receptor like polypeptides,
 FT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
 FT diabetes, psoriasis and glaucoma.
 XX Claim 19; Page -: 158pp; English.
 XX The invention describes novel nucleic acids encoding interleukin (IL) 17
 CC receptor like polypeptides useful as vaccines and in gene therapy. These
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-Alzheimer's, renal,
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and
 CC proteins may be used to prevent and treat diseases associated with
 CC inappropriate IL-17 receptor like polypeptide (IL17rip) expression. These
 CC include, for example immune disorders (e.g. inflammation, diabetes and
 CC transplant rejection), infections (e.g. hepatitis and septicemia),
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease

CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 CC (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
 CC breast cancer), reproductive disorders (e.g. infertility and
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 CC DNA and its complements may also be used as diagnostic probes to detect and
 CC quantitate the presence of similar nucleic acids in samples and identify
 CC patients needing restorative therapy. The IL17rip may also be used as
 CC antigens in the production of antibodies against the proteins and in
 CC assays to identify modulators of expression and activity. The
 CC anti-IL17rip antibodies and antagonists may also be used to down regulate
 CC expression and activity.
 CC Note: This sequence is not given in the specification but is based on the
 CC human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)
 CC and has been created according to information given in claim 19.
 XX Sequence 738 AA;
 SQ

Query Match 93.5%; Score 1416; DB 22; Length 738;
 Best Local Similarity 94.6%; Pred. No. 3.2e-150;
 Matches 262; Conservative 0; Mismatches 1; Indels 14; Gaps 1;

QY 2 DFCGWRMAARPRLCYANEGVGPASRNSGLNITFFKYDNCNTTTLNVPVGHVIAQAQNT 61
 Db 37 DFCGWR-----GVGPASRNSGLNITFFKYDNCNTTTLNVPVGHVIAQAQNT 82
 QY 62 ISOYACHDQVAVTILMSFGALGTEFLKGFVILELSEKSGRCCQOLILKDPKOLNSSPKR 121
 Db 83 ISOYACHDQVAVTILMSFGALGTEFLKGFVILELSEKSGRCCQOLILKDPKOLNSSPKR 142
 QY 122 TGESQPLNMFETDYKVVPPSPKSNTHPPFTRACDILLOPNLACKPWP 181
 Db 143 TGESQPLNMFETDYKVVPPSPKSNTHPPFTRACDILLOPNLACKPWP 202
 QY 182 RNLTISQSGDMQVSDHAPNFCGFFLYLHYLKEGFFKTKCKQBTETTSCLQN 241
 Db 203 RNLTISQSGDMQVSDHAPNFCGFFLYLHYLKEGFFKTKCKQBTETTSCLQN 262
 QY 242 VSPGDYIIELVDYDNTTKVNYALKPVHSPWAGPIR 278
 Db 263 VSPGDYIIELVDYDNTTKVNYALKPVHSPWAGPIR 299

RESULT 13
 AAU04958
 ID AAU04958 standard; Protein; 728 AA.
 AC AAU04958;
 DT 24-OCT-2001 (first entry)
 XX Human Interleukin 17 receptor, IL-17RH4.
 XX Human; Interleukin-17 receptor; IL-17RH4; agonist; antagonist;
 KW PRO20026; DNA 154095-2998; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; diabetes mellitus;
 KW allergic disease; asthma; demyelinating disease;
 KW degenerative cartilaginous disorder; transplantation associated disease.
 XX Homo sapiens.
 XX Key
 FH Location/Qualifiers
 FT Region 19..24
 FT Modified-site 31..34
 FT Modified-site 38..41
 FT Modified-site 56..59
 FT Modified-site 113..116
 FT Modified-site 147..150

XX WPI; 2001-611392/70.
 DR N-PSDB; AAS16201.
 XX
 XX Nucleic acids encoding interleukin 17 receptor like polypeptides,
 PT useful for preventing, diagnosing and treating, e.g. leukaemia, asthma,
 PT diabetes, psoriasis and glaucoma -
 XX
 XX Claim 2; Fig 1; 158pp; English.

XX The invention describes novel nucleic acids encoding interleukin (IL) 17
 CC receptor like polypeptides useful as vaccines and in gene therapy. These
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 CC osteopathic, vascular, cytostatic, anti-leukemic, anti-fertility and
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and
 CC proteins may be used to prevent and treat diseases associated with
 CC inappropriate IL-17 receptor like polypeptide (IL17rip) expression. These
 CC include, for example immune disorders (e.g. inflammation, diabetes and
 CC transplant rejection), infections (e.g. hepatitis and septicemia),
 CC dysfunctions (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 CC (e.g. stroke and atherosclerosis and cancers (e.g. leukaemia, myeloma and
 CC breast cancer), reproductive disorders (e.g. infertility and
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 CC DNA and its complements may also be used as diagnostic probes to detect and
 CC quantitate the presence of similar nucleic acids in samples and identify
 CC patients needing restorative therapy. The IL17rip may also be used as
 CC antigens in the production of antibodies against the proteins and in
 CC assays to identify modulators of expression and activity. The
 CC anti-IL17rip antibodies and antagonists may also be used to down regulate
 CC expression and activity. This is the amino acid sequence of human
 CC Interleukin 17 (IL-17) receptor like protein described in the method of
 CC the invention.
 CC Note: Residues 1-288 of this sequence correspond to residues 8-296 of the
 CC sequence shown in AA010601 which is incomplete in the specification.

XX Sequence 739 AA;

Query Match 91.5%; Score 1386; DB 22; Length 739;
 Best Local Similarity 98.8%; Pred. No. 7.7e-147;
 Matches 255; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 21 EGVGPASRNSGLYNTFFKYNCTTYLNPVKGKVIADQAQNTISQYACHDQVAVTILWSPG 80
 Db :|||||
 42 QGVGPASRNSGLYNTFFKYNCTTYLNPVKGKVIADQAQNTISQYACHDQVAVTILWSPG 101
 QY 81 ALGIEPLKGFVILEELKSGRQCOQLILDKPKQLNSFKRTGMESOPFLNMFETDYFV 140
 Db |||||
 102 ALGIEPLKGFVILEELKSGRQCOQLILDKPKQLNSFKRTGMESOPFLNMFETDYFV 161
 QY 141 KVPFSPKNSNYHPFFTRACDILLQPDNLACKPFWKPNLNISQHGSDMQVSDFA 200
 Db |||||
 162 KVPFSPKNSNYHPFFTRACDILLQPDNLACKPFWKPNLNISQHGSDMQVSDFA 221
 QY 201 PHNFGFRFYLHYLKHGEPFKRTCKEQTTTSCLLQNVSPGDIYIELVDVNTTRK 260
 Db |||||
 222 PHNFGFRFYLHYLKHGEPFKRTCKEQTTTSCLLQNVSPGDIYIELVDVNTTRK 281
 QY 261 VHYALKPVHSPWAGPIR 278
 Db |||||
 282 VHYALKPVHSPWAGPIR 299

RESULT 15

AAU11355

ID AAU11355 standard; Protein; 738 AA.

XX

AC AAU11355;

XX 26-MAR-2002 (first entry)
 XX Human DNAX cytokine receptor subunit 8 (DCRS8) polypeptide.
 XX
 XX Human; DNAX cytokine receptor subunit 8; DCRS8; phosphate labelling;
 KW gene therapy; protein therapy; immunological disorder.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 25 /label= Val
 FT /note= "Encoded by GYN"
 XX
 XX WO200190358-A2.
 XX
 XX 29-NOV-2001.
 XX
 XX 23-MAY-2001; 2001WO-US16767.
 XX
 XX 24-MAY-2000; 2000US-206862P.
 XX (SCHE) SCHEERIN CORP.
 XX
 XX Gorman DM;
 XX
 XX WPI; 2002-106198/14.
 XX N-PSDB; AAS18134.
 XX
 XX Isolated antigenic human or mouse DNAX receptor subunit-like
 PT polypeptide useful for detecting antibodies generated in response to
 PT presence of increased protein levels or immunological disorders -
 XX
 XX Claim 1; Page 25; 148pp; English.
 XX
 XX The invention relates to primate and rodent DNAX cytokine receptor
 CC subunit (DCRS) polypeptides and the polynucleotides encoding them. The
 CC receptors, or their portions may be useful as phosphate labelling enzymes
 CC to label general or specific substrates. The subunits may also be
 CC functional immunogens to elicit recognising antibodies or antigens
 CC capable of binding antibodies. A combination, e.g., including a DCRS can
 CC be used as an immunogen for the production of antisera or antibodies
 CC capable of distinguishing between other cytokine receptor family members.
 CC A purified DCRS can also be used as a reagent to detect antibodies
 CC generated in response to the presence of elevated levels of expression,
 CC or immunological disorders which lead to antibody production to the
 CC endogenous receptor. This sequence represents the human DCRS8
 CC polypeptide.
 XX
 XX Sequence 738 AA;
 SQ
 Query Match 88.7%; Score 1343.5; DB 23; Length 738;
 Best Local Similarity 90.6%; Pred. No. 4.8e-142;
 Matches 252; Conservative 2; Mismatches 9; Indels 15; Gaps 2;
 QY 1 ADTCGRWKAARPLCAVNEGVGPASRNSGLYNTFFKYNCTTYLNPVKGKVIADQAQNI 60
 Db |||||
 36 ADTCGW-----XGVGPASRNSGLYNTFFKYNCTTYLNPVKGKVIADQAQNI 81
 QY 61 TISQYACHDQVAVTILWSPGALGIEPLKGFVILEELKSGRQCOQLILDKPKQLNSFK 120
 Db |||||
 82 TISQYACHDQVAVTILWSPGALGIEPLKGFVILEELKSGRQCOQLILDKPKQLNSFK 141
 QY 121 RTGMESOPFLNMFETDYFVKVVPFSPKNSNYHPFFTRACDILLQPDNLACKPFWK 180
 Db |||||
 142 RTGMESOPFLNMFETDYFVR-LSPFSPKNSNYHPFFTRACDILLQPDNLACKPFWK 200
 QY 181 PENLNISQHGSDMQVSDFAHPNFGFRFYLHYLKHGEPFKRTCKEQTTTSCLLQ 240
 Db |||||
 201 PENLNISQHGSDMQVSDFAHPNFGFRFYLHYLKHGEPFKRTCKEQTTTSCLLQ 260
 QY 241 NVSPGDIYIELVDVNTTRKVVHYALKPVHSPWAGPIR 278

Mon May 19 09:52:38 2003

us-09-912-157-2_copy_36_313.rag

Page 12

DB 261 NVSPGDIIEVDVNTTRKMHYALKPVHSPWAGPIR 298

Search completed: May 19, 2003, 09:19:57
Job time : 25.9109 secs

GenCore version 5.1.4.p5.4578
Copyright: (c) 1993 - 2003 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: May 19, 2003, 09:16:08 ; Search time 10.263 seconds
(without alignments)
2604.041 Million cell updates/sec

Title: US-09-912-157-2_COPY_36_313

Perfect score: 1515

Sequence: 1 ADTCGRWKAARPRLCVAN.....RCVMHYALAPVHSPWAGPIR 278

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	691	45.6	564	2 T42695	hypothetical prote
2	99	6.5	341	2 H71716	190 kd antigen pre
3	95	6.3	1462	1 B36182	protein-tyrosine-p
4	93	6.1	353	2 T33782	hypothetical prote
5	93	6.1	872	2 T25186	hypothetical prote
6	91.5	6.0	421	1 Z28PIK	gene II protein -
7	91.5	6.0	758	2 T32210	3-isopropylmalate
8	88	5.8	1173	2 T51440	alpha-mannosidase
9	85.5	5.6	289	2 C36971	outer membrane pho
10	85.5	5.6	404	2 A28404	S-antigen - bovine
11	85	5.6	429	1 EHRT	Ig epsilon chain C
12	83	5.5	1121	2 T25715	hypothetical prote
13	82.5	5.4	420	2 T41870	ALK-EXO orf133 - B
14	82.5	5.4	461	2 T16225	hypothetical prote
15	82.5	5.4	632	2 T37257	hypothetical prote
16	82.5	5.4	1260	2 T20487	hypothetical prote
17	82	5.4	320	2 S70398	zona pellucida gly
18	81.5	5.4	320	1 A39479	homeotic protein m
19	81.5	5.4	839	2 F64171	hypothetical prote
20	81	5.3	286	2 D64400	hypothetical prote
21	80.5	5.3	363	2 S31780	peroxidase (EC 1.1
22	80.5	5.3	371	2 G86740	telcholic acid bios
23	80.5	5.3	498	2 H85040	hypothetical prote
24	80.5	5.3	526	2 T16124	hypothetical prote
25	80.5	5.3	538	2 T27433	hypothetical prote
26	80.5	5.3	670	2 AE2111	general secretion
27	80	5.3	2292	2 S35961	capsid polyprotein
28	79.5	5.2	377	2 JCS609	heat shock protein
29	79	5.2	2102	2 T15626	hypothetical prote

30	78	5.1	571	2 T38759	probable pyruvate
31	78	5.1	612	2 F81287	probable sugar tra
32	78	5.1	625	2 F81287	probable sugar tra
33	78	5.1	1014	2 H71602	protein with DnaJ
34	78	5.1	1795	2 F97713	190K antigen precu
35	78	5.1	2010	2 B71616	phosphatase (acid
36	78	5.1	2052	2 T18519	myosin X - bovine
37	77.5	5.1	226	2 AE1094	hypothetical prote
38	77	5.1	512	2 C64599	hypothetical prote
39	77	5.1	568	2 T39675	asparaginyl-trna s
40	77	5.1	1420	2 S54471	probable membrane
41	77	5.1	1589	1 RGEYC5	cell division cont
42	76.5	5.0	391	2 T38602	peroxidase (EC 1.1
43	76.5	5.0	321	1 S48390	hemocytic protein m
44	76.5	5.0	605	2 T07123	nine-cis-epoxycaro
45	76.5	5.0	711	2 T35281	hypothetical prote

ALIGNMENTS

RESULT 1

T42695 hypothetical protein DKFZp434N1928.1 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000

C:Accession: T42695

R:Boecker, H.; Boecker, M.; Brandt, P.; Meves, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, November 1999

A:Reference number: Z2230

A:Accession: T42695

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-564 <AAA>

A:Cross-references: EMBL:AL133097

A:Experimental source: adult testis; clone DKFZp434N1928

C:Genetics:

A>Note: DKFZp434N1928.1

Query Match 45.6% ; Score 691; DB 2; Length 564;

Best Local Similarity 99.2% ; Pred. No. 2.9e-56;

Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 155 HPFFFTTRACDLIQDNLACFPKPRNLNISQSGSDMQVSDFHAPHNFGFFFLHYK 214

Db 1 HPFFFTTRACDLIQDNLACFPKPRNLNISQSGSDMQVSDFHAPHNFGFFFLHYK 60

QY 215 LKHGPPFKRTCKOBTETTSCLLQNVSPGDIITELVDDTNTTKVMYALKPVHSPWA 274

Db 61 LKHGPPFKRTCKOBTETTSCLLQNVSPGDIITELVDDTNTTKVMYALKPVHSPWA 120

QY 275 GPIR 278

Db 121 GPIR 124

RESULT 2

H71716 190 kd antigen precursor (sca2) RP081 - Rickettsia prowazekii

C:Species: Rickettsia prowazekii

C>Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000

C:Accession: H71716

R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Slicheritz-Ponten, T.; Alsmark

Nature 396, 133-140, 1998

A>Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.

A:Reference number: A71630; MUID:99039499; PMID:9823893

A:Accession: H71716

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-341 <AND>

A:Cross-references: GB:AJ235270; GB:AJ235269; NID:g3860572; PID:CAA14551.1; PID:g386

A:Experimental source: strain Madrid E

C:Genetics:

A:Gene: sca2; RP001

Query Match 6.5%; Score 99; DB 2; Length 341;
 Best Local Similarity 22.1%; Pred. No. 0.21;
 Matches 69; Conservative 35; Mismatches 120; Indels 88; Gaps 15;

QY 15 RLIVANEGVGPASRN-----SGLNITP-----KYDNCVTYLVNPGKRVIAQAQ- 58
 DB 52 ELKVTIVGADGKTNVNGINISGLGVNKGQWKNIPKIQGRTT-----GLTIGADAEF 106
 QY 59 -----NTTISOYACHDOVAVTILMSPGALGI-EFLAGFRVILEEL 97
 DB 107 INNHEDVIGIAYSNLEKIYKNKLAGTAVGHELL-----SVYGLKELVKGFS--LQSI 157
 QY 98 KSEGRQCOQLIKDPKOLNSSP-KRTGMSQFELNMKFEYFVKVPPPSIKNE-----S 152
 DB 158 TSYG---HNTIKNSKNLKIIGKYONNFQTLNLYKYKYNLHPIPSIGFYDYSRAS 214
 QY 153 NYHPPFFTRACDILLOPN-----LACKPFWKPRN--LMSHGSDMQVSDH 199
 DB 215 NYKE--INVDIENLMQKSNQSFSSGAKIVSKPIISKNNIILTLASG----- 263
 QY 200 APHNGFRFFLYLKHEGPFKRTCKQRTTETTSCLQVSPGDYIIELVDDTNTTR 259
 DB 264 ---NIERFNKNTKVNAKATEFKQTLQTIIPKQPLGYNI--GNILMSIKINIVLL 318
 QY 260 KVMYALKPVHS 271
 DB 319 EYNYTHKKYHS 330

RESULT 3

B36182
 N:Alternate names: protein-tyrosine-phosphatase DPTP
 C:Species: Drosophila melanogaster
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 A:Accession: B36182
 R:Streuli, M.; Krueger, N.X.; Tsai, A.Y.M.; Salto, H.
 Proc. Natl. Acad. Sci. U.S.A. 86, 8698-8702, 1989
 A:Title: A family of receptor-linked protein tyrosine phosphatases in humans and Drosophila
 A:Reference number: A36182; PMID:90046860; PMID:2554325
 A:Accession: B36182
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-1462 <ST>
 A:Cross-references: GB:M27699; MID:g158188; PIDN:AAA28842.1; PID:g158189
 C:Genetics:
 A:Gene: Ptp69D
 A:Cross-references: FlyBase:FBgn0014007
 C:Superfamily: protein-tyrosine-phosphatase, receptor type PTP69D; fibronectin type III phosphatase homology
 C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-1462/Product: protein-tyrosine-phosphatase, receptor type PTP69D #status predicted
 F:29-806/Domain: extracellular #status predicted <EXT>
 F:38-114/Domain: immunoglobulin homology <IM>
 F:147-216/Domain: immunoglobulin homology <IM2>
 F:807-823/Domain: transmembrane #status predicted <TMN>
 F:824-1462/Domain: intracellular #status predicted <INT>
 F:917-1145/Domain: protein-tyrosine-phosphatase homology <PTP1>
 F:1213-1439/Domain: protein-tyrosine-phosphatase homology <PTP2>
 F:45-112,154-214/Disulfide bonds: #status predicted
 F:1097/Active site: Cys (phosphotyrosine intermediate) #status predicted
 F:1103/Binding site: substrate phosphate (Arg) #status predicted
 F:1391/Active site: Cys (phosphotyrosine intermediate) #status predicted
 F:1397/Binding site: substrate phosphate (Arg) #status predicted

Query Match 6.3%; Score 95; DB 1; Length 1462;
 Best Local Similarity 20.4%; Pred. No. 3.5;
 Matches 67; Conservative 45; Mismatches 100; Indels 116; Gaps 18;

QY 20 NEGVGVPASR-----NSGLNITFKYD-----NCTYLVNPGKRVIAQA 57

DB 259 NQGNDRPQKFFITLQAGTPTFTYHKDFINGSHSYLDHFKPNTTYFLRVGKNSING 318
 QY 58 -----QNTISOYACHDOV-----AVTILSPGALG-IEFLAGFRVILEEL 97
 DB 319 OPTQYQOGITLSY---DPIPIKVTGTASTIITIGWNPDPDIDYIOTYELIYSE- 374
 QY 98 KSEGRQCOQLIKDPKOLNSSP-KRTGMSQFELNMKFEYFVKVPPPSIKNESNTHPF 157
 DB 375 --SG-----EYKRVIEEAIYQNSRNLYM-----FDKLTATDYE-- 408
 QY 158 FFRTRACDILLOPNLACKPFW-----KPRNLNISOH-----GSDMQVSP 197
 DB 409 -FRVACSDLTK---TCGP-WSENVNVTMGVATKPTNLISIQCHDNVTRGSHAIW 462
 QY 198 DHAPHNFGFRFFLYLKHE-----GPFRTCKQRTTETTSCLQVSPGDY 247
 DB 463 DVPTKNGKVVSYLHLLGNPMSTVDREMGPKIRIDEPHKT-----LYESVSPNTY 517
 QY 248 IIELVDDTNTTRK---VMHYALKFVHSP.272
 DB 518 TTVTSATIRKKNKNGEPATGSCLPVSTP.545

RESULT 4

T33782
 hypothetical protein C39F7.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
 C:Accession: T33782
 R:Maggi, L.; Scheet, P.; Dubbelde, C.
 submitted to the EMBL Data Library, October 1998
 A:Description: The sequence of C. elegans cosmid C39F7.
 A:Reference number: 231407
 A:Accession: T33782
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-353 <MA>
 A:Cross-references: EMBL:AF101310; PIDN:AAC69214.1; GSPDB:GN00023; CESP:C39F7.5
 A:Experimental source: strain Bristol N2; clone C39F7
 C:Genetics:
 A:Gene: CESP:C39F7.5
 A:Map position: 5
 A:Introns: 14/2; 45/3; 224/1
 C:Superfamily: Caenorhabditis elegans hypothetical protein C39F7.5

Query Match 6.1%; Score 93; DB 2; Length 357;
 Best Local Similarity 23.4%; Pred. No. 0.82;
 Matches 51; Conservative 24; Mismatches 65; Indels 78; Gaps 10;

QY 101 GRCQOQLIKDPKOLNSSPKFR---TGMSQFP-----LNM---KEPTDYFKVV 143
 DB 26 GLSARNVLRAVSRLLKFSFKKSTRDQIRPFELIKSWPVDLNLALAEAD--SKLL 83
 QY 144 PPSIKNESNYPPFFTRACDILLOPNLACKPFWKPR---NLNI-----186
 DB 84 EF-----QRLCDNSRKFTNSFLRDFSGFTVSGNLNIFLFTSTRANRA 128
 QY 187 -SQHGSDMQVS--FOHAPHN-----GFRFFLYLKHEGPFKRTCKQEQ.230
 DB 129 VSRCTNLIAISYNDENFEDLCEQKFLAEQDAVEIPLASYYINEQWPNLEQ 188
 QY 231 TTTFTSCL-----LQVSPGDYIIELVDDTNT 257
 DB 189 LCTDFGCFKLEEDYKKNYKODLAHGLIIEVVDGNT 226

RESULT 5

T25186
 hypothetical protein T23P6.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
 C:Accession: T25186

Query Match 5.8%; Score 88; DB 2; Length 1173;
Best Local Similarity 21.8%; Pred. No. 12;
Matches 76; Conservative 38; Mismatches 102; Indels 132; Gaps 20;

QY 3 TCGNRKAAARPLCVANEGVGPASRNSGLYNIFKYNCTVTLNPKKH-VIADAQNT 61
DB 346 TCG-----PEPALCOFD-----FARMG-----FKYELC-----FWGHPVETLENVQ 385
QY 62 ISQACHQV-ANTILNSPGALGIFLKGKRVV-LEELKSEKQCOOLILKPKQLNSF 119
DB 386 ERAKLIDQYKXSTYRNTLLPLGDFYIISIDAEAFNYQMLF----- 434
QY 120 KRTGHSOPFLN--MKFET--DYF-----VKKVPFPPSKNE----- 151
DB 435 --DHINGNPILNAEALFGLEDYFRTVREADRYNRPQGVGSGVGFPSLSGDFTY 492
QY 152 -----SNVH-----PFEFTRACDILQ-----PDLNAC 175
DB 493 ADRODTWSGYYSRPF--KAVDRVLEHLRGAETNSFLGYCHRIQCEKFTSTY 549
QY 176 RPFKPNLNIQSGDMQ-VSFDHAPNFGFRFFLYLKLKHEGPKRKC----- 226
DB 550 KLTAAARNLALFQHDGVTGTAKDYVQDYGR---METSLOQLQIFNSKALEVLLGIRH 606
QY 227 KQEQTTETTSCLLQNSPGDYIIELVDDTNTKRVHYALKPVHSPWA 274
DB 607 EKEKSDQ-----SPSFFEAQMS-----KYDARPVKPIA 637

RESULT 9

C36971
outer membrane phospholipase A (EC 3.1.1.-) precursor - Proteus vulgaris
C:Species: Proteus vulgaris
C:Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 18-Jun-1999
C:Accession: C36971; S40130
R:Brook, R.G.P.M.; Brinkman, E.J. van Bortel, R.; Bekkers, A.C.A.P.A.; Verheij, H.M.; Tomm
J. Bacteriol. 176, 861-870, 1994
A:Title: Molecular characterization of enterobacterial plda genes encoding outer membra
A:Reference number: A36971; MUID:94131966; PMID:8300539
A:Accession: C36971
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-289 <BRO>
A:Cross-references: EMBL:X76902; NID:9436889; PIDN:CAA54224.1; PID:9436890
A:Note: authors translated the codon GAG for residue 74 as Gly and CGA for residue 115
C:Genetics:
A:Gene: plda
C:Superfamily: bacterial phospholipase A1
C:Keywords: carboxylic ester hydrolase

Query Match 5.6%; Score 85.5; DB 2; Length 289;
Best Local Similarity 26.5%; Pred. No. 3.1;
Matches 43; Conservative 16; Mismatches 58; Indels 45; Gaps 8;

QY 5 GWRKKAARPLCVANEGV-----GPASRNSGLYNITKYN-----CTYLL 46
DB 6 GLLAAALPFFCAQEAETIDKVDTPAVRGSIIANLQEHNDPFLTPYESNLLTYT 65
QY 47 NPVGKHVIAQAQNTISQYACHQDVAVTI-----LMSPGALGIEFLKGRVILE-----ELK 98
DB 66 SLDLKKAI-----ESYNSDNANKDEKVKFOLSAPLNR-GILGNSLGLASTQRSWOLS 121
QY 99 SEGRQCOOLILKPKQLNSFKRGMESOPPLANKFETDYFV 140
DB 122 NTGE-----SAPFETNYEPQLFLG--FATDIYV 148

RESULT 10

A28404
S-antigen - bovine
N:Antigen names: 48K rhodopsin-binding protein; arrestin
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 17-Nov-2000

C:Accession: B28404; A28404; A25826; A23619; S02144; S51073; I46054
R:Shinohara, T.; Dietschold, B.; Craft, C.M.; Wistow, G.; Early, J.J.; Donoso, L.A.;
Proc. Natl. Acad. Sci. U.S.A. 84, 6975-6979, 1987
A:Title: Primary and secondary structure of bovine retinal S antigen (48-kDa protein)
A:Reference number: A28404; MUID:88041034; PMID:3478675
A:Accession: B28404
A:Molecule type: mRNA
A:Residues: 1-404 <SHI>
A:Cross-references: GB:J02955; NID:g162671; PIDN:AAA30378.1; PID:g162672
A:Accession: A28404
A:Molecule type: protein
A:Residues: 2-53; 56-66; 74-96; 103-117; 133-165; 176-226; 251-257; 299-308; 322-333; 355-367;
R:Yamakita, K.; Takahashi, Y.; Sakuragi, S.; Matsubara, K.
Biochem. Biophys. Res. Commun. 142, 904-910, 1987
A:Title: Molecular cloning of the S-antigen cDNA from bovine retina.
A:Reference number: A25826; MUID:87156714; PMID:2950857
A:Accession: A25826
A:Molecule type: mRNA
A:Residues: 1-34; 136-118; 176-178; 316; 318-404 <YAM>
A:Cross-references: GB:M15115; NID:g162669; PIDN:AAA30377.1; PID:g162670
A:Experimental source: retina
A:Note: the authors translated the codon CTT for residue 35 as Val, GTG for residue 1
as Gln, and GAG for residue 379 as Gln
R:Wistow, G.J.; Katial, A.; Craft, C.; Shinohara, T.
FEBS Lett. 196, 23-28, 1986
A:Title: Sequence analysis of bovine retinal S-antigen. Relationships with alpha-tran
A:Reference number: A23619; MUID:86108925; PMID:3080338
A:Accession: A23619
A:Molecule type: mRNA
A:Residues: 166-404 <WIS>
A:Cross-references: GB:X03454; NID:975; PIDN:CAA27179.1; PID:g76
R:Taunasa, S.; Shichi, H.
Biochim. Biophys. Acta 994, 191-193, 1989
A:Title: The amino acid sequence of S-antigen: N-terminus and uveitogenic peptides.
A:Reference number: S02144; MUID:89088273; PMID:2910351
A:Accession: S02144
A:Molecule type: protein
A:Residues: 5-13; 198-229 <TSU>
R:Kieselbach, T.; Irrgang, K.D.; Rueppel, H.
Eur. J. Biochem. 226, 87-97, 1994
A:Title: A segment corresponding to amino acids Val170-Arg182 of bovine arrestin is c
A:Reference number: S51073; MUID:95045604; PMID:7957262
A:Accession: S51073
A:Status: preliminary
A:Molecule type: protein
A:Residues: 170-182 <KIE>
R:Smith, W.C.; Milam, A.H.; Dugger, D.; Arendt, A.; Hargrave, P.A.; Palczewski, K.
J. Biol. Chem. 269, 15407-15410, 1994
A:Title: A splice variant of arrestin. Molecular cloning and localization in bovine r
A:Reference number: A54008; MUID:94253112; PMID:7515057
A:Accession: I46054
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-369; A' <SMI>
A:Cross-references: EMBL:U08346; NID:g474378; PIDN:AAA20465.1; PID:g520467
C:Superfamily: arrestin
C:Keywords: blocked amino end; glycoprotein
F:1-404/Product: S-antigen, long form #status predicted <NAV>
F:5-404/Product: S-antigen, short form #status predicted <MA2>
F:170-182/Region: rhodopsin binding
F:1/Modified site: blocked amino end (Met) #status experimental
F:128-143/Disulfide bonds: #status predicted
F:228,271/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.6%; Score 85.5; DB 2; Length 404;
Best Local Similarity 20.6%; Pred. No. 4.9;
Matches 61; Conservative 32; Mismatches 88; Indels 115; Gaps 15;

QY 48 PVGKGV-----TADAQNTI-----SQFACH-----DOVANTILNSPGALGIEFLKGRVILE 95
DB 6 PAPNHYFKKISDKSVIILGKRYDIDHVERPVGWVLVDP-----ELVKGKRVY- 59
QY 96 ELKSEGRQCOOLILKPKQLNSFKRGMESOPPLANKFETD-YFVKVFPFPI----- 148

DB 60 -----SLTCAF-RYQEDIDVWGLSFRDLTFSQVQVPPVGCASCAT 100
QY 149 -----ANESNYHPPFFRACDILLQDNLACKPFWKPNLNISO----- 188
DB 101 TRLQESLKKLGANTYPP-----LTLFPDYLPCSVMLQAPQDVGSCGVDFEIKAF 152
QY 189 --HGSDQV-----SFDHAPHNFG-----FFFFLYHKL----- 216
DB 153 ATHSTVEDKIPKSSVRLIRKQVHAPRDMGQPPRAEASQWFFMSDKPLRLAVLSKE 212
QY 217 --HEGPFK---RKTCKQKQVTTTSCLLQNV-----PCDYIIEIIVDDVNTTRV 261
DB 213 IYIGEDIPVTVANTSTKTKIKVLYVEQVNVVLSYDIYIKVVAEAEQKV 268

RESULT 11
EHT

Ig epsilon chain C region - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999
C:Accession: A93442; A90937; A02143
R:Hellman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.
Nucleic Acids Res. 10, 6041-6049, 1982
A:Title: Structure and evolution of the heavy chain from rat immunoglobulin E.
A:Reference number: A93442; MUID:83064537; PMID:6292865
A:Accession: A93442
A:Molecule type: mRNA
A:Residues: 1-429 <HEL>
R:Experimental source: strain LOU/c/Nal, immunocytoxa IR2
DNA 1, 335-343, 1982
A:Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction,
A:Reference number: A90937; MUID:83182019; PMID:6820340
A:Contents: myeloma IR162

A:Accession: A90937
A:Molecule type: mRNA
A:Residues: 'N', 169-307, 'I', 309-342 <KIN>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:118-80/Domain: immunoglobulin homology <IM1>
F:118-186/Domain: immunoglobulin homology <IM2>
F:223-231/Domain: immunoglobulin homology <IM3>
F:327-398/Domain: immunoglobulin homology <IM4>
F:146,99,170,240,265,369,419/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match. 5.6%; Score 85; DB 1; Length 429;
Best Local Similarity 18.6%; Pred. No. 5.9;
Matches 52; Conservative 42; Mismatches 92; Indels 94; Gaps 11;

QY 56 DAQNTISQYAC---HQVATILNSPGALGIFELGPRVILEELKSGRCQQLIKDP 112
DB 115 NAFESTIQLTCFYGIHNDVSIHW-----LMDRKITYETHAQNVLIKE 159
QY 113 KOLNSFKRTGMSOPFLMFEFDYFKVVPFSPKSNESNYHPFFRTRACD----- 165
DB 160 GKLASTYSLNTQQQWMS---ESTETCKVT-----SQGENTWAHTRCSDDEPRGV 208
QY 166 --LLQPDNLACKPFWKR-----NLNIS-----HQGSDMQVSDHAPHN- 203
DB 209 IYILIPSPDLTYNGTFLCLVDLESEENITVTVWRERKKSIGSASQSRSTKH--HNA 266
QY 204 -----FGFRFFYLHY-----KLKHEGPFKRTK-----KQE 229
DB 267 TTSITSILPVDKMDIEGGYQCRVDHPFKPIVRSITKAPKRSAPETVFLPPREE 326
QY 230 QTTETTSCLQNVSPGDIYIELVDVNTTRKVMYALKPV 269
DB 327 KOKTILCLQNFPEDISVQMLQSLIPKASQSTTTL 366

RESULT 12

T25715
hypothetical protein F19F10.11a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T25715
R:Kellen, J.; Wamsley, P.
submitted to the EMBL Data Library, April 1997
A:Description: The sequence of C. elegans cosmid F19F10.
A:Reference number: Z20073
A:Accession: T25715
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1121 <REL>
A:Cross-references: EMBL:U97005; PIDN:AA52289.1; GSPDB:GN00023; CESP:F19F10.11a
A:Experimental source: strain Bristol N2; clone F19F10
C:Genetics:
A:Gene: CESP:F19F10.11a
A:Map position: 5
A:Introns: 19/3; 54/2; 87/2; 120/2; 162/2; 187/2; 337/2; 432/2; 466/3; 833/2; 868/2

Query Match 5.5%; Score 83; DB 2; Length 1121;
Best Local Similarity 24.3%; Pred. No. 32;
Matches 50; Conservative 29; Mismatches 79; Indels 48; Gaps 10;

QY 79 PGALGTEFLGPRVILEELKSGRCQQLIKDPKOLNSFKRTGMSQPP--LNKFFET 136
DB 769 PKLAESFTEPVRI-----PEIRSSQQLIAGSPSETLDKDKVQEPETEKEKIVKREA 822
QY 137 -----DYFV-KVVPFSPKSNESNY--HPFFR-TRACD---LLQPDNLACKPFWKPNL 184
DB 823 VEDETFYVEREIPAPSLSPRAEILKPAWFRATSKYDKAKIALAKDKPAPKPVKVPVST 882
QY 185 NISQHSQMQVSDHAPHNFGFRFFLYHKLHEGPFKRTKCKQVTTTSCLLQNVSP 244
DB 883 SCVQCCTP-----KHEGLRKECVDDR-----LPFLNVRK 915
QY 245 GDYIIEIIVDDVNTTRKVMYALKPVH 270
DB 916 GAIPLELTPPI-FNRKAIFCLEHMH 940

RESULT 13

T41870
ALK-EXO orf133 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
C:Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV
A:Variety: isolate T3
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: T41870
R:Gomi, S.; Matilma, K.; Maeda, S.
J. Gen. Virol. 80, 1323-1337, 1999
A:Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A:Reference number: Z22020; MUID:99281911; PMID:10355780
A:Accession: T41870
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-420 <KAM>
A:Cross-references: EMBL:L33180; MID:93745835; PIDN:AA63799.1; PID:93745952
A:Experimental source: isolate T3
C:Genetics:
A:Note: alk-exo
C:Superfamily: OpMVNP alkaline exonuclease

Query Match 5.4%; Score 82.5; DB 2; Length 420;
Best Local Similarity 21.2%; Pred. No. 9.8;
Matches 48; Conservative 27; Mismatches 74; Indels 77; Gaps 11;

QY 48 PVCKHVIADAQNTISQYACHQVNTI-----LNSPGALGTEFLGPRVILEEL 97
DB 227 FMGFTYVFKQNL-----VAVSVPRDETFCKNKLFTENNAIYAF----- 265
QY 98 KSEGRQCQQLIKDPKOLNSFKR-----TCMESQPPFNKFFETDY-FKVVVPPFSIK 149

Db 266 AVNSNCERYQCADRRRL--SFRMHSNHNYSQDEIDAMVDGRGIYLDYGHKLCAYCNDFS 323
 QY 150 NESNYPPFFRTRACDLLOPNDNLACKPFWKPRNLNLSOHGSDMQVSFDDA-----P 201
 Db 324 SNR-----EACDSVLKREHTNCKSF-----NLAKNFNDNFTYDFVVKRLQSLKAS 369
 QY 202 HNF---GFREFFLYHKLKHEGPFKTKCKBOETTETTSLLQNVSP 244
 Db 370 HFRNDATKLAIFGIYHTG-----TLKTFCCGVQNSP 404

RESULT 14
 T16225
 hypothetical protein F31E8.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C/Accession: T16225
 R:Du, Z.
 submitted to the EMBL Data Library, April 1996
 A:Description: The sequence of C. elegans cosmid F31E8.
 A:Reference number: Z18481
 A:Accession: T16225
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-461 <DU>
 A:Cross-references: EMBL:U55856; NID:g1280154; PID:g1280157; PIDN:AAA98022.1; GSPDB:GNOC
 A:Experimental source: strain Bristol N2; clone F31E8
 C:Genetics:
 A:Gene: CESP:F31E8.5
 A:Map position: 2
 A:Introns: 30/1, 42/2, 78/2, 148/3, 185/2, 245/3, 302/3, 361/1, 388/3, 432/3

Query Match 5.4%; Score 82.5; DB 2; Length 461;
 Best Local Similarity 19.3%; Pred. No. 11;
 Matches 59; Conservative 39; Mismatches 103; Indels 105; Gaps 14;

QY 29 NSGLNITFKYN-C-TYLLNPVGVKHVIADAQNITISQVACHD----- 69
 Db 62 NNGFFHISPPNCHAIYCPVKONYDAHNLAIATSTCEERYVIYTPHADKLLIKES 121
 QY 70 -QVAVILWSPGALGIEFLKGRVILEELKSEGRCQOOLILKDPKQLNSSFKRTGMSQP 128
 Db 122 GQSEVKYWARNL--EP-----IIDOLISK---VHVLKSPENHEFTSAVDKGETV 170
 QY 129 FLNKRFTDYFKVVPFISKNE--SNYHFFRTRACDLLOPNDNLACKPFWKPRNLNI 186
 Db 171 ANMLK-DTDLILNTRNCQVKNIGSTYPLPKA-----VQDKTKGLPKRW-----LND 219
 QY 187 SQSGSDMQVSFDHAPNFGFEFFLYHKLKHEGPFKRTCK-----PVKENDAKKSIDLLAYLKTLDKMGVNL 257
 Db 220 RR-----TQVATDYL-----SCLLQNVSPGDIYIELVDDTNTTRKVMYALK 267
 QY 228 --QEQTTET-----SCLLQNVSPGDIYIELVDDTNTTRKVMYALK 267
 Db 258 ANREKCESVGGLKAGRKKONPLIQKALFRVSVNTYIPVHPNDQVSNAYKMFILS 317
 QY 268 PVHSPW 273
 Db 318 TRKCHW 323

RESULT 15
 T37257
 hypothetical protein R02D1.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C/Accession: T37257
 R:Clarke, K.; David, M.
 submitted to the EMBL Data Library, June 1999
 A:Description: The sequence of C. elegans cosmid R02D1.
 A:Reference number: Z21650
 A:Accession: T37257
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-622 <CL>
 A:Cross-references: EMBL:AF024495; PIDN:AAB70338.2
 A:Experimental source: strain Bristol N2; clone R02D1
 C:Genetics:
 A:Gene: R02D1.1
 A:Map position: V
 A:Introns: 38/2, 77/1, 191/2, 280/3, 308/2, 335/3, 472/3, 587/3

Query Match 5.4%; Score 82.5; DB 2; Length 622;
 Best Local Similarity 23.4%; Pred. No. 16;
 Matches 49; Conservative 31; Mismatches 64; Indels 65; Gaps 14;

QY 18 VANEGV-GPASRNSGLYNIT--PKYDNTTLYLPVGVKEVIADAQNITISQVACHDQAVT 74
 Db 135 TINGYETPASGRNOLNTEGFKY-----IKVDMNLSSSKYASKD--AII 179
 QY 75 IIMSPGALGIEFLKGRVILEELKSEGRCQOOL-ILKDPKQLNSSF-----PKR 121
 Db 180 SNW-----EYI--FFTTRYLSVO--HCRFEDILGTLRLKLPSELETITLPAQICFEH 228
 QY 122 TGMESQ-----PFLNKKFET--DYFVKVVPFISKNSNHYHFFRTRACDLLOPD 171
 Db 229 AGKRNQGDIMKVTEQFLDSLANDLHDYV-----NEMNSRYFLRLTQ---LLKIN 276
 QY 172 NLACKPFWKPR-NLNLISQSGSDMQVSFDR 199
 Db 277 QAIQKIGWESRPMKMGELGRVFNVLKIEFSH 305

Search completed: May 19, 2003, 09:25:13
 Job time : 15.263 secs

GenCore version 5.1.4.p5.4578
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OK protein - protein search, using sw model

Run on: May 19, 2003, 09:08:53 Search time 5.64467 Seconds
(without alignments)
2042.709 Million cell updates/sec

Title: US-09-912-157-2_COPY_36_313

Perfect score: 1515

Sequence: 1 ADTCGWKAAAPRLCVAN.....KVMHYALKPVHFWAGPTR 278

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	6.3	1462	1 PTP6_DROME	P16620 drosophila
2	91.5	6.0	421	1 VG2_BPIKE	P03660 bacterioph
3	91.5	6.0	758	1 LEU2_SCHPO	Q14289 schizosacch
4	85.5	5.6	289	1 PAIL_PROVU	P37447 proteus vul
5	85.5	5.6	404	1 ARRS_BOVIN	P08168 bos taurus
6	85	5.6	429	1 EPC_RAT	P01855 rattus norv
7	84	5.5	405	1 ARRS_PIG	P79260 sus scrofa
8	84	5.5	449	1 MCE1_CANAL	P78587 candida alb
9	82	5.4	716	1 ZP2_FELCA	P47984 felis silve
10	81.5	5.4	320	1 MEC3_CAEVU	P34765 caenorhabdi
11	81.5	5.4	839	1 YDDE_HAEIN	P45182 haemophilus
12	81	5.3	286	1 Y804_METJA	Q58214 methanococc
13	80.5	5.3	363	1 PER_COPCI	P28314 coprinus ci
14	80.5	5.3	364	1 PER_ARTRA	P28313 arthromyces
15	79	5.2	405	1 ARRS_CANFA	P28281 canis fami
16	78	5.1	518	1 TBX5_HUMAN	Q99593 homo sapien
17	78	5.1	571	1 DCPI_SCHPO	Q09737 schizosacch
18	78	5.1	2052	1 MY10_BOVIN	P79114 bos taurus
19	77.5	5.1	1001	1 TP3A_HUMAN	Q13472 homo sapien
20	77	5.1	1420	1 YN8E_YEAST	Q03496 saccharomyc
21	77	5.1	1589	1 CC25_YEAST	P04821 saccharomyc
22	76.5	5.0	321	1 MEC3_CAEEL	P09088 caenorhabdi
23	76.5	5.0	770	1 LEU2_CANNA	Q00464 candida mal
24	76.5	5.0	3433	1 QTRQ_HUMAN	P46939 homo sapien
25	76	5.0	295	1 MEC3_CAEER	P34764 caenorhabdi
26	76	5.0	342	1 LYCA_BPCP7	P19385 bacterioph
27	76	5.0	456	1 Y172_DROME	P04283 drosophila
28	76	5.0	518	1 TBX5_MOUSE	P70326 mus musculu
29	76	5.0	537	1 STR_MYCPN	P75222 mycoplasma
30	76	5.0	566	1 Y397_MYTCGE	P47637 mycoplasma
31	76	5.0	858	1 SYL_VIBCH	Q9K766 vibrio chol
32	76	5.0	2290	1 POLG_EMCV	P03304 encephalomy
33	75.5	5.0	667	1 VTER_HSV60	P24443 human herpe

ALIGNMENTS

RESULT 1

PTP6_DROME

ID PTP6_DROME STANDARD; PRT: 1462 AA.

AC P16620; 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Protein-tyrosine phosphatase DPTP precursor (EC 3.1.3.48) (Protein-

DE tyrosine-phosphate phosphohydrolase).

GN PTP69D OR DPTP.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90046860; PubMed=2554325;

RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;

RT "A family of receptor-linked protein tyrosine phosphatases in humans

and Drosophila."

RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).

CC - FUNCTION: IT IS POSSIBLE THAT DPTP IS A CELL ADHESION RECEPTOR.

CC - CATALYTIC ACTIVITY: Protein tyrosine phosphate + H2O -> protein

tyrosine + phosphate.

CC - SUBCELLULAR LOCATION: Type I membrane protein.

CC - SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

CC - SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC - SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.

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CC EMBL; M27699; AAA28842.1;

CC PIR; B36182; B36182.

CC KSRP; P18052; IYFO.

CC FlyBase; FBgn0014007; Ptp69D.

CC InterPro; IPR003961; FN_III.

CC InterPro; IPR003006; Ig_MHC.

CC InterPro; IPR003598; Ig_C2.

CC InterPro; IPR003600; Ig-like.

CC InterPro; IPR000387; Tyr_phosphatase.

CC InterPro; IPR000242; Tyr_PP.

CC Pfam; PF00041; fn3; 3.

CC Pfam; PF00047; Ig; 2.

CC Pfam; PF00102; Y_phosphatase; 2.

CC PRINTS; PR00700; PRTYPPHPTASE.

CC SMART; SM00060; FN3; 3.

CC SMART; SM00410; IG_1like; 1.

CC SMART; SM00408; IGG2; 1.

CC SMART; SM00194; PTPC; 2.

DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.
 DR PROSITE; PS0056; TYR_PHOSPHATASE 2; 2.
 DR PROSITE; PS0055; TYR_PHOSPHATASE_PTP; 2.
 KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
 KW Cell adhesion; Immunoglobulin domain; Repeat.
 FT SIGNAL 1 23
 FT CHAIN 24 1462
 FT DOMAIN 24 805
 FT TRANSMEM 806 823
 FT DOMAIN 824 1462
 FT DOMAIN 138 119
 FT DOMAIN 147 221
 FT DOMAIN 332 437
 FT DOMAIN 438 538
 FT DOMAIN 912 1165
 FT DOMAIN 1208 1459
 FT ACT_SITE 1097 1097
 FT ACT_SITE 1391 1391
 FT DISULFID 45 112
 FT DISULFID 154 214
 FT CARBOHYD 40 40
 FT CARBOHYD 58 58
 FT CARBOHYD 64 64
 FT CARBOHYD 85 85
 FT CARBOHYD 105 105
 FT CARBOHYD 109 109
 FT CARBOHYD 119 119
 FT CARBOHYD 162 162
 FT CARBOHYD 191 191
 FT CARBOHYD 196 196
 FT CARBOHYD 209 209
 FT CARBOHYD 255 255
 FT CARBOHYD 288 288
 FT CARBOHYD 302 302
 FT CARBOHYD 429 429
 FT CARBOHYD 442 442
 FT CARBOHYD 451 451
 FT CARBOHYD 516 516
 FT CARBOHYD 613 613
 FT CARBOHYD 701 701
 FT CARBOHYD 755 755
 SQ SEQUENCE 1462 AA; 16741 MW; F8091D69E8230EB CRC64;

Query Match 6.3%; Score 95; DB 1; Length 1462;
 Best Local Similarity 20.4%; Pred. No. 1;
 Matches 67; Conservative 45; Mismatches 100; Indels 116; Gaps 18;

QY 20 NEGVCPSR-----NSGLNITFKYD-----NCTYLNPGKHVIADA 57
 DB 259 NGNDPIQKPTITLQAGTPTFTYHKDFINGSHYSYLDHFKPNTYFLRYGRKNSIGNG 318
 QY 58 -----QNITISQYACHDQV-----AVTILSPGALG-IEELKGFVILEEL 97
 DB 319 OPTQYPOGTTLSY---DPIFIPKVTGTGTAITIGWNPDPDLIDYIQYELIVSE- 374
 QY 98 KSEGRCCQLIKDKPOLNSFKRTGMSOPPLANKFETDYFKVYVPPSPISNESYHPF 157
 DB 375 --SG-----EYFKVIEAIIYQNSRLPYH-----FKLKTADYE-- 408
 QY 158 FFRTRACDLQLQDNLACKPFW-----KPNRLNISQH-----GSDMQVSP 197
 DB 409 -FRVRASDLTK-----TCGP-NSENVNGTMDGVATKPTNLSIQCHDNVTRGNSAINW 462
 QY 198 DHAPHNFGFRFYLHYLKHHE-----GPKKKCKQKQKQTTTSCILQNVSPG-DY 247
 DB 463 DVPKTPGKVSYLILHGNPASTVDREMGWGFKIRRIDEPHHTK-----LYESVSPNTNY 517
 QY 248 IELVDDTNTK-----VNHVATKPVHSP 272
 DB 518 TVTVSAITRRKKNGEPATGSCLMPVSTP 545

RESULT 2

VG2_BPIKE
 ID VG2_BPIKE STANDARD; PRT; 421 AA.
 AC P03660;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Gene II protein [Contains: Gene X protein].
 GN II AND X.
 OS Bacteriophage Ike.
 OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
 OX NCBI_TaxID=10867;
 RN [1]
 RP SEQUENCE FROM N.A. PubMed=3981635;
 RA MEDLINE=85160831; PubMed=3981635;
 RA Peeters B.P.H., Peters R.M., Schoenmakers J.G.G., Konings R.N.H.;
 RT "Nucleotide sequence and genetic organization of the genome of the N-
 specific filamentous bacteriophage Ike. Comparison with the genome of
 the F-specific filamentous phages M13, fd and fl.";
 RL J. Mol. Biol. 181:27-39(1985).
 CC - FUNCTION: GENE II PROTEIN IS REQUIRED FOR DNA REPLICATION. THE
 CC - FUNCTION OF THE GENE X PROTEIN IS UNKNOWN.
 CC
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 CC
 CC EMBL; X02139; CAA26067.1;
 CC EMBL; X02139; CAA26068.1;
 DR PIR; A04265; Z2BPIK.
 KW DNA replication; Alternative initiation.
 FT CHAIN 1 421 GENE II PROTEIN.
 FT INIT_MET 301 421 GENE X PROTEIN.
 FT INIT_MET 301 421 FOR GENE X PROTEIN.
 SQ SEQUENCE 421 AA; 47594 MW; 626ACIFDDF45215 CRC64;

Query Match 6.0%; Score 91.5; DB 1; Length 421;
 Best Local Similarity 21.4%; Pred. No. 0.47;
 Matches 71; Conservative 44; Mismatches 98; Indels 119; Gaps 18;

QY 10 AARPRCLVANEGVGPASRNSGLNITFKYDNCYTLNPGKHVIADAQNITISQYACHD 69
 DB 123 AAMPEL-----YDLCDVTNVTGVR-----IDVTFSAKVAND 154
 QY 70 QVA-----VTILSPGALGIEFLKGFVILEELKSGROQ 105
 DB 155 HIANQVTSFLRNVSGQTKKTRALDYETTVNNEGS-----RHRTLVAYLKHEVQAO 207
 QY 106 QLILKDPKQLN--SSFKRTGME--SQPFLNMKFTDYFKVYVPPSPISNESYHPFFRT- 161
 DB 208 IKRLQKKKSHLLIYEKNCLEVLSPDLQL-----YAVGLVRE-----EARLRTFFENF 257
 QY 162 -----RACDLILQPD-----NLACKPFWK--RNLNISQSDMQV-----SFDHAPHN 203
 DB 258 GLPKRPFDIIVKYODNTSGSSPNLIC-DLWKKSKDLDFAFKGSMDNVDSDSVYDALINN 316
 QY 204 FGF-----RFFLYLHYLKHHEGPPKRTKQEQTT-----ETTS-----CLL 239
 DB 317 FSSVTKSGNISNSKANRLPGFPYRLVNSG-YDNVAQMTERTTWSRLKELTSGVLSKAQL 375
 QY 240 QNVSPGDIIELYDDTNT--TRKVMETALKPV 269
 DB 376 MLUSTDRNVVPLQVIMINVDFOQTPETVYEPV 407

RESULT 3
 LEU2_SCHPO
 ID LEU2_SCHPO STANDARD; PRT; 758 AA.
 AC O14289;
 DT 15-JUL-1998 (Rel. 36, Created)

FT SIGNAL 1 20 BY SIMILARITY.
 FT CHAIN 21 289 PHOSPHOLIPASE A1.
 FT ACT_SITE 164 164 BY SIMILARITY.
 SQ SEQUENCE 289 AA: 32944 MW: D75516CFEB406997 CRC64;

Query Match 5.68; Score 85.5; DB 1; Length 289;
 Best Local Similarity 26.58; Pred. No. 1.1;
 Matches 43; Conservative 16; Mismatches 58; Indels 45; Gaps 8;

QY 5 GWKMAAARPRVCANEGV-----GPSRNSGLYNITFKYDN-----CTYTL 46
 DB 6 GMLAAALFFPACAEATIDKVDHTPAVRGSIAMQLQEDNPFTLYPVESNYLYT 65
 QY 47 NPVGKVIADQNIITISYACHQDVAVTI-----LWSPGALGIEFLKGFVILE---ELK 98
 DB 66 SLDLKKAI---ESYNWSDNANKDEKPOLSLAPPLNR--GLGDSNLLGASTQSRWQLS 121
 QY 99 SEGRCCQQLIKPKLNSFKRGMESQPLNKKFETDFV 140
 DB 122 NTGE-----SAPFRETNYPQLFLG--FATDYSV 148

RESULT 5
 ARRS_BOVIN STANDARD; PRT; 404 AA.
 AC P08168;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE S-arrestin (Retinal S-antigen) (48 kDa protein) (S-Ag) (Rod
 DE photoreceptor arrestin).
 GN SAG.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_Taxid:9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-88041034; PubMed-3478675;
 RA Shinozaki T., Dietzschold B., Craft C.M., Wistow G., Early J.J.,
 RA Donoso L.A., Horwitz J., Tao R.;
 RA "Primary and secondary structure of bovine retinal S antigen (48-kDa
 RA protein)."
 RT Proc. Natl. Acad. Sci. U.S.A. 84:6975-6979(1987).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Retina;
 RX MEDLINE-87156714; PubMed-2950857;
 RA Yamaki K., Takahashi Y., Sakuragi S., Matsubara K.;
 RA "Molecular cloning of the S-antigen cDNA from bovine retina."
 RL Biochem. Biophys. Res. Commun. 142:904-910(1987).
 RN [3]
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RX MEDLINE-94253112; PubMed-7515057;
 RA Smith W.C., Milam A.H., Dugger D., Arcand A., Hargrave P.A.,
 RA Palczewski K.;
 RA "A splice variant of arrestin. Molecular cloning and localization in
 RA bovine retina."
 RT J. Biol. Chem. 269:15407-15410(1994).
 RL [4]
 RP SEQUENCE OF 166-404 FROM N.A.
 RX MEDLINE-86108925; PubMed-3080338;
 RA Wistow G.J., Katial A., Craft C.M., Shinozaki T.;
 RA "Sequence analysis of bovine retinal S-antigen. Relationships with
 RA alpha-transducin and G-proteins."
 RL FEBS Lett. 196:23-28(1986).
 RN [5]
 RP SEQUENCE OF 1-12 AND 198-229.
 RX MEDLINE-89088273; PubMed-2910351;
 RA Tanasawa S., Shichi H.;
 RA "The amino acid sequence of S-antigen: N-terminus and uveitogenic
 RA peptides."

RL Biochim. Biophys. Acta 994:191-193(1989).
 [6]
 RN CALCIN-BINDING DATA.
 RX MEDLINE-90264449; PubMed-2160981;
 RA Hupertz B., Weyand I., Bauer P.J.;
 RT "Calc-binding capacity of cytoplasmic proteins from rod
 RT photoreceptors is mainly due to arrestin."
 RL J. Biol. Chem. 265:9470-9475(1990).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
 RX MEDLINE-98154736; PubMed-9495348;
 RA Granzin J., Wilden U., Choe H.W., Labahn J., Krafft B., Buldt G.;
 RT "X-ray crystal structure of arrestin from bovine rod outer segments."
 RL Nature 391:918-921(1998).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE-99235986; PubMed-10219246;
 RA Hirsch J.A., Schubert C., Gurevich V.V., Sigler P.B.;
 RT "The 2.8 A crystal structure of visual arrestin: a model for
 RT arrestin's regulation."
 RL Cell 97:257-269(1999).
 CC 1- FUNCTION: ARRESTIN IS ONE OF THE MAJOR PROTEINS OF THE ROS
 CC (RETINAL ROD OUTER SEGMENTS); IT BINDS TO PHOTOACTIVATED-
 CC PHOSPHORYLATED RHODOPSIN, THEREBY APPARENTLY PREVENTING THE
 CC TRANSDUCIN-MEDIATED ACTIVATION OF PHOSPHODIESTERASE.
 CC 1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM (P44); ARE PRODUCED BY ALTERNATIVE SPLICING. THE SHORT
 CC FORM PLAYS A ROLE IN THE PHOTOTRANSDUCTION CASCADE.
 CC 1- TISSUE SPECIFICITY: RETINA AND PINEAL GLAND. THE P44 ISOFORM IS
 CC LOCALIZED IN THE PHOTORECEPTOR OUTER SEGMENT.
 CC 1- DISEASE: S-ANTIGEN INDUCES AUTOIMMUNE UVEITIS.
 CC 1- MISCELLANEOUS: ARRESTIN BINDS CALCIUM.
 CC 1- SIMILARITY: BELONGS TO THE ARRESTIN FAMILY.
 CC
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 CC EMBL: J02955; AAA30378.1;
 CC EMBL: M15115; AAA30377.1;
 CC EMBL: U08346; AAA20465.1;
 CC EMBL: X03454; CAA27179.1;
 CC FIC; A23619; CAA23619.
 CC PIR; A28404; A28404.
 CC PIR; S02144; S02144.
 CC PIR; A25826; A25826.
 CC PDB; 1AYR; 13-JAN-99.
 CC PDB; 1CF1; 16-APR-99.
 CC InterPro: IPR000698; Arrestin.
 CC Pfam: PF00339; arrestin; 1.
 CC Pfam: PF02752; arrestin_C; 1.
 CC PRINTS; PR00309; ARRESTIN.
 CC PROSITE; PD002099; Arrestin; 1.
 CC PROSITE; PS00295; ARRESTINS; 1.
 CC Sensory transduction; Vision; Autoimmune uveitis; Acetylation;
 CC Calcium-binding; Alternative splicing; 3D-structure.
 KW MOD_RES 1 4
 FT PROPEP 1 4
 FT REMOVED (IN 30% OF THE CHAINS).
 FT DISULFID 128 143
 FT PROBABLE.
 FT VARSPPLIC 370 370
 FT F -> A (IN SHORT ISOFORM).
 FT MISSING (IN SHORT ISOFORM).
 FT V -> L (IN REF. 2).
 FT CONFLICT 35 35
 FT L -> V (IN REF. 2).
 FT CONFLICT 119 119
 FT V -> I (IN REF. 2).
 FT CONFLICT 177 177
 FT D -> H (IN REF. 2).
 FT CONFLICT 317 317
 FT SEQUENCE 404 AA; 45275 MW; 26B1D80B52AF1EF CRC64;
 SQ

Query Match 5.68; Score 85.5; DB 1; Length 404;
 Best Local Similarity 20.6%; Pred. No. 1.6;

Matches 61: Conservative 32; Mismatches 88; Indels 115; Gaps 15;

QY 48 PVGKHV---TADQNTI---SOYACH---DOAVATILWSPGALGIEFLKGRVILE 95
 DB 6 PAPNHVIFKISDKSVTLVGLKROYIDVERVEPVGVLYDP-----ELVKGKRVV- 59
 QY 96 ELKSEGRQCOOLILDKPKLNSFKTGESQPFNLKMTFD-IFYKVVPPFSI----- 148
 DB 60-----SLACAF-RYQEDIDVGLSFRDLIFYSOVQVFPVPGASGAT 100
 QY 149-----KNESNHPFFETRACDILLOPDNLACKPFWKPNLMSO----- 188
 DB 101 TLQSLRILKLGANTYP-----LLTFDILPCSVMLQAPQDVGSCGVDFEIKAF 152
 QY 189---HSDNOV-----SPDHAPHNG-----PFFFLYHLYLK----- 216
 DB 153 ATHSTVDKDKPKKSVLLIRKVOHAPDMGPPQRAEASOFFNSDKPLRLAVLSLKE 212
 QY 217---HEGPFK---RTCKQSTTETSCILLONVS-----PDYIIELVDDTNTTRKV 261
 DB 213 IYHGEPIPVVAVTNTSTKTKVKKLVLEQVNTVNVLYSSDYIKYVAEEAEQKV 268

RESULT 6

EPIC_RAT STANDARD; PRT; 429 AA.

AC P01855;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig epsilon chain C region.
 OS Rattus norvegicus (Rat)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (IMMUNOCYTOMA IR2).
 RC STRAIN=LOU/C/WSL;
 RX MEDLINE=83064537; PubMed=6292865;
 RA Hellman L., Pettersson U., Engstrom A., Karlsson T., Bennich H.;
 RT "Structure and evolution of the heavy chain from rat immunoglobulin
 E".
 RL Nucleic Acids Res. 10:6041-6049(1982).
 RN [2]
 RP SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).
 RX MEDLINE=83182019; PubMed=6820340;
 RA Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;
 RT "A cloned cDNA probe for rat immunoglobulin epsilon heavy chain:
 construction, identification, and DNA sequence.";
 RL DNA 1:335-343(1982).
 RN [3]
 RP SEQUENCE OF 205-306 FROM N.A.
 RX MEDLINE=82114576; PubMed=6803238;
 RA Hellman L., Pettersson U., Bennich H.;
 RT "Characterization and molecular cloning of the mRNA for the heavy
 (epsilon) chain of rat immunoglobulin E";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).
 CC [3]
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 CC EMBL; J00744; AAA41379.1; ALT_INIT.
 DR PIR; A02143; EHRT.
 DR HSP; P01854; LIGE.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003600; Ig_Like.
 DR Pfam; PF00047; Ig. 4.

DR SMART: SK00410; IG_Like; 3.
 DR SMART: SK00407; IG_C1; 1.
 DR PROSITE: PS00290; IG_MHC; 3.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 168 168 R->N (IN REF. 2).
 FT CONFLICT 308 308 P->L (IN REF. 2).
 FT CONFLICT 308 308 P->L (IN REF. 2).
 SQ SEQUENCE 429 AA; 48671 MW; D2970B34EF8A7B0 CRC64;

Query Match 5.6%; Score 85; DB 1; Length 429;
 Best Local Similarity 18.6%; Pred. No. 2;
 Matches 52; Conservative 42; Mismatches 92; Indels 94; Gaps 11;

QY 56 DAQNTIISQYAC---HDQVATILWSPGALGIEFLKGRVILEELKSGRQCOOLILKDP 112
 DB 115 NAFESTIOLYCFYGHIONDYSIH-----LADDRKIYETRAONVLIKEE 159
 QY 113 KOLNSFKTKGESQPFNLKMTFDIFYKVVPPFSIKNESNHPFFETRACD----- 165
 DB 160 GKLASTYSRLNITQQQWMS---ESTETCKVT-----SQGENTWARTSRCSDDPRGY 208
 QY 166---LLLOPDNLACKPFWKPR-----NLNIS-----QHSQDMQVSYFDHAPHN- 203
 DB 209 IYILPPSPDLIYENGTPRLTCLVLDLESEENITVTVWRERKKSIGSASQSTKH--HNA 266
 QY 204-----FQFFFLYH-----KLKHEGPFKRTK-----KOE 229
 DB 267 TTSITSLPVDARKWIEGEGYQCRVDPHPKPIVRSITKAPKRSAPVTVFLPPEEE 326
 QY 230 QTETTSCLLQVSPGDVIIELVDDTNTTRKVHYALKPV 269
 DB 327 KDRATLTLCLIQNFEDDISVQWLQDSKLIPKSOESTTTP 366

RESULT 7

ARRS_PIG STANDARD; PRT; 405 AA.

AC P79260;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE S-arrestin (Retinal S-antigen) (48 kDa protein) (S-AG) (Rod
 DE photoreceptor arrestin).
 GN SAG.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=96273620; PubMed=8690040;
 RA Singh A.K., Kumar G., Shinohara T., Shichi H.;
 RT "Porcine S-antigen: cDNA sequence and expression in retina, ciliary
 RT epithelium and iris";
 RL Exp. Eye Res. 62:299-308(1996).
 CC [1]
 CC FUNCTION: ARRESTIN IS ONE OF THE MAJOR PROTEINS OF THE ROS
 CC (RETINAL ROD OUTER SEGMENTS); IT BINDS TO PHOTOACTIVATED-
 CC PHOSPHORYLATED RHODOPSIN, THEREBY APPARENTLY PREVENTING THE
 CC TRANSDUCIN-MEDIATED ACTIVATION OF PHOSPHODIESTERASE.
 CC [1]
 CC TISSUE SPECIFICITY: RETINA AND PINEAL GLAND. ALSO EXPRESSED IN THE
 CC ANTERIOR TISSUES SUCH AS THE CILIARY EPITHELIUM AND IRIS
 CC EPITHELIUM.
 CC [1]
 CC DISEASE: S-ANTIGEN INDUCES AUTOIMMUNE UVEITIS.
 CC [1]
 CC MISCELLANEOUS: ARRESTIN BINDS CALCIUM (BY SIMILARITY).
 CC [1]
 CC SIMILARITY: BELONGS TO THE ARRESTIN FAMILY.
 CC [1]
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 CC EMBL; J00744; AAA41379.1; ALT_INIT.
 DR PIR; A02143; EHRT.
 DR HSP; P01854; LIGE.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003600; Ig_Like.
 DR Pfam; PF00047; Ig. 4.

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CC      ENBL; S82664; A946757.2;
CC      HSP; P08168; 1CF1.
CC      InterPro: IPR000698; Arrestin.
CC      Pfam: PF00339; arrestin; 1.
CC      PRINTS: PR02752; arrestin; C.1.
CC      PRINTS: PR00309; ARRESTIN.
CC      PRODOM: PD002099; Arrestin; 1.
CC      PROSITE: PS00495; ARRESTINS; 1.
CC      Sensory transduction; Vision; Autoimmune uveitis; Calcium-binding.
CC      DISULFID 131 146 PROBABLE.
CC      SQ SEQUENCE 405 AA; 54102 MW; F9C0C8658CBEA73E CRC64;

Query Match 5.5%; Score 84; DB 1; Length 405;
Best Local Similarity 21.5%; Pred. No. 2.3;
Matches 68; Conservative 31; Mismatches 97; Indels 120; Gaps 17;

QY 19 ANEGVGPASRNSGLNIFKDKNTTILNPGKHVIADQNITISQYACH-DQVAV---T 74
DB 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
3 ANVQASKSPNVIKPKTSRDKSVIYL---GKR-----DYIDRVQVPEVDGV 48
QY 75 ILWSPGALGIEFLKGRFVILELSEKGRQCOQLILDKPKQLNSKFKTGMSQPELNMKF 134
DB 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
49 VLVDP-----ELVKGRVTV-----SLTCAF-RVQGEDIDVIGLSP 83
QY 135 ETD-IVKVVPPPSI-----KNESNHPFFTRACDILLQPDNLACKPFW 179
DB 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
84 RDLISQVQVPPVGAASQTKLQESLIRKLGHTYF-----LTFPDLPCSVML 135
QY 180 KPNRLNISQ-HGSDMOV-----SFDHAPNFG-----205
DB 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
136 QPAQDVQKCCGVDPEVAKAFATSDAGDEKIPKSSVALLIRKVOHAPLEMGQPBEA 195
QY 206 -PRFFY---LHYLKL-----HEGPFK---RKCKQKQETTTSCILQNVS-----PC 245
DB 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
196 ANQFFMSDKPLHLTVLSKELYGEPIPVTVTVNTEKVKIKALVEQVANNVLYS 255
QY 246 DYIIELVDNTTRKV 261
DB 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
256 DYIKPVAPEEQQRV 271.

RESULT 8
MCEL CANAL STANDARD; PRT; 449 AA.
AC P78587:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE mRNA capping enzyme alpha subunit (mRNA guanylyltransferase)
DE (EC 2.7.7.50) (GTP--RNA guanylyltransferase) (Gtase).
GN COT1.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_Taxid=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO 1060;
RX MEDLINE=96423877; PubMed=8828219;
RA Yamada-Okabe T., Shimmi O., Doi R., Mizumoto K., Arisawa M.,
RA Yamada-Okabe H.
RT "Isolation of the mRNA-capping enzyme and ferric-reductase-related
RL genes from Candida albicans."
RL Microbiology 142:2515-2523(1996).
CC -1- FUNCTION: SECOND STEP OF M-RNA CAPPING. TRANSFER OF THE GMP MOIETY
CC OF GTP TO THE 5' END OF RNA YIELDING A 5' 2'-5' LINKAGE.
CC REACTION INTERMEDIATE.
CC -1- CATALYTIC ACTIVITY: GTP + (5')ppp-mRNA - diphosphate +
CC G(5')ppp-mRNA.
CC -1- SUBUNIT: THE M-RNA CAPPING ENZYME IS COMPOSED OF TWO SEPARATE
CC CHAINS ALPHA AND BETA, RESPECTIVELY A mRNA GUANYLYLTRANSFERASE AND

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CC      AN RNA 5'-TRIPHOSPHATASE.
CC      -1- SUBCELLULAR LOCATION: Nuclear.
CC      -1- SIMILARITY: BELONGS TO THE EUKARYOTIC GTASE FAMILY.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@lsb-sib.ch)
CC      EMBL; D83180; BAAL1833.1;
CC      InterPro: IPR001339; mRNA_cap_enzyme.
CC      Pfam: PF01331; mRNA_cap_enzyme; 1.
CC      Transferase; Nucleotidyltransferase; mRNA processing; mRNA capping;
CC      Nuclear protein. 67 67 GUANYLYLATION SITE (POTENTIAL).
CC      ACT_SITE 427 435 POLY-GLN.
CC      DOMAIN 427 435
CC      SQ SEQUENCE 449 AA; 52253 MW; D93F44BF1123058B CRC64;

Query Match 5.5%; Score 84; DB 1; Length 449;
Best Local Similarity 20.4%; Pred. No. 2.6;
Matches 56; Conservative 34; Mismatches 92; Indels 92; Gaps 13;

QY 79 PGALGIEFLKGRFVILEEL-----KSEGRQCOQLILDKPKQLNSKFKTGMSQPF 129
DB 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
41 PGQSPVSEF---RLEETLMQKDYFVCKTDLGRLCLFLINDPD-----KGGV---F 88
QY 130 LMKFETDYFVKVVPFSPKSNSEHPFFTRACD---LLQPDNLACKPFW---180
DB 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
89 LVTRENDYIPTPNHPLPSVNETREKPTVHGCTLLDGLVLENVNS-EPVLRYVIFDAL 147
QY 181 -----PRLN-----NISQSGSDQVSDHAPNFGPFYLYH---213
DB 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
148 AIHGKCIIDRLPLRGUYITENVKPFDPNFKHNPDI-VNSPEFFKVGFTMLSTHAD 206
QY 214 -----KLHGEFKKTKQKQETTTSCILQNVSPG-----DYIIELV-----252
DB 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
207 DVLSEMDKLFHASDGLIYTCETPYVFGTQDQLLAKWPAENTYDFOLEFVFNVDPL 266
QY 253 DDNTTRKVMHYALKP-----VHSPWA 274
DB 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
267 DERDPTSTLYDYDAKPNLKLKRVWQGSNVHTDFA 300

RESULT 9
ZP2_FELCA STANDARD; PRT; 716 AA.
AC P47984;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Zona pellucida sperm-binding protein 2 precursor (Zona pellucida
DE glycoprotein ZP2) (Zona pellucida protein A).
GN ZP2 OR ZPA.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_Taxid=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=95143578; PubMed=7841460;
RA Harris J.D., Hibler D.W., Fontenot G.K., Hsu K.T., Yurewicz E.C.,
RA Sacco A.G.
RT "Cloning and characterization of zona pellucida genes and cDNAs from
RT a variety of mammalian species: the ZPA, ZPB and ZPC gene families."
RL DNA Seq. 4:361-393(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Okazaki Y., Isojima S., Sugimoto M.;

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GN HI1369.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma. subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=777;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=93350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saubek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RD".
RL Science 269:496-512(1995).
CC 1- SIMILARITY: TO E. COLI YDDB.
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DR EMBL: U32817; AAC23016.1;
DR TIGR: HI1369;
DR InterPro: IPR000531; TonB_box.
DR Pfam: PF00593; TonB_box; 1.
RW Hypothetical protein; Complete proteome.
SQ SEQUENCE 839 AA; 96409 MW; D419EFF3BF91E503 CRC64;
Query Match 5.4%; Score 81.5; DB 1; Length 839;
Best Local Similarity 18.2%; Pred. No. 9.7;
Matches 36; Conservative 42; Mismatches 69; Indels 51; Gaps 7;
QY 91 RVILEELKSGKCOQILKDKP-----OLNSSFKRTGMSOPPLNM-KFTDYF 139
DB 477 KIILSLSDS-----MEPTSTNTSKGRVTSYQNIAYEDLIKKKFLRPG 530
QY 140 VIVVPPSIKNE-----SNVHPF-----FFTRACDILLOPOMLACK 176
DB 531 IRIERDDYLNANNIAPRFVARYHPMDNTGTLGLNRYTGRSFASLKLKANGILKLNDSR 590
QY 177 PFWKPRNINISOHSDMQVSDHAPNFGFRFFLYHLKHEGFKKTKCKBOTV---- 232
DB 591 QHONFSLK-SPYADELSLSDQNGNFGALGLYIHRDNKRIILKEPIQGRKTSYIN 649
QY 233 -----ETTSCLLNQVSP 244
DB 650 GHPPGVDTYITQLANNIEP 667
RESULT 12
Y804_METJA STANDARD; PRT; 286 AA.
ID Y804_METJA
AC Q5814;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein M70804.
GN M70804.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=9688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Keane B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Weese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RD jannaschii".
RL Science 273:1058-1073(1996).
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CC or send an email to license@isb-sib.ch).
DR EMBL: U67525; AAB98804.1;
DR TIGR: M70804;
DR Pfam: PF01444; MoaA_WiF_PqQE; 1.
RW Hypothetical protein; Complete proteome.
SQ SEQUENCE 286 AA; 32920 MW; CACCA47C3A3B4E63A CRC64;
Query Match 5.3%; Score 81; DB 1; Length 286;
Best Local Similarity 28.2%; Pred. No. 2.8;
Matches 46; Conservative 22; Mismatches 53; Indels 42; Gaps 11;
QY 15 RLCVANGVG-----PASRNSGLINITYFKDNCITLYNPVGHV---TADAQNTI 62
DB 23 RHCIGCGIMLETENPOHPHSIELFKKNCIY--CYSRLKTVRGYIGNLEAEVTVI 80
QY 63 SOYACHDOQAVATILNSPGA-LGIEFLK--GPRVILEELKSGKCOQILKDKPKNL--- 116
DB 81 SOY-----CEPILDLLEGVKAIEFCQDLGRV---DLQNTGLLEELIKELKDLGLD 131
QY 117 -----SSFKTGNESOPPLNMKFTDYFYVVPVPSIKNESNY 154
DB 132 IMISLSFSR---EKYLLTGR---DYENRVL---NNIKIASKY 166
RESULT 13
PER_COPCI STANDARD; PRT; 363 AA.
ID PER_COPCI
AC P28314; P28315;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Peroxidase precursor (EC 1.11.1.7).
GN CIP1.
OS Coprinus cinereus (Inky cap fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Psathyrellaceae; Coprinopsis.
OX NCBI_TaxID=5346;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=IFO 8371;
RX MEDLINE=93239741; PubMed=8477731;
RA Baunsgaard L., Dalboe H., Houen G., Rasmussen E.M., Welinder K.G.;
RT "Amino acid sequence of Coprinus macrothizus peroxidase and cDNA
RD sequence encoding Coprinus cinereus peroxidase. A new family of
RN fungal peroxidases".
RL Eur. J. Biochem. 213:605-611(1993).
RN [2]
RP SEQUENCE OF 161-185.
RX MEDLINE=92247803; PubMed=1576150;
RA Kjaer M., Andersen M.B., Schneider P., Christensen B.,
RA Schuelein M., Welinder K.G.;

RT *Comparison of structure and activities of peroxidases from Coprinus
 RL cinereus, Coprinus macrohizus and Arthromyces ramosus.
 RN [3] Biochim. Biophys. Acta 1120:248-256(1992).
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE=94156050; PubMed=8112469;
 RA Petersen J.F.W., Kadriola A., Larsen S.;
 RT "three-dimensional structure of a recombinant peroxidase from
 RL Coprinus cinereus at 2.6-A resolution.";
 RN FEBS Lett. 339:291-296(1994).
 RP STRUCTURE BY NMR OF MUTANT ASN-265;
 RX MEDLINE=97074497; PubMed=8916924;
 RA Velich N.C., Gao Y., Welinder K.G.;
 RT "The Asp245-->Asn mutant of Coprinus cinereus peroxidase.
 RP Characterization by 1H-NMR spectroscopy and comparison with the wild-
 type enzyme.";
 RL Biochemistry 35:14370-14380(1996).
 CC -1- CATALYTIC ACTIVITY: Donor + H(2)O(2) -> oxidized donor + 2 H(2)O.
 CC -1- COFACTOR: Binds 1 protoheme IX, 1 iron(III) ion and 2 calcium ions
 CC per subunit.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY.
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 CC ENGL; X69457; CAA94216.1;
 DR HSP: P28313; 1AFV.
 DR InterPro: IPR02016; Peroxidase.
 DR Pfam: PF00141; Peroxidase; 1.
 DR PRINTS: PR00458; PEROXIDASE.
 DR PROSITE: PS00435; PEROXIDASE_1; 1.
 DR PROSITE: PS00436; PEROXIDASE_2; 1.
 KW Oxidoreductase; Glycoprotein; Peroxidase; Heme; Calcium-binding;
 KW SIGNAL.
 FT CHAIN 1 20
 FT CA_BIND 21 363
 FT CA_BIND 76 76
 FT CA_BIND 94 94
 FT CA_BIND 96 96
 FT CA_BIND 98 98
 FT CA_BIND 204 204
 FT CA_BIND 221 221
 FT CA_BIND 223 223
 FT CA_BIND 226 226
 FT CA_BIND 228 228
 FT ACT_SITE 71 71
 FT ACT_SITE 75 75
 FT ACT_SITE 112 112
 FT ACT_SITE 265 265
 FT METAL 203 203
 FT MOD_RES 21 21
 FT DISULFID 31 43
 FT DISULFID 42 312
 FT DISULFID 62 148
 FT DISULFID 276 341
 FT CARBOHYD 162 162
 FT CARBOHYD 358 358
 FT VARIANT 99 99
 SQ SEQUENCE 363 AA; 37640 MW; E56E53B963C3DB5 CRC64;
 Query Match 5.3%; Score 80.5; DB 1; Length 363;
 Best Local Similarity 22.8%; Pred. No. 4.2;
 Matches 31; Conservative 23; Mismatches 43; Indels 39; Gaps 6;
 QY 79 PGLGTEFLG-----FVILEELKSGKQCQQLI-----LKPD 112
 ||: ||| |
 ||: ||| |

Db 149 PGSPLRELTGRSSSPSPSPSLIPGNTVTAIDRMGDAGFPDVEVLLAHSLSQ 208
 QY 113 KOLNSFKRTGMSOPFLNKKFTDYFKVW-----PPSKIKESNYHPF--FFTRAC 164
 Db 209 EGLNSAIFRSPLDSTR--QVDTQFYETLLKGTQPCPSLGFAEELSPPGFFMRSD 265
 QY 165 DILLQPDNLACKPFWK 180
 Db 266 ALIARDSTRACK--WQ 279
 RESULT 14
 PER_ARTRA STANDARD; PRT; 364 AA.
 ID P28313.
 AC 01-DEC-1992 (Rel. 24, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Peroxidase precursor (EC 1.11.1.7).
 OS Arthromyces ramosus.
 OC Eukaryota; Fungi; Fungi Incertae sedis; 'Arthromyces'.
 OX NCBI_TaxID=5451;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95399997; PubMed=7670182;
 RA Sawai-Hatanaka H., Ashikari T., Tanaka Y., Asada Y., Nakayama T.,
 RA Minakata H., Kunishima N., Fukuyama K., Yamada H., Shibano Y.,
 RA Amachi T.;
 RT "Cloning, sequencing, and heterologous expression of a gene coding
 RT for Arthromyces ramosus peroxidase.";
 RL Biosci. Biotechnol. Biochem. 59:1221-1228(1995).
 RN [2]
 RP SEQUENCE OF 162-186
 RX MEDLINE=92247803; PubMed=1576150;
 RA Kjaer M., Andersen M.B., Schneider P., Christensen B.,
 RA Schuelein M., Welinder K.G.;
 RT "Comparison of structure and activities of peroxidases from Coprinus
 RT cinereus, Coprinus macrohizus and Arthromyces ramosus.";
 RN Biochim. Biophys. Acta 1120:248-256(1992).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=94118276; PubMed=8289254;
 RA Kunishima N., Fukuyama K., Matsubara H., Hatanaka H., Shibano Y.,
 RA Amachi T.;
 RT "Crystal structure of the fungal peroxidase from Arthromyces ramosus
 RT at 1.9-A resolution. Structural comparisons with the lignin and
 RT cytochrome c peroxidases.";
 RL J. Mol. Biol. 235:331-344(1994).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RX MEDLINE=97400206; PubMed=9257700;
 RA Itakura H., Oda Y., Fukuyama K.;
 RT "Binding mode of benzhydroxamic acid to Arthromyces ramosus
 RT peroxidase shown by X-ray crystallographic analysis of the complex at
 RT 1.6-A resolution.";
 RL FEBS Lett. 412:107-110(1997).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 36-350.
 RX MEDLINE=99435728; PubMed=10504224;
 RA Tsukamoto K., Itakura H., Sato K., Fukuyama K., Miura S.,
 RA Takahashi S., Ikezawa H., Hosoya T.;
 RT "Binding of salicylhydroxamic acid and several aromatic donor
 RT molecules to Arthromyces ramosus peroxidase, investigated by X-ray
 RT crystallography, optical difference spectroscopy, NMR relaxation,
 RT molecular dynamics, and kinetics.";
 RL Biochemistry 38:12558-12568(1999).
 CC -1- CATALYTIC ACTIVITY: Donor + H(2)O(2) -> oxidized donor + 2 H(2)O.
 CC -1- COFACTOR: Binds 1 protoheme IX, 1 iron(III) ion and 2 calcium ions
 CC per subunit.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch)

[illegible]

```

Query Match      5.3% Score 80.5; DB 1; Length 364;
Best Local Similarity 22.8%; Pred. No. 4.2;
Matches 31; Conservative 23; Mismatches 43; Indels 39; Gaps
        16;

QY   79 PGALGIEFLKG-----FVILEELKPSGRCCOLI-----LKDP 112
DDB  150 PGPREFLELTGRSNSOPSPSLIPGGNTVTAILDRMGDAGSPDEVDLLAAHSLSAQ 209
QY   113 KQLNSFKFTGHESOPFLMKPFDIDFVV-----PPFSIKNESNYHPP--FFRTRAC 164
DDB  210 ECLNSAIFRPJLDSTP---QVFOTQFIETLLKGTTPGPGSLGFABEELSFPFGFRMSD 266
QY   165 DLLLQPDNLACKPFWK 180
DDB  267 ALLARDSRTACR-WQ 280

RESULT 15
ARRS_CAFNA
ID: ARRS_CAFNA STANDARD; PRT: 405 AA.
AC: Q282B1;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
```

Db 107 LQESLAKKLGNTYP-----LLAFFDYLPCSVMLQAPQDMKCCGVDFFVKAFAR 158
 QY 196 -----SEDHAPNFG-----FRFF-----YLYKXKHEGP 220
 Db 159 DSTEDEDKVPKSSVRLIRKVOBAPSEMGQOPRAEAAWQFFMSDKPLHLAVLSKEY 218
 QY 221 FRRK-----TCROOTTETTSCLLOVNS-----PGDYIIELVDDNTTRKY 261
 Db 219 FHGEPIVTVTVTNNTEKIVKIKALVEQVANYVLSSDIYTKPVAQETOEKY 272

Search completed: May 19, 2003, 09:20:48
 Job time : 10.6447 secs

GenCore version 5.1.4.p5_4578
Copyright (c) 1993, 2003 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: May 19, 2003, 09:14:29 ; Search time 21.809 Seconds
(without alignments)
2626.495 Million cell updates/sec

Title: US-09-912-157-2_COPY_36_313

Perfect score: 1515

Sequence: 1 ADTCGRWKAARPLCVAN.....RNVHYALKPVHSPWAGPTR 278

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 2060471115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp.archaea:*
- 2: sp.bacteria:*
- 3: sp.fungi:*
- 4: sp.human:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mhc:*
- 8: sp.organelle:*
- 9: sp.phage:*
- 10: sp.plant:*
- 11: sp.rodent:*
- 12: sp.virus:*
- 13: sp.vertebrate:*
- 14: sp.unclassified:*
- 15: sp.virus:*
- 16: sp.bacteriap:*
- 17: sp.archesp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	788	52.0	745	13 Q8QHJ9	Q8QHJ9 brachydanio
2	779	51.4	745	13 Q8QHJ6	Q8QHJ6 brachydanio
3	695	45.9	582	11 Q8F5J8	Q8F5J8 mus musculus
4	691	45.6	564	4 Q9UPA0	Q9UPA0 homo sapien
5	99	6.5	341	16 Q9Z866	Q9Z866 rickettsia
6	95.5	6.3	1341	12 Q8B304	Q8B304 sandfly fev
7	93	6.1	662	5 Q9UA07	Q9UA07 caenorhabdi
8	93	6.1	872	5 Q9XU67	Q9XU67 caenorhabdi
9	92	6.1	1428	5 Q9VU03	Q9VU03 drosophila
10	91	6.0	506	10 Q94LT2	Q94LT2 oryza sativ
11	90.5	6.0	519	13 Q9W7C2	Q9W7C2 xenopus lae
12	89.5	5.9	368	13 Q9PW79	Q9PW79 gallus gall
13	89.5	5.9	368	13 Q9IAR7	Q9IAR7 gallus gall
14	89.5	5.9	660	3 Q9C1M9	Q9C1M9 aspergillus
15	89	5.9	509	2 Q9X9S1	Q9X9S1 streptococc
16	88	5.8	344	11 Q924K7	Q924K7 meriones un

17	88	5.8	451	13 Q73719	Q73719 gallus gall
18	88	5.8	521	13 Q9PWE8	Q9PWE8 gallus gall
19	88	5.8	1173	10 Q9LFR0	Q9LFR0 arabidopsis
20	86.5	5.7	770	12 Q12935	Q12935 spodoptera
21	86	5.7	294	12 Q89248	Q89248 woodchuck h
22	85	5.6	980	2 Q8RR74	Q8RR74 bacillus sp
23	83.5	5.5	278	11 Q9QYL3	Q9QYL3 mus musculu
24	83	5.5	1121	5 Q01526	Q01526 caenorhabdi
25	82.5	5.4	318	2 Q9RG67	Q9RG67 lactobacill
26	82.5	5.4	420	12 Q92487	Q92487 bombyx mori
27	82.5	5.4	461	5 Q19938	Q19938 caenorhabdi
28	82.5	5.4	622	5 Q17082	Q17082 caenorhabdi
29	82.5	5.4	1260	5 Q19103	Q19103 caenorhabdi
30	82.5	5.4	1276	5 Q9W247	Q9W247 drosophila
31	82	5.4	465	10 Q8VZ10	Q8VZ10 oryza sativ
32	82	5.4	1096	13 Q90ZT1	Q90ZT1 brachydanio
33	82	5.4	1901	12 Q9DHH8	Q9DHH8 yaba-like d
34	81.5	5.4	465	5 Q8T6K4	Q8T6K4 plasmodium
35	81	5.3	3085	5 Q97283	Q97283 plasmodium
36	80.5	5.3	360	11 Q8R438	Q8R438 rattus norv
37	80.5	5.3	363	3 Q12575	Q12575 coprinus ci
38	80.5	5.3	371	16 Q9CH14	Q9CH14 lactococcus
39	80.5	5.3	498	10 Q9ZR09	Q9ZR09 arabidopsis
40	80.5	5.3	538	5 Q9XV22	Q9XV22 caenorhabdi
41	80.5	5.3	549	5 Q19655	Q19655 caenorhabdi
42	80.5	5.3	670	16 Q9YU48	Q9YU48 anabaena sp
43	80	5.3	501	6 Q95LS4	Q95LS4 macaca fasc
44	80	5.3	572	17 Q8TNJ1	Q8TNJ1 methanosarc
45	80	5.3	2292	12 Q66850	Q66850 encephalomy

ALIGNMENTS

RESULT 1

Q8QHJ9 PRELIMINARY; PRT; 745 AA.
ID Q8QHJ9
AC Q8QHJ9
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Sef.
GN Sef.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21824236; PubMed=11802164;
RA Tsang W, Friesel R., Kudo H T., David I.;
RT Identification of Sef, a novel modulator of FGF signalling.*;
RL Nat. Cell Biol. 4:165-169(2002).
DR EMBL; AF364103; AAL76112.1;
SQ SEQUENCE 745 AA; 83431 MW; 56FE1F0B9D98DB4 CRC64;

Query Match	52.0%	Score 788;	DB 13;	Length 745;
Best Local Similarity	53.8%	Pred. No. 4,3e-71;		
Matches 142;	Conservative 40;	Mismatches 80;	Indels 2;	Gaps 1;
QY 17	CVANGVGPSRNSGL--YNTFTYDNCYTLNPKVHVIADQNTIVTSYACHDQVAVT 74			
Db 35	CSYKQGTSTSSMOBGRKLGATFRIDNCVSNVNPGLKHAHEVNNITFSLSCDQAAYV 94			
QY 75	ILWSPGALIEFLKGFVLEELKSGRCCQLILKDPQLNSSFRTGHESSOPFLNMF 134			
Db 95	VHWASPLGIEHVKGFTYLEDNPKKCOQHLLKDPQLNFKYKIRMSQPFSSLA 154			
QY 135	ETDYFKVVPVPSKKNESNTHPFFTRACDILLQPDMLACKPFWKPNRNINISQHSQHQ 194			
Db 155	ETDYNVRIVPPTFLNDSFFPPSFLRNCSEVLLGPDNLCKPFWKPKMLNVSQLSNLH 214			

QY 195 VSFDHAPNFGFFFLHYLKLKHEGPFKRTCKQBOTETTSCLLQNVSPGDIYIELVDD 254
 DB 195 VSFDHAPNFGFFFLHYLKLKHEGPFKRTCKQBOTETTSCLLQNVSPGDIYIELVDD 274
 QY 255 TMTTRKVMHYALKPVSHPWAGPIR 278
 DB 275 SNNTRRQTOYHVSOVHSPWAGPIR 298

RESULT 2

Q8QBJ6 PRELIMINARY; PRT; 745 AA.
 AC Q8QBJ6;
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE FGF signalling antagonist Sef.
 GN Sef.
 OS Brachydanio rerio (zebrafish) (zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21824237; PubMed-11802165;
 RA Furchauer M., Lin W., Ang S.L., Thisse B., Thisse C.;
 RT "Sef is a feedback-induced antagonist of Ras/MAPK-mediated FGF
 RT signalling."
 RL Nat. Cell Biol. 4:170-174(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21824237; PubMed-11802165;
 RA Furchauer M., Lin W., Ang S.L., Thisse B., Thisse C.;
 RT "Sef is a feedback-induced antagonist of Ras/MAPK-mediated FGF
 RT signalling."
 RL Nat. Cell Biol. 4:170-174(2002).
 RN [2]

Query Match 51.4%; Score 779; DB 13; Length 745;
 Best Local Similarity 53.0%; Pred. No. 3.5e-70;
 Matches 140; Conservative 42; Mismatches 80; Indels 2; Gaps 1;

QY 17 CVANEGVGPASRNSGL-TNITFYKNDCTYLNFGVGHVIAADQNTISQYACHDQVAVT 74
 DB 35 CSTQGGTQTSMDGAKLGVTFRYDNCVNVNSPLGKHAHEVNNISFSLSCDQAAV 94
 QY 75 ILWSPGALGIEFLKGFVILELKGEGCOOLILKDPKOLNSFKETGNEOPLNKFF 134
 DB 95 VHWASPLGIEHVGKGFVILELKNPKOCQHLKDPKOLNSFKETGNEOPLNKFF 154
 QY 135 ETDYFVYVPPSPKKNESNTHPFFTRACDILLOPNLACKPFWKPRNLNISQSGSDMQ 194
 DB 155 ETDYFVYVPPSPKKNESNTHPFFTRACDILLOPNLACKPFWKPRNLNISQSGSDMQ 214
 QY 195 VSFDHAPNFGFFFLHYLKLKHEGPFKRTCKQBOTETTSCLLQNVSPGDIYIELVDD 254
 DB 215 VSFDHAPNFGFFFLHYLKLKHEGPFKRTCKQBOTETTSCLLQNVSPGDIYIELVDD 274
 QY 255 TMTTRKVMHYALKPVSHPWAGPIR 278
 DB 275 SNNTRRQTOYHVSOVHSPWAGPIR 298

RESULT 3

Q8R5J8 PRELIMINARY; PRT; 582 AA.
 AC Q8R5J8;
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Similar expression to FGF protein (Fragment).
 GN Sef.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21824237; PubMed-11802165;
 RA Furchauer M., Lin W., Ang S.L., Thisse B., Thisse C.;
 RT "Sef is a feedback-induced antagonist of Ras/MAPK-mediated FGF
 RT signalling."
 RL Nat. Cell Biol. 4:170-174(2002).
 DR EMBL; AF424804; AAL79530.1;
 FT NON_TER
 FT SEQUENCE 582 AA; 65263 MW; 56663B2981C4268E CRC64;
 Query Match 45.9%; Score 695; DB 11; Length 582;
 Best Local Similarity 86.0%; Pred. No. 8.5e-62;
 Matches 123; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 136 TDYFVYVPPSPKKNESNTHPFFTRACDILLOPNLACKPFWKPRNLNISQSGSDMQV 195
 DB 1 TDYFVYVPPSPKKNESNTHPFFTRACDILLOPNLACKPFWKPRNLNISQSGSDMQV 60
 QY 196 SFDHAPNFGFFFLHYLKLKHEGPFKRTCKQBOTETTSCLLQNVSPGDIYIELVDD 255
 DB 61 SFDHAPNFGFFFLHYLKLKHEGPFKRTCKQBOTETTSCLLQNVSPGDIYIELVDD 120
 QY 256 TMTTRKVMHYALKPVSHPWAGPIR 278
 DB 121 TMTTRKVMHYALKPVSHPWAGPIR 143

RESULT 4

Q9UFA0 PRELIMINARY; PRT; 564 AA.
 AC Q9UFA0;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
 DE Hypothetical 63.1 KDa protein (Fragment).
 GN DKF2P434N1928.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RA Bioecker H., Bioecker M., Brandt P., Mewes H.W., Gassenhuder J.,
 RA Wiemann S.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL133097; CAB61408.1;
 KW Hypothetical protein.
 FT NON_TER
 FT SEQUENCE 564 AA; 63134 MW; 6B3AA5BD4523E88C CRC64;

Query Match 45.6%; Score 691; DB 4; Length 564;
 Best Local Similarity 99.2%; Pred. No. 2.1e-61;
 Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 155 HPFFTRACDILLOPNLACKPFWKPRNLNISQSGSDMQVSDHAPNFGFFFLHYL 214
 DB 1 HPFFTRACDILLOPNLACKPFWKPRNLNISQSGSDMQVSDHAPNFGFFFLHYL 60
 QY 215 LKHEGPFKRTCKQBOTETTSCLLQNVSPGDIYIELVDDTNTTRKVMHYALKPVSHPA 274
 DB 61 LKHEGPFKRTCKQBOTETTSCLLQNVSPGDIYIELVDDTNTTRKVMHYALKPVSHPA 120
 QY 275 GPIR 278
 DB 121 GPIR 124

RESULT 5

Q9ZB56


```

Db 259 NCNDPIQKFFITLQAGTPTFTYHKDFNGSHTSYLHDHFKPNTYFLRVCKNSIGNG 318
QY 58 -----ONTISOTACHOV-----AVTILWSPGALG-TEFLKGFVILEEL 97
Db 319 OPTPOPGITLSTY--DPIFKVETGTASTITIGWPPDLADIOTIELIVSB- 374
QY 98 KSGRCQOLILKOPKQNSFKRTGSEOPFLMKFTDYFKVVPFSPKINSYHPF 157
Db 375 --SG-----EVPKIEEATYQNSRLPYN-----FDKLATATDE-- 408
QY 158 FFRTRACILLQPNLACKPFW-----KPNRLNISOH-----GSDMOVSF 197
Db 409 -FVRACSDLTK-----TCGP-WSENVNGTMDGVATKPTNLSIQCHDNVTRNSAINW 462
QY 198 DHAPNFGFRFYLYLKHEGFKKTC-----KQTTTTSCLLQNVSPGDIY 249
Db 463 D-VKYPNGKILY-----ESVSTNTYTVTSATIRHKKNGEPATGSLMPVSTDAIGR 516
QY 250 ELVDYNTTRKVMYALK---PVHSPWAGPI 277
Db 517 TMRKVNLDK---YVLKLYLPKISERNGPI 544
RESULT 10
Q94LT2 PRELIMINARY; PRT; 506 AA.
AC Q94LT2
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 56.6 kDa protein.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=CV, NIPPONBARE;
RA Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Taitrin T.,
RA Riggs F., Hsiao J., Zismann V., Blunt S., Pal G., Vanaken S.E.,
RA Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,
RA White O., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSJNB0011A08 genomic sequence.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC034238; AAK5491.1;
DR InterPro; IPR004263; Exostosin.
DR Pfam; PF03016; Exostosin; 1.
KW Hypothetical protein.
SQ SEQUENCE 506 AA; 56612 MW; B35878D1F1CE24CE CRC64;

Query Match 6.0%; Score 91; DB 10; Length 506;
Best Local Similarity 20.8%; Pred. No. 1.3;
Matches 60; Conservative 34; Mismatches 82; Indels 112; Gaps 14;

QY 18 VANEGVGPASRNSGLNITFKYDNCYTLNPKVGRKVIADQNITISYAC--HDOVAVTI 75
Db 113 VYNDGFGPAGGALPERDYD-----TDQYMLAIYHMRREYELTGDAARAADA 164
QY 76 LMSFGALGIEFLKGFVILEELSE-----GRCQOLILKPKQLNS----- 117
Db 165 FEVP-----FYAGFDAANLAKSLDAERDALPRLQAEWLRPEWNRAGGRDHFNVAAR 218
QY 118 ----SFKRTG-----MESQPLANKPETDYFKVVPFSPKINSN 153
Db 219 PVWDYRGGDGMGNALLTYPAINTVTLTVEANPWGIDFG-----VFPF-----SH 266
QY 154 HPFFFRTRACDILLQPNLACKPKFKPRLNLSISGRSDMVSPDHAPHNFGFRFYLYH 213
Db 267 FHP-----TSDADVL-----WQDR---MRRGRRLWAFAGAPR----- 298
QY 214 KLKHEGFPKRTCKQ---EQTTTTSCLLQNVSPGDIY-----ILEVD 253

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Db 299 -----PGSKTYRAQIIEQCTASPTSCFTGSSPGHNSPGRINELLE 340
RESULT 11
Q9W7C2 PRELIMINARY; PRT; 519 AA.
AC Q9W7C2
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE T-box transcription factor Tbx5.
GN TBX5.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE-99180578; PubMed-10079235;
RA Horb M.E.; Thomsen G.H.;
RT "Tbx5 is essential for heart development.";
RL Development 126:1739-1751(1999).
DR EMBL; AF133036; AAD23592.1;
DR HSSP; P24781; LXR.
DR TRANSFAC; T04422;
DR InterPro; IPR001699; TF-T-box.
DR Pfam; PF00907; T-box; 1.
DR PRINTS; PR00937; TBOX.
DR SMART; SM00425; TBOX_1.
DR PROSITE; PS01283; TBOX_1; 1.
DR PROSITE; PS01284; TBOX_2; 1.
DR PROSITE; PS0252; TBOX_3; 1.
SQ SEQUENCE 519 AA; 58080 MW; 8B5E096C67FC3D1E CRC64;

Query Match 6.0%; Score 90.5; DB 13; Length 519;
Best Local Similarity 20.9%; Pred. No. 1.5;
Matches 61; Conservative 42; Mismatches 90; Indels 99; Gaps 15;

QY 13 RPLCV--ANEVGPASRNSGLNITFKYDNCYTLNPKVGRKVIADQNITISYACHDQ 70
Db 180 QRLVHVDADNNGFGSKTAF-----CT-----HVSETDIATVTONKI 222
QY 71 VAVTILWSPGALGIEFLKGFVILEELSEGRQCOQLILKPKQLNSFKRTGMSQPL 130
Db 223 TQLAIENP-----PAKGRG-----SDDMELH---RNSRMQSKY- 255
QY 131 NMKFETDYFKVVPFSPKINSN---SNTHPPFPFRTR-----ACDILL 167
Db 256 -----PVVPRSTVRQKVSNNHSPFSQETRNIGSSTLNSQYOCENGVSYSQDILL 305
QY 168 LOPDNLACKPKFKPRLNLSISGRSDMVSPDHAPHNFGFRFYLYHKLKHEGFPKRTCK 227
Db 306 --PSSAYTSL--PHESGTIYHCTKRVKSEPAHS--YKKPYMDTSPSEDPFTRSGP 359
QY 228 Q--EQTTTTS-----CLLQNVSPGDIYILEVD--TNTTRKVMHYA 265
Db 360 QPSSSSSTTSFTESAQRQAQACHTASSAPTEVPVSTEDISCHNSVSPSIS 411
RESULT 12
Q9PW79 PRELIMINARY; PRT; 368 AA.
AC Q9PW79
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TBBS3.
GN TBBS.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

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DR PFam: PF00020; TNFR_C6; 2.  
DR SMART: SKN00005; DEATH; 1.  
DR SMART: SKN00208; TNFR; 2.  
DR PROSITE: PS00198; 4FEAS_FERREDOXIN; UNKNOWN_1.  
DR PROSITE: PS50017; DEATH_DOMAIN; 1.  
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.  
DR PROSITE: PS50050; TNFR_NGFR_2; 2.  
DR SQ SEQUENCE 368 AA; 41531 MW; 0553CE531DBE47C6 CRC64;  
  
Query Match          5.9%; Score 89.5; DB 13; Length 368;  
Best Local Similarity 22.9%; Pred. No. 1.2;  
Matches 36; Conservative 19; Mismatches 49; Indels 53; Gaps  
  
QY 77 WSPCALGIIEFLKGRVILEELKSEGRQCQOILTKDPQLNSFKRTGNESOPFLNM-----132  
Db 195 WKPSAV-----VNRLQRLGLIODNRNCNEOIYNQQCOBELLTAGSVEVPGBGVEMGTGTE 247  
  
QY 133 -----KPEF-----DYFKVVPPPSIKNESHTHPFFFTTRACD- 165  
Db 248 RRPDPKVETVKLQPVVLGENPALLHRSFTFYDYVFPPEAKRG-----RALDL 298  
  
QY 166 -----LLQPDNLACKPFWKPRNLNISQHSMDQVS 196  
Db 299 QENDLYLAEDHDHRVSCPEPTOMLTWLNMOOGSKASVN 335  
  
RESULT 14  
Q9CIM9 PRELIMINARY; PRT: 660 AA.  
ID O9CLM9  
AC O9CLM9  
DT 01-JUN-2001 (TRENBLrel. 17, Created)  
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
DE 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
DE ALPHA-L-rhamnosidase A precursor (EC 3.2.1.40).  
GN RHAA.  
OS Aspergillus aculeatus.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eurytiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillius.  
NCBI_TaxID=5053;  
RX RN [1]  
RN RX [1]  
RP MEDLINE=21218536; PubMed=11319105;  
RA Manzanares P., van Den Broeck H.C., de Graaff L.H., Vlaser J.;  
RT Purification and Characterization of Two Different alpha-L-  
RT Rhamnosidases, Rhna and Rhap, from Aspergillus aculeatus.*;  
RL Appl. Environ. Microbiol. 67:2230-2234(2001).  
DE ENBL; AF284761; AAA16249.1;  
KW Glycosidase; Hydrolase; Signal.  
RW SIGNAL  
FX 1 19 POTENTIAL.  
SQ SEQUENCE 660 AA; 71218 MW; A550A9FAFD0E42984 CRC64;  
  
Query Match          5.9%; Score 89.5; DB 3; Length 660;  
Best Local Similarity 22.4%; Pred. No. 2.6;  
Matches 57; Conservative 29; Mismatches 92; Indels 77; Gaps  
  
QY 3 TCGRWKAARPPLCVANEGVGPSNSGLNTYTFKDNYCTTYLPVPGKHVIADAQNITY 62  
Db 403 TAASKIAANAARLWA-----QNSLR-----DNFTTLHPDGNAWAIAKANLXL 448  
  
QY 63 SOYACHD-QVAVTVLWSGP-----GALGIEFLKGRVILEELASEGRCCQLI-----108  
Db 449 SSNOSEAISALAARWGYPGAPAPEAGSTVSPFTGGGFELQAHLANEPRDALDLLRLQWG 508  
  
QY 109 --LKDPQLNSFKRTGNESOPPLANKKETDIFYKKVVPFPSIKNESYH-----PFFFT 161  
Db 509 FMDDPPMTNSTVF-----IES-----YSTDGSLAYAPHYNTRVSHAGWSTGPTSALT 557  
  
QY 162 R-----ACDLLLOPDNLACKPFWKPRNLNISQHSMDQVSDFORAPHNGFRFFT 210  
Db 558 HYTAGLRUTPGAGSTWLTFK-----QPGNLTEVQAGFETOLG-----LEA 597  
QY 211 LHYLKLBHGPFKRKT 225
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Db 598 TOTQKSAAGTFOOLT 612

RESULT 15

Q9X9S1 PRELIMINARY; PRT; 509 AA.
AC Q9X9S1;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Polysaccharide synthase.
GN TTS.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID-1313;
RN [1]
RP SEQUENCE FROM N.A.
RA Liuli D., Munoz R., Lopez R., Garcia E.;
RT "A single gene (tts) located outside the cap locus directs the
RT formation of Streptococcus pneumoniae type 37 capsular polysaccharide:
RT type 37 pneumococci are natural, genetically binary strains."
RL J. Exp. Med. 19:241-251(1999).
DR EMBL: AJ131985; CAB51329.1;
DR InterPro: IPR001173; Glycos.transf_2.
DR Pfam: PF00535; Glycos.transf_2; 1.
SQ SEQUENCE 509 AA; 5888 MW; C6C38D2ACFAB0D8A CRC64;

Query Match 5.94; Score 89; DB 2; Length 509;
Best Local Similarity 23.1%; Pred. No. 2.1;
Matches 62; Conservative 43; Mismatches 117; Indels 46; Gaps 14;
QY 32 LYNITFKYDNCCTTILNPVKHV-----IADAQNITISQYACHDOVAVTILSPGALGIEF 86
DB 70 IYVSTFYLN-----YHYGSGFKSSISEAKKVIILYCTANDFVPECLVES---MOQDY 123
QY 87 LKGRVILEELKSGROQQLILKDPQLNSSF---KRTGMS---QPELNMKFETDYF 139
DB 124 ANFETVILDDSKSE--VTKQVDEFAKYNVSVIRDDDRNGFKAGNINNTLNKNNDYDF 181
QY 140 V-----KVPPEPSIKNESNHPFEETRACDILLQPDNLACKPFKPNLNISQHGSDMQ 194
DB 182 VLLDSEIIPSNFKSLAY---FERNRLG-ILQATHVA-----SRNRLFM--DTLA 229
QY 195 VSFD-HAPNFGFRFFLYHLKHEGPFKRKTKQ-----EOTTETSCILQNVSPGDY 247
DB 230 IGVDSEHPYQKVHYTGFLSLGHGAMISKDCYQAAGGFPVHVAEDLCFSIESRIKGDY 289
QY 248 ITELVDNTNTRK--VMHYALKPVHSPW 273
DB 290 HVGFAADDIVCQEEYPPDYLAFAKRSKW 317

Search completed: May 19, 2003, 09:23:47
Job time : 28.809 secs

GenCore version 5.1.4_p5.4578
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OM protein - protein search, using sw model

Run on: May 19, 2003, 09:07:58 ; Search time 54.0074 Seconds
(without alignments)
1771.498 Million cell updates/sec

Title: US-09-912-157-2_COPY_36_753

Perfect score: 3829

Sequence: 1 ADTCGRWMAARPLCVAN.....CYADLCGRSYTDELHVAFL 718

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues.

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3829	100.0	753	23	Human cytokine rec
2	3819	99.7	753	23	Human cytokine rec
3	3741	97.3	739	23	Human cytokine rec
4	3725	97.3	738	22	Human Interleukin
5	3721	97.2	738	22	Human Interleukin
6	3720	97.2	738	22	Human Interleukin
7	3718	97.1	738	22	Human Interleukin
8	3718	97.1	738	22	Human Interleukin
9	3718	97.1	738	22	Human Interleukin
10	3714	97.0	738	22	Human Interleukin

11	3714	97.0	738	22	AAU09957	Human Interleukin
12	3703	96.7	728	22	AAU04958	Human Interleukin
13	3700	96.6	739	22	AAU10602	Human Interleukin
14	3657	95.5	738	23	AAU11355	Human DNAX cytokin
15	3208	83.8	739	23	ABB07630	Murine cytokine re
16	2515	65.7	554	22	AAU91330	Human novel secret
17	1334	34.8	296	22	AAU10601	5' portion of Huma
18	312	8.1	866	19	AAW04185	Human Interleukin-
19	312	8.1	866	19	AAW61272	Human Interleukin-
20	312	8.1	866	21	AAW92409	Human IL-17R prote
21	312	8.1	866	21	AAW99941	Human IL-17R prote
22	312	8.1	866	21	AAW97131	Human Interleukin-
23	312	8.1	866	21	AAW97181	Human Interleukin-
24	312	8.1	866	21	AAW03807	Human IL-17R (NCTL
25	312	8.1	866	22	AAW82086	Human Interleukin-
26	312	8.1	866	22	AAW72754	Murine Interleukin
27	306	8.0	864	19	AAW04184	Mouse Interleukin-
28	306	8.0	864	19	AAW61271	Murine IL-17R prot
29	306	8.0	864	21	AAW92408	Murine IL-17R prot
30	306	8.0	864	21	AAW99935	Murine Interleukin
31	306	8.0	864	21	AAW97130	Murine Interleukin
32	306	8.0	864	21	AAW97180	Murine Interleukin
33	306	8.0	864	21	AAW03806	Murine IL-17R poly
34	306	8.0	864	22	AAW82086	Murine Interleukin
35	306	8.0	864	22	AAW72748	Human IL-17 recept
36	271.5	7.1	539	23	AAW47457	Human IL-17RH matu
37	135.5	3.5	238	20	AAW31624	Human secreted pro
38	135.5	3.5	385	21	AAW25795	Human secreted pro
39	135.5	3.5	385	22	AAW75381	Human IL-17 recept
40	135.5	3.5	385	23	AAW47459	Human PRO polypept
41	135.5	3.5	502	22	AAU29233	Human EST encoded
42	135.5	3.5	502	22	AAW24349	Human Interleukin
43	135.5	3.5	502	22	AAU04955	Human protein havi
44	135.5	3.5	502	22	AAW06386	Human PRO5801. Ho
45	135.5	3.5	502	22	AAW97604	

ALIGNMENTS

RESULT 1
ABB07626
ID ABB07626 standard; Protein; 753 AA.

AC ABB07626;

DT 20-MAY-2002 (first entry)

DE Human cytokine receptor, Zcytor18 amino acid sequence.

DE Cytokine receptor; Zcytor18; cell proliferation; antiproliferative; human;
pulmonary alveolar proteinosis; familial periodic fever; antitumor;
erythroleukemia; chromosome 3p14.3; gene therapy.

OS Homo sapiens.

PN WO200208259-A2.

PD 31-JAN-2002.

PF 23-JUL-2001; 2001WO-US23253.

PR 26-JUL-2000; 2000US-220747P.

XX (ZYMO) ZYMOGENETICS INC.

XX Presnell SR, Kuestner RE, Gao Z;

XX WPI; 2002-217048/27.

XX N-PSDB; ABA95031, ABA95032.

XX New cytokine receptor polypeptide designated zcytor18, useful for
inhibiting cell proliferation associated with psoriasis or tumor

PT growth, and modulating immune system by binding to endogenous zcytor18;
 PT ligand;
 XX Claim 1; Page 2; 119pp; English.
 XX The invention relates to an isolated cytokine receptor polypeptide
 CC designated zcytor18. The zcytor18 polypeptides can be expressed by
 CC standard recombinant methodology. The polypeptides can be used to inhibit
 CC cell proliferation associated with psoriasis or tumour growth. The
 CC encoding nucleic acids are useful for providing zcytor18 in vivo by gene
 CC therapy techniques. zcytor18 oligonucleotide probes are useful for in
 CC vivo diagnosis, and the zcytor18 probes and primers can be used to detect
 CC and localize zcytor18 gene expression in tissue samples. The probes are
 CC also useful for detecting gross aberrations in chromosome 3 in which
 CC zcytor18 gene resides. The zcytor18 polynucleotides can also be used in
 CC linkage-based testing of pulmonary alveolar proteinosis, familial
 CC periodic fever and erythroleukemia, and erythroleukemia associated with
 CC polymorphisms of cytokine receptors. The present sequence represents a
 CC human zcytor18 amino acid sequence.
 XX Sequence 753 AA;

Query Match 100.0%; Score 3829; DB 23; Length 753;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 716; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADTCGWRKAAARPRLCVANEVGPASRNSGLYNTFKYDNCYTLNPGKRVIAADQNI 60
 DB 36 ADTCGWRKAAARPRLCVANEVGPASRNSGLYNTFKYDNCYTLNPGKRVIAADQNI 95
 QY 61 TISQYACHDQVAVTIWSPGALGIEFLAGFRVILEELKSGRCCQOLILKDPQLNLSFK 120
 DB 96 TISQYACHDQVAVTIWSPGALGIEFLAGFRVILEELKSGRCCQOLILKDPQLNLSFK 155
 QY 121 RTGESQFFLMKFETDYFVKKVPPPSIKNESYHPFFTRACDILLQPDNLACKPFWK 180
 DB 156 RTGESQFFLMKFETDYFVKKVPPPSIKNESYHPFFTRACDILLQPDNLACKPFWK 215
 QY 181 PRNLISQSGSDMOVSDHAPNCFREFYLYLKHGEPFRKTKQBTETTSCLLQ 240
 DB 216 PRNLISQSGSDMOVSDHAPNCFREFYLYLKHGEPFRKTKQBTETTSCLLQ 275
 QY 241 NVSPGDYIIEVDVNTTRKVNHYALKFVPSWAGPIRAVITVPLVLSAFATLFTVC 300
 DB 276 NVSPGDYIIEVDVNTTRKVNHYALKFVPSWAGPIRAVITVPLVLSAFATLFTVC 335
 QY 301 RKQOENYSHLDESSSESTYTAALPRERLRPRKPYELCYSKDQGNHNVQCFAYFL 360
 DB 336 RKQOENYSHLDESSSESTYTAALPRERLRPRKPYELCYSKDQGNHNVQCFAYFL 395
 QY 361 QDFCGEVALDWEDFSLCREGQREWVQIKIHESQFIIVVCSKGMKIFVYDKNKKHGGG 420
 DB 396 QDFCGEVALDWEDFSLCREGQREWVQIKIHESQFIIVVCSKGMKIFVYDKNKKHGGG 455
 QY 421 RGSKGELFVAVSAELKRAQSSAALSKEFIATVFDYSGEDVPCILDLSTKRLM 480
 DB 456 RGSKGELFVAVSAELKRAQSSAALSKEFIATVFDYSGEDVPCILDLSTKRLM 515
 QY 481 DNLPLCSHLHSDHGLQEPQHTQGRSRRNTRFSKGRSLVAICNKHQFIDEPDWE 540
 DB 516 DNLPLCSHLHSDHGLQEPQHTQGRSRRNTRFSKGRSLVAICNKHQFIDEPDWE 575
 QY 541 KQFVPEPPLPYRREPVELEKDSGLVNDVMCKPGSPESDCLKVEAVLIGATGADSOHE 600
 DB 576 KQFVPEPPLPYRREPVELEKDSGLVNDVMCKPGSPESDCLKVEAVLIGATGADSOHE 635
 QY 601 SQHGLDQGEARPALDGAALQPLHTVTRAGSPDNPRDGSIGYSSVPSSELSLPLMEG 660
 DB 636 SQHGLDQGEARPALDGAALQPLHTVTRAGSPDNPRDGSIGYSSVPSSELSLPLMEG 695
 QY 661 LSTDQETSSLTESVSSSSGLGEEPEPALPSPKLLSSGCKADLGCSTYDDELHVAVPL 718
 DB 696 LSTDQETSSLTESVSSSSGLGEEPEPALPSPKLLSSGCKADLGCSTYDDELHVAVPL 753

RESULT 2

ABB07627
 ID ABB07627 standard; Protein; 753 AA.
 AC ABB07627;
 XX 20-MAY-2002 (first entry)
 DT Human cytokine receptor, zcytor18 variant sequence.
 DE Cytokine receptor; zcytor18; cell proliferation; antiproliferative; human;
 KW pulmonary alveolar proteinosis; familial periodic fever; antitumor;
 KW erythroleukemia; chromosome 3p14.3; gene therapy; variant.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT Misc-difference 269 /label- R269M
 FT /note- "wild-type Thr is replaced with Met"
 FT Misc-difference 750 /label- V750A
 FT /note- "wild-type Val is replaced with Ala"
 XX W020208259-A2.
 XX 31-JAN-2002.
 XX 23-JUL-2001; 2001WO-US23253.
 XX 26-JUL-2000; 2000US-220747P.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Presnell SR, Kuestner RE, Gao Z;
 DR WPI; 2002-217048/27.
 DR N-PSDB; ABA95033, ABA95034.
 XX New cytokine receptor polypeptide designated zcytor18, useful for
 PT inhibiting cell proliferation associated with psoriasis or tumor
 PT growth, and modulating immune system by binding to endogenous zcytor18
 PT ligand
 XX Disclosure; Page 94-98; 119pp; English.
 XX The invention relates to an isolated cytokine receptor polypeptide
 CC designated zcytor18. The zcytor18 polypeptides can be expressed by
 CC standard recombinant methodology. The polypeptides can be used to inhibit
 CC cell proliferation associated with psoriasis or tumour growth. The
 CC encoding nucleic acids are useful for providing zcytor18 in vivo by gene
 CC therapy techniques. zcytor18 oligonucleotide probes are useful for in
 CC vivo diagnosis, and the zcytor18 probes and primers can be used to detect
 CC and localize zcytor18 gene expression in tissue samples. The probes are
 CC also useful for detecting gross aberrations in chromosome 3 in which
 CC zcytor18 gene resides. The zcytor18 polynucleotides can also be used in
 CC linkage-based testing of pulmonary alveolar proteinosis, familial
 CC periodic fever and erythroleukemia, and erythroleukemia associated with
 CC polymorphisms of cytokine receptors. The present sequence represents a
 CC human zcytor18 variant amino acid sequence.
 XX Sequence 753 AA;

Query Match 99.7%; Score 3819; DB 23; Length 753;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 716; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ADTCGWRKAAARPRLCVANEVGPASRNSGLYNTFKYDNCYTLNPGKRVIAADQNI 60
 DB 36 ADTCGWRKAAARPRLCVANEVGPASRNSGLYNTFKYDNCYTLNPGKRVIAADQNI 95

QY 61 TISQACHDOAVATILMSGALGIEFLKGRVILEELKSGRQCOOLILKDPKOLNSPK 120
 DB 96 TISQACHDOAVATILMSGALGIEFLKGRVILEELKSGRQCOOLILKDPKOLNSPK 155
 QY 121 RTGMSQPLANKFTDYFVAVPFPSPKSNYHEFFERTACDLLOPDLACKPFWK 180
 DB 156 RTGMSQPLANKFTDYFVAVPFPSPKSNYHEFFERTACDLLOPDLACKPFWK 215
 QY 181 PRLNISQSGDMQVSDHAPNHFGRFFLYLKLHKGEPFRKTKCOEOTTTSCILQ 240
 DB 216 PRLNISQSGDMQVSDHAPNHFGRFFLYLKLHKGEPFRKTKCOEOTTTSCILQ 275
 QY 241 NVSPGDIYIELVDOTNTTRKVMHYALAPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
 DB 276 NVSPGDIYIELVDOTNTTRKVMHYALAPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 335
 QY 301 RKQOENIYSHLDESSSESTYTAALPRELRPRKPVLCYSSKDGQHNHNVQCFAYFL 360
 DB 336 RKQOENIYSHLDESSSESTYTAALPRELRPRKPVLCYSSKDGQHNHNVQCFAYFL 395
 QY 361 QDFCGEVALDWMEDFSLCRGQREWYIQIHESQFIIVVCSKGMKTFYDKKTKHKG 420
 DB 396 QDFCGEVALDWMEDFSLCRGQREWYIQIHESQFIIVVCSKGMKTFYDKKTKHKG 455
 QY 421 RGSKGELFLVAVSAIAELKROAKOSSAALSFKFIATVDFYSCGDVPGIILSTKRLM 480
 DB 456 RGSKGELFLVAVSAIAELKROAKOSSAALSFKFIATVDFYSCGDVPGIILSTKRLM 515
 QY 481 DNLPLQCSHLHSRDHGLQBPQGTROGSRNRYFRSKSGLYVAICNMHOIDEEDPWE 540
 DB 516 DNLPLQCSHLHSRDHGLQBPQGTROGSRNRYFRSKSGLYVAICNMHOIDEEDPWE 575
 QY 541 KQFVFPHPPLRYREPVLKFDGLVNDVMCKPGPESDCLKVEAAVLGATGADPSQHE 600
 DB 576 KQFVFPHPPLRYREPVLKFDGLVNDVMCKPGPESDCLKVEAAVLGATGADPSQHE 635
 QY 601 SOHGLDQDGEARPAIDGSAALQPLLTHTVKAQSPDMRDSGITDSSVPSSELSPLMEG 660
 DB 636 SOHGLDQDGEARPAIDGSAALQPLLTHTVKAQSPDMRDSGITDSSVPSSELSPLMEG 695
 QY 661 LSTDQETSSLTSSVSSSGIGEEPPALPSPKLLSSGCKADLACRSTYTDLHAAVPL 718
 DB 696 LSTDQETSSLTSSVSSSGIGEEPPALPSPKLLSSGCKADLACRSTYTDLHAAVPL 753

RESULT 3

ABB07628
 ID ABB07628 standard; Protein; 739 AA.
 AC ABB07628;
 XX ABB07628;
 XX

20-MAY-2002 (first entry)

Human cytokine receptor, zcytor18 splice variant.

Cytokine receptor; zcytor18; cell proliferation; antipsoriatic; human;
 pulmonary alveolar proteinosis; familial periodic fever; antitumor;
 erythroleukemia; chromosome 3p14.3; gene therapy; splice variant.

Homo sapiens.

WO200208259-A2.

31-JAN-2002.

23-JUL-2001; 2001MO-US23253.

26-JUL-2000; 2000US-22047P.

(Zymo) ZYMOGENETICS INC.

Presnell SR, Kuestner RE, Gao Z;

DR WP1; 2002-217048/27.
 DR N-PSDB; ABA95035, ABA95036.
 XX
 PT New cytokine receptor polypeptide designated zcytor18, useful for
 PT inhibiting cell proliferation associated with psoriasis or tumor
 PT growth, and modulating immune system by binding to endogenous zcytor18
 PT ligand
 XX
 PS Claim 1; Page 102-106; 119pp; English.
 XX
 CC The invention relates to an isolated cytokine receptor polypeptide
 CC designated zcytor18. The zcytor18 polypeptides can be expressed by
 CC standard recombinant methodology. The polypeptides can be used to inhibit
 CC cell proliferation associated with psoriasis or tumour growth. The
 CC encoding nucleic acids are useful for providing zcytor18 in vivo by gene
 CC therapy techniques. zcytor18 oligonucleotide probes are useful for in
 CC vivo diagnosis, and the zcytor18 probes and primers can be used to detect
 CC and localize zcytor18 gene expression in tissue samples. The probes are
 CC also useful for detecting gross aberrations in chromosome 3 in which
 CC zcytor18 gene resides. The zcytor18 polynucleotides can also be used in
 CC linkage-based testing of pulmonary alveolar proteinosis, familial
 CC periodic fever and erythroleukemia, and erythroleukemia associated with
 CC polymorphisms of cytokine receptors. The present sequence represents a
 CC human zcytor18 splice variant.
 XX
 SQ Sequence 739 AA;

Query Match 97.7%; Score 3741; DB 23; Length 739;
 Best Local Similarity 98.1%; Pred. No. 0;
 Matches 704; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 ADTCGRMKAAARPLCVANEGVGPASRNSGLYNTTFKIDNCTTYLNPVKGRVIAADQNI 60
 DB 36 ADTCGR -----GVGPASRNSGLYNTTFKIDNCTTYLNPVKGRVIAADQNI 81
 QY 61 TISQACHDOAVATILMSGALGIEFLKGRVILEELKSGRQCOOLILKDPKOLNSPK 120
 DB 82 TISQACHDOAVATILMSGALGIEFLKGRVILEELKSGRQCOOLILKDPKOLNSPK 141
 QY 121 RTGMSQPLANKFTDYFVAVPFPSPKSNYHEFFERTACDLLOPDLACKPFWK 180
 DB 142 RTGMSQPLANKFTDYFVAVPFPSPKSNYHEFFERTACDLLOPDLACKPFWK 201
 QY 181 PRLNISQSGDMQVSDHAPNHFGRFFLYLKLHKGEPFRKTKCOEOTTTSCILQ 240
 DB 202 PRLNISQSGDMQVSDHAPNHFGRFFLYLKLHKGEPFRKTKCOEOTTTSCILQ 261
 QY 241 NVSPGDIYIELVDOTNTTRKVMHYALAPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
 DB 262 NVSPGDIYIELVDOTNTTRKVMHYALAPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 321
 QY 301 RKQOENIYSHLDESSSESTYTAALPRELRPRKPVLCYSSKDGQHNHNVQCFAYFL 360
 DB 322 RKQOENIYSHLDESSSESTYTAALPRELRPRKPVLCYSSKDGQHNHNVQCFAYFL 381
 QY 361 QDFCGEVALDWMEDFSLCRGQREWYIQIHESQFIIVVCSKGMKTFYDKKTKHKG 420
 DB 382 QDFCGEVALDWMEDFSLCRGQREWYIQIHESQFIIVVCSKGMKTFYDKKTKHKG 441
 QY 421 RGSKGELFLVAVSAIAELKROAKOSSAALSFKFIATVDFYSCGDVPGIILSTKRLM 480
 DB 442 RGSKGELFLVAVSAIAELKROAKOSSAALSFKFIATVDFYSCGDVPGIILSTKRLM 501
 QY 481 DNLPLQCSHLHSRDHGLQBPQGTROGSRNRYFRSKSGLYVAICNMHOIDEEDPWE 540
 DB 502 DNLPLQCSHLHSRDHGLQBPQGTROGSRNRYFRSKSGLYVAICNMHOIDEEDPWE 561
 QY 541 KQFVFPHPPLRYREPVLKFDGLVNDVMCKPGPESDCLKVEAAVLGATGADPSQHE 600
 DB 562 KQFVFPHPPLRYREPVLKFDGLVNDVMCKPGPESDCLKVEAAVLGATGADPSQHE 621
 QY 601 SOHGLDQDGEARPAIDGSAALQPLLTHTVKAQSPDMRDSGITDSSVPSSELSPLMEG 660

Db 622 SOHGLDQGEARPDGSAALQPLHTVKAQSPDMRDSGGYDSSVPSSELSPLMEG 681
 QY 661 LSTDTTSLTSSVSSGLGEEPPALPSKLLSSGCKADGCRSTYDELHAYAPL 718
 Db 682 LSTDTTSLTSSVSSGLGEEPPALPSKLLSSGCKADGCRSTYDELHAYAPL 739

RESULT 4

AAU09904
 ID AAU09904 standard; Protein; 738 AA.

XX AC AAU09904:
 XX DT 14-FEB-2002 (first entry)
 XX DE Human Interleukin 17 (hIL-17) receptor-like protein.

XX DE Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 XX KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 XX KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 XX KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 XX KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
 XX KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 XX KW bone disease; vascular disorder; eye disorder; cancer; human.

XX OS Homo sapiens.

XX PN WO200168859-A2.

XX PD 20-SEP-2001.

XX PF 15-MAR-2001; 2001WO-US08678.

XX PR 16-MAR-2000; 2000US-189816P.

XX PR 28-NOV-2000; 2000US-0724460.

XX PA (AMGE-) AMGEN INC.

XX PI Jling S;

XX WPI; 2001-611392/70.

XX DR NP-FSD8; AAS15346.

XX PT Nucleic acids encoding interleukin 17 receptor like polypeptides,
 XX PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
 XX PT diabetes, psoriasis and glaucoma -
 XX PS Claim 2; Page 152-154; 158pp; English.

XX CC The invention describes novel nucleic acids encoding interleukin (IL) 17
 XX CC receptor like polypeptides useful as vaccines and in gene therapy. These
 XX CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 XX CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
 XX CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 XX CC osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
 XX CC ophthalmological activities. The IL-17 receptor like nucleic acids and
 XX CC proteins may be used to prevent and treat diseases associated with
 XX CC inappropriate IL-17 receptor like polypeptide (IL17R) expression. These
 XX CC include, for example immune disorders (e.g. inflammation, diabetes and
 XX CC transplant rejection), infections (e.g. hepatitis and septicemia),
 XX CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
 XX CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 XX CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 XX CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 XX CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 XX CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
 XX CC breast cancer), reproductive disorders (e.g. infertility and
 XX CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 XX CC DNA and its complements may also be used as diagnostic probes to detect and
 XX CC quantitate the presence of similar nucleic acids in samples and identify
 XX CC patients needing restorative therapy. The IL17R may also be used as
 XX CC antigens in the production of antibodies against the proteins and in
 XX CC assays to identify modulators of expression and activity. The

CC anti-IL17r/p antibodies and antagonists may also be used to down regulate
 CC expression and activity. This is the amino acid sequence of the human
 CC interleukin 17 (IL-17) receptor like protein described in the method of
 CC the invention.
 XX SQ Sequence 738 AA;

Query Match 97.38; Score 3725; DB 22; Length 738;
 Best local similarity 97.8%; Pred. No. 0;

Matches 700; Conservative 1; Mismatches 1; Indels 14; Gaps 1;

QY 2 DTGCGWKAARPRICVANEGVGPASRNGLYNITFKYDNCCTTTLNVPVGRVIADAGNIT 61
 Db 37 DTGCGW-----GVGPASRNGLYNITFKYDNCCTTTLNVPVGRVIADAGNIT 82
 QY 62 ISOYACHDOVAVTIILWSPGALGIEFLAGFRVILEELKSGROCOOLILKDPQLNSFKR 121
 Db 83 ISOYACHDOVAVTIILWSPGALGIEFLAGFRVILEELKSGROCOOLILKDPQLNSFKR 142
 QY 122 TGMESQPFLLMKFETDYEVVVPPEPSIKNESYHPFFETRACDLLLQPDNLACKPWP 181
 Db 143 TGMESQPFLLMKFETDYEVVVPPEPSIKNESYHPFFETRACDLLLQPDNLACKPWP 202
 QY 182 RNINISQHSQDMQVSDHAPNFGFRFFLYLHKHEGPFKTKCKQRTTETTSCLLON 241
 Db 203 RNINISQHSQDMQVSDHAPNFGFRFFLYLHKHEGPFKTKCKQRTTETTSCLLON 262
 QY 242 VSPGDYIIELVDVTNTRKVMYALAKPVSPWAGPIRAVAITVPLVWISAFATLFTVNCR 301
 Db 263 VSPGDYIIELVDVTNTRKVMYALAKPVSPWAGPIRAVAITVPLVWISAFATLFTVNCR 322
 QY 302 KKOENIYSHLDESSSESTYTAALPRERLRPRKPVFLCYTSKDCQNMNMVQCFAYFLQ 361
 Db 323 KKOENIYSHLDESSSESTYTAALPRERLRPRKPVFLCYTSKDCQNMNMVQCFAYFLQ 382
 QY 362 DFCGCEVALDLWEDFSICREGREWVIOKHESQFIIVVCSKGMKIFVDKKNYKRGGR 421
 Db 383 DFCGCEVALDLWEDFSICREGREWVIOKHESQFIIVVCSKGMKIFVDKKNYKRGGR 442
 QY 422 GSGKGLFLVAVSAIAEKLRQAKOSSAALSKEFIAYFYDSCGDPVGLDLSTKYRLMD 481
 Db 443 GSGKGLFLVAVSAIAEKLRQAKOSSAALSKEFIAYFYDSCGDPVGLDLSTKYRLMD 502
 QY 482 NLPQLCSHLSRHDGLQSPGQHTROGSRNNYFRSKSRSLYVAICNMHOFIDEPDWFEX 541
 Db 503 NLPQLCSHLSRHDGLQSPGQHTROGSRNNYFRSKSRSLYVAICNMHOFIDEPDWFEX 562
 QY 542 QYVFFHPPLRTREPVLKESGLVLDNVMCKRGPESDPCLKVEAAVLGATGPAQSORES 601
 Db 563 QYVFFHPPLRTREPVLKESGLVLDNVMCKRGPESDPCLKVEAAVLGATGPAQSORES 622
 QY 602 QHGLDQDCEARPDALDGAALQPLHTVKAQSPDMRDSGGYDSSVPSSELSPLMEGL 661
 Db 623 QHGLDQDCEARPDALDGAALQPLHTVKAQSPDMRDSGGYDSSVPSSELSPLMEGL 682
 QY 662 STDQTTSLTSSVSSGLGEEPPALPSKLLSSGCKADGCRSTYDELHAYAP 717
 Db 683 STDQTTSLTSSVSSGLGEEPPALPSKLLSSGCKADGCRSTYDELHAYAP 738

RESULT 5

AAU09953
 ID AAU09953 standard; Protein; 738 AA.

XX AC AAU09953;
 XX DT 14-FEB-2002 (first entry)

XX DE Human Interleukin 17 (hIL-17) receptor like protein substitution #3.

XX KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 XX KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 XX KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;

KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 KW muten.

OS Homo sapiens
 OS Synthetic

XX Key Location/Qualifiers

FT Misc-difference 363 /label= Ser, Thr, Ala, Cys

XX WO200168859-A2.

XX 20-SEP-2001

XX 15-MAR-2001; 2001WO-US08678.

XX 16-MAR-2000; 2000US-189816P.

PR 28-NOV-2000; 2000US-0724460.

XX (AMGE-) AMGEN INC.

XX Jing S.

XX WPI; 2001-611392/70.

XX Nucleic acids encoding interleukin 17 receptor like polypeptides,
 useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
 diabetes, psoriasis and glaucoma

XX Claim 20; Page 7; 158pp; English.

XX The invention describes novel nucleic acids encoding interleukin (IL) 17
 receptor like polypeptides useful as vaccines and in gene therapy. These
 have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
 anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and
 ophthalmological activities. The IL-17 receptor like nucleic acids and
 proteins may be used to prevent and treat diseases associated with
 inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These
 include, for example immune disorders (e.g. inflammation, diabetes and
 transplant rejection), infections (e.g. hepatitis and septicemia),
 weight disorders (e.g. anorexia, cachexia and obesity), neuronal
 dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
 breast cancer), reproductive disorders (e.g. infertility and
 miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 DNA and its complements may also be used as diagnostic probes to detect and
 quantitate the presence of similar nucleic acids in samples and identify
 patients needing restorative therapy. The IL17rp may also be used as
 antigens in the production of antibodies against the proteins and in
 assays to identify modulators of expression and activity. The
 anti-IL17rp antibodies and antagonists may also be used to down regulate
 expression and activity.

XX Note: This sequence is not given in the specification but is based on the
 human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)
 and has been created according to information given in claim 20.

XX Sequence 738 AA;

Query Match 97.2%; Score 3721; DB 22; Length 738;

Best Local Similarity 97.6%; Pred. No. 0;

Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;

OY 2 DTCCWKAARPLCVANEGVGPASRNSGLYNTFFKIDNTYLPVGVKHYDAQNIT 61

DB 37 DTCCWR-----GVGPASRNSGLYNTFFKIDNTYLPVGVKHYDAQNIT 82

OY 62 ISYACHDOVAVTILWSPGALGIEFLAGFRVILEELKSEGRCCOOLILKDPKQLNSSEFKR 121
 DB 83 ISYACHDOVAVTILWSPGALGIEFLAGFRVILEELKSEGRCCOOLILKDPKQLNSSEFKR 142
 OY 122 TGHESQPEFLNMFEDYDFKVVVPPPSIKNSNTHPPFFTRACDILLLOPNLACKPWP 181
 DB 143 TGHESQPEFLNMFEDYDFKVVVPPPSIKNSNTHPPFFTRACDILLLOPNLACKPWP 202
 OY 182 RNLNLSQSGDSQVDFDHAPNFGFRFFLYHLYKLHKGFPKRTCKQOTTETTSCLQN 241
 DB 203 RNLNLSQSGDSQVDFDHAPNFGFRFFLYHLYKLHKGFPKRTCKQOTTETTSCLQN 262
 OY 242 VSPGDYIIEVDVDTNTRVNHAYALKPVHSPWAGPIRAVAITVPLVISAATLFTVWCR 301
 DB 263 VSPGDYIIEVDVDTNTRVNHAYALKPVHSPWAGPIRAVAITVPLVISAATLFTVWCR 322
 OY 302 KKOENIYSHLDESESESTYTAALPRERLRPRKPYLYCYSSKQGNHNVVOCFAIFLQ 361
 DB 323 KKOENIYSHLDESESESTYTAALPRERLRPRKPYLYCYTSKQGNHNVVOCFAIFLQ 382
 OY 362 DFCGCEVALDLWEDSLCRGOREWVIOKTHESQFIIVVCSKGMKYFYDKNKYHKGGR 421
 DB 383 DFCGCEVALDLWEDSLCRGOREWVIOKTHESQFIIVVCSKGMKYFYDKNKYHKGGR 442
 OY 422 GSGKGEFLVAVSAIAEKLRQAKOSSAALSKFIIVFYSCGDPVPGILDLSTKRLMD 481
 DB 443 GSGKGEFLVAVSAIAEKLRQAKOSSAALSKFIIVFYSCGDPVPGILDLSTKRLMD 502
 OY 482 NLPQLCSHLESRDHGLQEPGQTRQSGRRNTFRSKGSRSLYVAICNMHOFIDEPDNFEK 541
 DB 503 NLPQLCSHLESRDHGLQEPGQTRQSGRRNTFRSKGSRSLYVAICNMHOFIDEPDNFEK 562
 OY 542 QFYVPEPPPLRYRREVPVLEKFGSLVLDVWCKPGPESDFCLVAYAVLGATGPAADSHES 601
 DB 563 QFYVPEPPPLRYRREVPVLEKFGSLVLDVWCKPGPESDFCLVAYAVLGATGPAADSHES 622
 OY 602 QHGLDQDGEARPALDGSAAALQPLLTFTVKAAGSPDMRPSDGIYDSVPSSELSLPLMEGL 661
 DB 623 QHGLDQDGEARPALDGSAAALQPLLTFTVKAAGSPDMRPSDGIYDSVPSSELSLPLMEGL 682
 OY 662 STQQTETSSLTSSVSSSGIEEPPPALPKLLSSGSKADLCGRSYTDELHNAV 717
 DB 683 STQQTETSSLTSSVSSSGIEEPPPALPKLLSSGSKADLCGRSYTDELHNAV 738

RESULT 6

AAU09954

ID AAU09954 standard; Protein; 738 AA.

XX AC AAU09954;

XX 14-FEB-2002 (first entry)

Human Interleukin 17 (hIL-17) receptor like protein substitution #4.
 Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;
 hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 muten.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 374 /label= Val, Ile, Met, Leu, Phe, Ala, Nle

XX WO200168859-A2.

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XX PD - 20-SEP-2001.
XX XL
XX PF 15-MAR-2001; 2001WO-US08678.
XX PR 16-MAR-2000; 2000US-189816P.
XX PP 28-NOV-2000; 2000US-0724460.
XX PA (AMGE-) AMGEN INC.
XX PI Jing S;
XX PL WPI; 2001-611392/70.
XX DR Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma -
XX PT Claim 21; Page -: 158pp; English.
XX CC The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, osteopthalmic, vascular, cytostatic, IL-17 leukemic, anti-inferility and ophthalmologic activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These include, for example immune disorders (e.g., inflammation, diabetes and transplant rejection), infections (e.g., hepatitis and septicemia), weight disorders (e.g., anorexia, cachexia and obesity), neuronal dysfunction (e.g., Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g., cystic fibrosis, asthma and emphysema), skin disease (e.g., eczema and psoriasis), kidney disease (e.g., glomerulonephritis), bone diseases (e.g., osteoporosis and hypercalcaemia), vascular disorders (e.g., stroke and arteriosclerosis), cancers (e.g., leukemia, myeloma and breast cancer), reproductive disorders (e.g., infertility and miscarriage), eye disorders (e.g., glaucoma and retinal neuropathy). The DNA and its complements may also be used as diagnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17rlp may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-IL17rlp antibodies and antagonists may also be used to down regulate expression and activity.
XX CC Note: This sequence is not given in the specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AAU99904) and has been created according to information given in claim 21.
XX SS Sequence 738 AA:
Query Match          97.2%; Score 3720; DB 22; Length 738;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;
QY      2' DTCCGRRKKAAPRLCVANEGVGPSRNSGLYNITFKYDNCCTYLNPVKGVIADAQNIT 61
DB      ||||| |-----GGGPSARNSSGLYNITFRIDNCTLYLNPVKRAVIADAQNIT 82
QY      62 ISQTACHDVAVTILWSPGALIGIEFLKGFVRVILEELKSGRCCOOLILKPQLNGSFKR 121
DB      83 ISQTACHDVAVTILWSPGALIGIEFLKGFVRVILEELKSGRCCOOLILKPQLNGSFKR 142
QY      122 TGMESQPLANKPETDYFVKVPVPPSIKNESNYHPFFFTACDLILLQPDNLACKPWPK 181
DB      143 TGMESQPLANKPETDYFVKVPVPPSIKNESNYHPFFFTACDLILLQPDNLACKPWPK 202
QY      182 RLNIISQRSDMQVSDFHAPHNFGRPFYLYLKIHGEPFKRKTCQQQTTFETTSCLIQN 241
DB      203 RLNIISQRSDMQVSDFHAPHNFGRPFYLYLKIHGEPFKRKTCQBQTTTFETTSCLIQN 262
QY      242 VSPGDYTIELVDONTNTREKVHYALKPVHSGPWAGPRVAIVTVPLWIWSAFATLEFWCMCR 301

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Db	263	VSPGDYIIELVDNTRKVMYIAKPVHSPWAGPIRAMAITYPLVVISAFATLFTVNCR	322
QY	302	KKOENIYSHLDESSSESYTAAALPRERLRPRKPYELCTSSKDGQGNHNVVQCFAIFLQ	361
Db	323	KKOENIYSHLDESSSESYTAAALPRERLRPRKPYELCTSSKDGQGNHNVVQCFAIFLQ	382
QY	362	DFCCEVALDLWEDFSICREGQRENVIOKIHESOFILVCSKGMKYFVDKKNYKHKGGR	421
Db	383	DFCCEVALDLWEDFSICREGQRENVIOKIHESOFILVCSKGMKYFVDKKNYKHKGGR	442
QY	422	GSKGELFLVAVSAIAEKURQAKQSSSAALSKFTANTFYDSCEGDVPGIILDSIKYRLMD	481
Db	443	GSKGELFLVAVSAIAEKURQAKQSSSAALSKFTANTFYDSCEGDVPGIILDSIKYRLMD	502
QY	482	NLPQLCSHLHSRDBGLQEPQRTROGSRNRNFRSKSGRSILYAICNMHQFIDEEPDMFEK	541
Db	503	NLPQLCSHLHSRDBGLQEPQRTROGSRNRNFRSKSGRSILYAICNMHQFIDEEPDMFEK	562
QY	542	QFVFPHPPLRYREPVLKFDGSLVNDVMCKPSPDSFCLKYAAAVLCATGPAADSQRES	601
Db	563	QFVFPHPPLRYREPVLKFDGSLVNDVMCKPSPDSFCLKYAAAVLCATGPAADSQRES	622
QY	602	QHGGLDQGEARPALDGSAAALOPILHTVKAGSPDMRDSGIYDSSVSPSELSPLMBGL	661
Db	623	QHGGLDQGEARPALDGSAAALOPILHTVKAGSPDMRDSGIYDSSVSPSELSPLMBGL	682
QY	662	STDQTTSSITSSVSSSGLGEPEPPALPKLLSGSGCKADLCGRSYTDELHAVAP	717
Db	683	STDQTTSSITSSVSSSGLGEPEPPALPKLLSGSGCKADLCGRSYTDELHAVAP	738
RESULT 7			
ID	AAU09951	standard; Protein; 738 AA.	
XX	AAU09951		
AC	AAU09951		
DT	XX	14-FEB-2002 (first entry)	
DE	XX	Human Interleukin 17 (hIL-17) receptor like protein substitution #1.	
DE	XX	Interleukin 17; hIL-17 receptor like protein; immunomodulatory;	
KW	KW	anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;	
KW	KW	hepatic; anabolic; anorectic; anti- α -glucosidase; anti-parkinsonian;	
KW	KW	anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;	
KW	KW	vascular; cytostatic; anti-leukemic; anti-infective; ophthalmological;	
KW	KW	hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;	
KW	KW	bone disease; vascular disorder; eye disorder; cancer; human; mutant;	
XX	XX	mutin.	
OS	OS	Homo sapiens.	
OS	OS	Synthetic.	
FH	FH	Key Location/Qualifiers	
FT	FT	Misc-difference 45 /label= Gly, Pro or Ala	
XX	XX	WO200168859-A2.	
PN	PN	20-SEP-2001.	
PD	PD	XX	
PF	PF	XX	
XX	XX	15-MAR-2001; 2001WO-US08678.	
PR	PR	16-MAR-2000; 2000US-189816P.	
PR	PR	28-NOV-2000; 2000US-0724460.	
PA	PA	(AMGE-) AMGEN INC.	
XX	XX	Jing S;	
PI	PI	WPI; 2001-611392/70.	
XX	XX		

PT Nucleic acids encoding interleukin 17 receptor like polypeptides, 541
 PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
 PT diabetes, psoriasis and glaucoma.
 XX Claim: 18, Page 1, 158pp; English.
 XX
 CC The invention describes novel nucleic acids encoding Interleukin (IL) 17
 CC receptor like polypeptides useful as vaccines and in gene therapy. These
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 CC immunosuppressive, hepatic, anorectic, anorectic, anti-alzheimer's, renal,
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and
 CC proteins may be used to prevent and treat diseases associated with
 CC inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These
 CC include, for example immune disorders (e.g. inflammation, diabetes and
 CC transplant rejection), infections (e.g. hepatitis and septicemia),
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
 CC breast cancer), reproductive disorders (e.g. infertility and
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 CC DNA and its complements may also be used as diagnostic probes to detect and
 CC quantitate the presence of similar nucleic acids in samples and identify
 CC patients needing restorative therapy. The IL17rp may also be used as
 CC antigens in the production of antibodies against the proteins and in
 CC assays to identify modulators of expression and activity. The
 CC anti-IL17rp antibodies and antagonists may also be used to down regulate
 CC expression and activity.
 CC Note: This sequence is not given in the specification but is based on the
 CC human Interleukin 17 (IL-17) receptor like protein sequence (AA009904)
 CC and has been created according to information given in claim 18.
 XX
 SQ Sequence 738 AA;

Query Match 97.1%; Score 3718; DB:22; Length 738;
 Best Local Similarity 97.6%; Pred. No. 0;
 Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;
 QY 2 DTCGTRKAAARPLVAGNEGVGPASRNSGLNITFTNDCTTTLAPVGHVIAQAQNT 61
 DB 37 DTCGWR-----GVXPSRNSGLNITFTNDCTTTLAPVGHVIAQAQNT 82
 QY 62 ISQACHDOAVATILSPGALGIEFLKGFVRVILELSEKQCOQLILADPKQLANSFFR 121
 DB 83 ISQACHDOAVATILSPGALGIEFLKGFVRVILELSEKQCOQLILADPKQLANSFFR 142
 QY 122 TGMESQPLAKMETDYEVKVPFFSIRKESNYHPPFRACDILLOPDLNACFPWKP 181
 DB 143 TGMESQPLAKMETDYEVKVPFFSIRKESNYHPPFRACDILLOPDLNACFPWKP 202
 QY 182 RLNLISQSGDMQVSDPHAFNFGFRFFLYLKLHKGPPFRKTKCOQTETTSCLQN 241
 DB 203 RLNLISQSGDMQVSDPHAFNFGFRFFLYLKLHKGPPFRKTKCOQTETTSCLQN 262
 QY 242 VSRGDIIELVDDNTTRKVMHVKPVHSPWAGPIRAVATVPLVVISAFATLFTWCR 301
 DB 263 VSRGDIIELVDDNTTRKVMHVKPVHSPWAGPIRAVATVPLVVISAFATLFTWCR 322
 QY 302 KQQENIYSHLDESSSTTTAALPRERLPRPKVFLCYSSKDGQNNHNVVOCFAFLQ 361
 DB 323 KQQENIYSHLDESSSTTTAALPRERLPRPKVFLCYSSKDGQNNHNVVOCFAFLQ 382
 QY 362 DFCGCEVALDLWEDFSLCRGQREWYQIKHESQFIIVVCSKGMKYVDKKNYKRGGR 421
 DB 383 DFCGCEVALDLWEDFSLCRGQREWYQIKHESQFIIVVCSKGMKYVDKKNYKRGGR 442
 QY 422 GSGKGLFLVAVSAIAELKRAQKQSSAALSFKFIIVFYDSCGDVPGIILSTKRLMD 481
 DB 443 GSGKGLFLVAVSAIAELKRAQKQSSAALSFKFIIVFYDSCGDVPGIILSTKRLMD 502

QY 482 NLPLQCSHLHSRDLQEPQOBTROGSRNRYFRSKGRSLYVAICNMHOFIDEPDWFEX 541
 DB 503 NLPLQCSHLHSRDLQEPQOBTROGSRNRYFRSKGRSLYVAICNMHOFIDEPDWFEX 562
 QY 542 QVTFPPPPPLRTREPVLKFKPSGLVLDVWCKPQPSDPCLVKVAAYLGATGAPADSQHES 601
 DB 563 QVTFPPPPPLRTREPVLKFKPSGLVLDVWCKPQPSDPCLVKVAAYLGATGAPADSQHES 622
 QY 602 QHGGLQDQCEARPDALGSAALQPLLTFTVKAGSPDMPDPSGIYDSSVSSSELSPLKEGL 661
 DB 623 QHGGLQDQCEARPDALGSAALQPLLTFTVKAGSPDMPDPSGIYDSSVSSSELSPLKEGL 682
 QY 662 STQDTFSSLTSTSVSSSGLGEPPEPPALPSKLLSSGCKADLGCSYTDLEAVAP 717
 DB 683 STQDTFSSLTSTSVSSSGLGEPPEPPALPSKLLSSGCKADLGCSYTDLEAVAP 738
 RESULT 8
 AAU09952
 ID AAU09952 standard; Protein: 738 AA.
 XX AC AAU09952;
 XX 14-FEB-2002 (first entry)
 DT Human Interleukin 17 (hIL-17) receptor like protein substitution #2.
 DE Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KW hepatic; anorectic; anorectic; anti-alzheimer's; anti-parkinsonian;
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 KW mutin.
 XX Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 227 /label- Phe, Leu, Val, Ile, Ala, Tyr
 XX WO200168859-A2.
 XX 20-SEP-2001.
 XX 15-MAR-2001; 2001WO-US08678.
 XX 16-MAR-2000; 2000US-189816P.
 XX 28-NOV-2000; 2000US-0724460.
 XX (AMGE-) AMGEN INC.
 XX Jing S;
 XX MPI; 2001-611392/70.
 XX Nucleic acids encoding interleukin 17 receptor like polypeptides,
 XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
 XX diabetes, psoriasis and glaucoma.
 XX Claim 19; Page 1; 158pp; English.
 XX The invention describes novel nucleic acids encoding Interleukin (IL) 17
 XX receptor like polypeptides useful as vaccines and in gene therapy. These
 XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 XX immunosuppressive, hepatic, anorectic, anorectic, anti-alzheimer's, renal,
 XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 XX osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and
 XX ophthalmological activities. The IL-17 receptor like nucleic acids and
 XX proteins may be used to prevent and treat diseases associated with

CC inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These
 CC include, for example immune disorders (e.g. hepatitis and septicemia),
 CC transplant rejection), anorexia, cachexia and obesity), neuronal
 CC weight disorders (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 CC dysfunction (e.g. cystic fibrosis, asthma and emphysema), skin disease
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
 CC breast cancer), reproductive disorders (e.g. infertility and
 CC DNA and its complements may also be used as diagnostic probes to detect and
 CC quantify the presence of similar nucleic acids in samples and identify
 CC patients needing restorative therapy. The IL17rp may also be used as
 CC antigens in the production of antibodies against the proteins and in
 CC assays to identify modulators of expression and activity. The
 CC anti-IL17rp antibodies and antagonists may also be used to down-regulate
 CC expression and activity.
 CC Note: This sequence is not given in the specification but is based on the
 CC human Interleukin 17 (IL-17) receptor like protein sequence (AA09904)
 CC and has been created according to information given in claim 19.
 XX Sequence: 738 AA;

Query Match 97.1%; Score 3718; DB 22; Length 738;
 Best Local Similarity 97.6%; Pred. No. 0;
 Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;

QY 2 DTCGRKAAARPLCVANEGVPASRNSGLYNTFKYDNCCTYLPVCKRKHVIAQAQMIT 61
 DB 37 DTCGRK-----GVGPASRNSGLYNTFKYDNCCTYLPVCKRKHVIAQAQMIT 82
 QY 62 ISQACHQVAVTILMSPALGIEFLKGRVILELSEKSGROCOQLIKDPQLNSFKR 121
 DB 83 ISQACHQVAVTILMSPALGIEFLKGRVILELSEKSGROCOQLIKDPQLNSFKR 142
 QY 122 TGMESQPLFNKFTDIFVKVVPFPIKNSNTHPFFTRACDILLOPDLNACKPFWKP 181
 DB 143 TGMESQPLFNKFTDIFVKVVPFPIKNSNTHPFFTRACDILLOPDLNACKPFWKP 202
 QY 182 RNLSQSGDMQVSDHAPHNGFPEYLLKHEGPFKTKQKQOTTTSCILON 241
 DB 203 RNLSQSGDMQVSDHAPHNGFPEYLLKHEGPFKTKQKQOTTTSCILON 262
 QY 242 VSPGDIYIELVDNTTRKVMHAYLKPVHSPWAGPIRAVAITVPLVISAFAITFTVCR 301
 DB 263 VSPGDIYIELVDNTTRKVMHAYLKPVHSPWAGPIRAVAITVPLVISAFAITFTVCR 322
 QY 302 KKOENIYSHLDESSESTYTAALPRELRPRKPKVPLCYSSKQGNHNVVQCFAYFLQ 361
 DB 373 KKOENIYSHLDESSESTYTAALPRELRPRKPKVPLCYSSKQGNHNVVQCFAYFLQ 382
 QY 382 DFCCEVALDWDPSLCREGRENVVIOKIHESQFIIVVCSKGMFYVDKNYKHKGGGR 421
 DB 393 DFCCEVALDWDPSLCREGRENVVIOKIHESQFIIVVCSKGMFYVDKNYKHKGGGR 442
 QY 422 GSGKGLFLVAVSAIAELKRAKQSSAALSKTAVTFYSCGDDVGTLDLSKYRLMD 481
 DB 443 GSGKGLFLVAVSAIAELKRAKQSSAALSKTAVTFYSCGDDVGTLDLSKYRLMD 502
 QY 482 NLPLQCSHLHSDHGLQPGQHTGGRNRYFRSKGRSLYVAICNMQHOFIDEPDWFEX 541
 DB 503 NLPLQCSHLHSDHGLQPGQHTGGRNRYFRSKGRSLYVAICNMQHOFIDEPDWFEX 562
 QY 542 QFYVPEPPLRYREPVLEKFGSLVNDVCKPQSPDSCFLKVAEVLGATGPDADSHES 601
 DB 563 QFYVPEPPLRYREPVLEKFGSLVNDVCKPQSPDSCFLKVAEVLGATGPDADSHES 622
 QY 602 QHGGLDQDGEARPALDGAALQPLHRTVAKGSPDMPRSGIYDSSVPSSELSPLMEGL 661
 DB 623 QHGGLDQDGEARPALDGAALQPLHRTVAKGSPDMPRSGIYDSSVPSSELSPLMEGL 682
 QY 662 STQDTSSLTSSVSSSGIEEPFPALPSKLLSSGSCADLGCRSYTDELEAVP 717

DB 683 STQDTSSLTSSVSSSGIEEPFPALPSKLLSSGSCADLGCRSYTDELEAVP 738
 RESULT 9
 AAU09956
 ID AAU09956 standard; Protein: 738 AA.
 AC AAU09956;
 XX 14-FEB-2002 (first entry)
 DE Human Interleukin 17 (hIL-17) receptor like protein substitution #6.
 KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone-disease; vascular disorder; eye disorder; cancer; human; mutant;
 KW mutain.
 OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 515
 FN /label- Asp, Glu
 XX W0200169859-A2.
 XX 20-SEP-2001.
 XX 15-MAR-2001; 2001WO-US08678.
 XX 16-MAR-2000; 2000US-189816P.
 XX 28-NOV-2000; 2000US-074460.
 XX (ANGE-) AMGEN INC.
 XX Jing S;
 XX WPI; 2001-611392/70.
 XX Nucleic acids encoding interleukin 17 receptor like polypeptides,
 XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
 XX diabetes, psoriasis and glaucoma.
 XX Claim 23; Page -: 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17
 receptor like polypeptides useful as vaccines and in gene therapy. These
 have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
 anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and
 ophthalmological activities. The IL-17 receptor like nucleic acids and
 proteins may be used to prevent and treat diseases associated with
 inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These
 include, for example immune disorders (e.g. inflammation, diabetes and
 transplant rejection), infections (e.g. hepatitis and septicemia),
 weight disorders (e.g. anorexia, cachexia and obesity), neuronal
 dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
 breast cancer), reproductive disorders (e.g. infertility and
 miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 DNA and its complements may also be used as diagnostic probes to detect and
 quantify the presence of similar nucleic acids in samples and identify
 patients needing restorative therapy. The IL17rp may also be used as

CC antigens in the production of antibodies against the proteins and in
CC assays to identify modulators of expression and activity. The
CC anti-IL17rlp antibodies and antagonists may also be used to down regulate
CC expression and activity.
CC Note: This sequence is not given in the specification but is based on the
CC human Interleukin 17 (IL-17) receptor like protein sequence. (AAU09904)
CC and has been created according to information given in claim 23.
XX

Sequence 738 AA;

Query Match 97.1%; Score 3718; DB 22; Length 738;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;

QY	2	DTGGRKAAARPRLCVANGVGPASRNSGLYNITPKYKCTTYLNPVGRKVIADAQNI	61
DB	37	DTGGRK-----GVGPASRNSGLYNITPKYKCTTYLNPVGRKVIADAQNI	82
QY	62	ISYACHDVAVTIWSPGALGIEFLKFRVILEELKSGROCOQLIKDPKQLNSFKR	121
DB	83	ISYACHDVAVTIWSPGALGIEFLKFRVILEELKSGROCOQLIKDPKQLNSFKR	142
QY	122	TGESQFFLNMFEDYFVKVVPFSPKSNHYPFFTRACDILLQDMLACKPWKP	181
DB	143	TGESQFFLNMFEDYFVKVVPFSPKSNHYPFFTRACDILLQDMLACKPWKP	202
QY	182	RNLNISQSGDMOVSDHAPNFCFRFFYLHYLKHGEPFKCKQKQOTTETTSCLLN	241
DB	203	RNLNISQSGDMOVSDHAPNFCFRFFYLHYLKHGEPFKCKQKQOTTETTSCLLN	262
QY	242	VSPGDYIIEVDVTTTRKVMYALKVPSWAGPIRAVAIVPLVWISAFATLFTVNCR	301
DB	263	VSPGDYIIEVDVTTTRKVMYALKVPSWAGPIRAVAIVPLVWISAFATLFTVNCR	322
QY	302	KKOENITSHLDESESTYTAALPRERLRPRKPVLCYSSKQGNMNVVQCFAFLQ	361
DB	323	KKOENITSHLDESESTYTAALPRERLRPRKPVLCYSSKQGNMNVVQCFAFLQ	382
QY	362	DFGCGVALDMEFSLCREGQREWVTKIHESQFIIVVCSKGMKIFVDKKNYKHGGGR	421
DB	383	DFGCGVALDMEFSLCREGQREWVTKIHESQFIIVVCSKGMKIFVDKKNYKHGGGR	442
QY	422	GSCKGLFVAVSAIAELKQAKOSSAALSKEIAYFDYSCGDPGVLILSTKYRLMD	481
DB	443	GSCKGLFVAVSAIAELKQAKOSSAALSKEIAYFDYSCGDPGVLILSTKYRLMD	502
QY	482	NLPQLCHLSRDLGQEPGQRTQGRNRYFRSKGRSLVAICNMHQFIDEPDWFKE	541
DB	503	NLPQLCHLSRDLGQEPGQRTQGRNRYFRSKGRSLVAICNMHQFIDEPDWFKE	562
QY	542	QVFPFPPPLRYRREPLVEKFGVLNDVNMCKPGSPDCLVAEAVLGATGPAQSQES	601
DB	563	QVFPFPPPLRYRREPLVEKFGVLNDVNMCKPGSPDCLVAEAVLGATGPAQSQES	622
QY	602	QHGGLDGEAPALDGAALQPLHVVKAGSPDPRSGIYDSVPSSLSPLMEGL	661
DB	623	QHGGLDGEAPALDGAALQPLHVVKAGSPDPRSGIYDSVPSSLSPLMEGL	682
QY	662	STDQTETSLTSSVSSSGLGEEPPALPSKLSSGCKADIGCSYTDDELHAYAP	717
DB	683	STDQTETSLTSSVSSSGLGEEPPALPSKLSSGCKADIGCSYTDDELHAYAP	738

RESULT 10

AAU09955
ID AAU09955 standard; Protein; 738 AA.

XX AAU09955;

XX AC

XX 14-FEB-2002 (first entry)

XX Human Interleukin 17 (hIL-17) receptor like protein substitution #5.

KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
mutin.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

PT Misc-difference 385

XX /label- Cys, Ser, Ala

XX WO200168859-A2.

XX 20-SEP-2001.

XX 15-MAR-2001; 2001WO-US08678.

XX 16-MAR-2000; 2000US-189816P.

XX 28-NOV-2000; 2000US-0724460.

XX (AMGE-) AMGEN INC.

XX JIng S;

XX WPI; 2001-611392/70.

XX Nucleic acids encoding interleukin 17 receptor like polypeptides,
XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
XX diabetes, psoriasis and glaucoma.

XX Claim 22; Page 1; 158pp; English.

XX The invention describes novel nucleic acids encoding interleukin (IL) 17
XX receptor like polypeptides useful as vaccines and in gene therapy. These
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
XX osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and
XX ophthalmological activities. The IL-17 receptor like nucleic acids and
XX proteins may be used to prevent and treat diseases associated with
XX inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
XX include, for example immune disorders (e.g. inflammation, diabetes and
XX transplant rejection), infections (e.g. hepatitis and septicemia),
XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal
XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
XX lung disorders (e.g. cystic-fibrosis, asthma and emphysema), skin disease
XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
XX (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
XX breast cancer), reproductive disorders (e.g. infertility and
XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
XX DNA and its complements may also be used as diagnostic probes to detect and
XX quantitate the presence of similar nucleic acids in samples and identify
XX patients needing restorative therapy. The IL17rlp may also be used as
XX antigens in the production of antibodies against the proteins and in
XX assays to identify modulators of expression and activity. The
XX anti-IL17rlp antibodies and antagonists may also be used to down regulate
XX expression and activity.
XX Note: This sequence is not given in the specification but is based on the
XX human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)
XX and has been created according to information given in claim 22.

XX Sequence 738 AA;

XX Query Match 97.0%; Score 3714; DB 22; Length 738;

XX Best Local Similarity 97.6%; Pred. No. 0;

XX Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;

QY 2 DTCGRKAAARPRCLVANGVGPASRNSGLNITFKYDNTYTLNPGVGRVIADQNT 61
 DB 37 DTCGRW-----GVGPASRNSGLNITFKYDNTYTLNPGVGRVIADQNT 82
 QY 62 ISQYACHDOVAVTILNSPGALGTEFLKGRFVILEELKSGRQCOOLILKDPKOLNSFKR 121
 DB 83 ISQYACHDOVAVTILNSPGALGTEFLKGRFVILEELKSGRQCOOLILKDPKOLNSFKR 142
 QY 122 TGMESQPLNKKFTDYFVAVVPPPSIKNESNYHFFRFRACDILLOPDNLACKPFWKP 181
 DB 143 TGMESQPLNKKFTDYFVAVVPPPSIKNESNYHFFRFRACDILLOPDNLACKPFWKP 202
 QY 182 RNINISQSGSDQVSDHAPHNGFRFFLYLTKLKHGSPFRKTCBOQTETTSCLLQN 241
 DB 203 RNINISQSGSDQVSDHAPHNGFRFFLYLTKLKHGSPFRKTCBOQTETTSCLLQN 262
 QY 242 VSPGDYIELVDNTTRKVMYALKPVHSPWAGPIRAVAITVPLVVISAFATLVACR 301
 DB 263 VSPGDYIELVDNTTRKVMYALKPVHSPWAGPIRAMALTVPVVISAFATLVACR 322
 QY 302 KQQENIYSHLDSESSSTYTAALPRELPRKPVFLCYSSKDGQNHNVVOCFAIFLO 361
 DB 323 KQQENIYSHLDSESSSTYTAALPRELPRKPVFLCYSSKDGQNHNVVOCFAIFLO 382
 QY 362 DPCGEVALDWEFSLCGRQREWIQIHESOFIIVC-SKGMKYFVKKYKKGGR 421
 DB 383 DFCGEVALDWEFSLCGRQREWIQIHESOFIIVC-SKGMKYFVKKYKKGGR 442
 QY 422 GSGGELFLVAVSAIAELKROAKQSSAALSKFTAVTFDYSCEGDPGLDLSKYRLMD 481
 DB 443 GSGGELFLVAVSAIAELKROAKQSSAALSKFTAVTFDYSCEGDPGLDLSKYRLMD 502
 QY 482 NLQCLSHLSRDRGLOEQGHTROGSRNFRSKGRSLVACNMHGFIDEEDPWEK 541
 DB 503 NLQCLSHLSRDRGLOEQGHTROGSRNFRSKGRSLVACNMHGFIDEEDPWEK 562
 QY 542 QVFPFPPPLRYREPVLKFDGLVNDVMCKPGPESDCLKYEAAVLGATGAPDSQES 601
 DB 563 QVFPFPPPLRYREPVLKFDGLVNDVMCKPGPESDCLKYEAAVLGATGAPDSQES 622
 QY 602 QRGGLDQGEARALDGSALQPLHTVAKGSDMDPRDGIYDSSVPSSELSPLMBGL 661
 DB 623 QRGGLDQGEARALDGSALQPLHTVAKGSDMDPRDGIYDSSVPSSELSPLMBGL 682
 QY 662 STDQTSSTLTVSSVSSGLGEEPPALPSPKLLSSGCKADLCGRSYTDELHAVAP 717
 DB 683 STDQTSSTLTVSSVSSGLGEEPPALPSPKLLSSGCKADLCGRSYTDELHAVAP 738

RESULT 11

AAU09957
 ID AAU09957 standard; Protein; 738 AA.
 AC AAU09957;

14-FEB-2002 (first entry)

Human Interleukin 17 (hIL-17) receptor like protein substitution #7.

Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;
 hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 mitein.

OS Homo sapiens.
 OS Synthetic.

Key Location/Qualifiers
 Misc-difference 602

FT XX /label= Cys, Ala, Ser
 PN WO200168859-A2.
 PD 20-SEP-2001.
 PP 15-MAR-2001; 2001WO-US086678.
 PR 16-MAR-2000; 2000US-189818P.
 PX 28-NOV-2000; 2000US-0724460.
 PA (ANGE-) AMGEN INC.
 PI Jing S;
 XX WPI; 2001-611392/70.
 DR Nucleic acids encoding interleukin 17 receptor like polypeptides,
 useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
 diabetes, psoriasis and glaucoma
 PS Claim 24; Page 1; 158pp; English.
 CC The invention describes novel nucleic acids encoding interleukin (IL) 17
 receptor like polypeptides useful as vaccines and in gene therapy. These
 have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
 anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and
 ophthalmological activities. The IL-17 receptor like nucleic acids and
 proteins may be used to prevent and treat diseases associated with
 inappropriate IL-17 receptor like polypeptide (IL17rip) expression. These
 include, for example immune disorders (e.g. inflammation, diabetes and
 transplant rejection), infections (e.g. hepatitis and septicemia),
 weight disorders (e.g. anorexia, cachexia and obesity), neuronal
 dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
 breast cancer), reproductive disorders (e.g. infertility and
 miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 DNA and its complements may also be used as diagnostic probes to detect and
 quantitate the presence of similar nucleic acids in samples and identify
 patients needing restorative therapy. The IL17rip may also be used as
 antigens in the production of antibodies against the proteins and in
 assays to identify modulators of expression and activity--the
 anti-IL17rip antibodies and antagonists may also be used to down regulate
 expression and activity.
 CC Note: This sequence is not given in the specification but is based on the
 human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)
 and has been created according to information given in claim 24.

Sequence 738 AA;

Query Match 97.0%; Score 3714; DB 22; Length 738;
 Best Local Similarity 97.6%; Pred. No. 0;

Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;

QY 2 DTCGRKAAARPRCLVANGVGPASRNSGLNITFKYDNTYTLNPGVGRVIADQNT 61
 DB 37 DTCGRW-----GVGPASRNSGLNITFKYDNTYTLNPGVGRVIADQNT 82
 QY 62 ISQYACHDOVAVTILNSPGALGTEFLKGRFVILEELKSGRQCOOLILKDPKOLNSFKR 121
 DB 83 ISQYACHDOVAVTILNSPGALGTEFLKGRFVILEELKSGRQCOOLILKDPKOLNSFKR 142
 QY 122 TGMESQPLNKKFTDYFVAVVPPPSIKNESNYHFFRFRACDILLOPDNLACKPFWKP 181
 DB 143 TGMESQPLNKKFTDYFVAVVPPPSIKNESNYHFFRFRACDILLOPDNLACKPFWKP 202
 QY 182 RNINISQSGSDQVSDHAPHNGFRFFLYLTKLKHGSPFRKTCBOQTETTSCLLQN 241
 DB 203 RNINISQSGSDQVSDHAPHNGFRFFLYLTKLKHGSPFRKTCBOQTETTSCLLQN 262

Db 203 RLNIISGSDMQVDFHAPNFRFPFYLYLTKLHKGFPKRTCKBQTTETTSCLQN 262
 QY 242 VSPGDYIIELVDVNTTRKVVHYALKVPSWAGPRAVAIVLPLVLSAPATLFTWCR 301
 Db 263 VSPGDYIIELVDVNTTRKVVHYALKVPSWAGPRAVAIVLPLVLSAPATLFTWCR 332
 QY 302 KKOENYIHLDESESESTTAALPRERLRPRPKVFLCYSSKQGNBNVQCFATFLQ 361
 Db 323 KKOENYIHLDESESESTTAALPRERLRPRPKVFLCYSSKQGNBNVQCFATFLQ 382
 QY 362 DFCCEVALDWEFSLCREGREWIQKHESQFIIVVCSKGMKIFVDRKNTKKGGR 431
 Db 383 DFCCEVALDWEFSLCREGREWIQKHESQFIIVVCSKGMKIFVDRKNTKKGGR 442
 QY 422 GSKGELFLVAVSAEKLKRAKSSAALSKEFIIVFSCGDDVPGILDLSTKYLMD 481
 Db 443 GSKGELFLVAVSAEKLKRAKSSAALSKEFIIVFSCGDDVPGILDLSTKYLMD 502
 QY 482 NLPQLCSHLSDHGLQPGQHTQSGRRNYFRSKGRSLYVAICNMHQFIDEEPWFEX 541
 Db 503 NLPQLCSHLSDHGLQPGQHTQSGRRNYFRSKGRSLYVAICNMHQFIDEEPWFEX 562
 QY 542 QFYVFPPLRYREPLVEKFGSLVNDVCKPESDPCLKVAEVLGATGPADSQHS 601
 Db 563 QFYVFPPLRYREPLVEKFGSLVNDVCKPESDPCLKVAEVLGATGPADSQHS 622
 QY 602 QHGLDQDGEARPDGSAALQPLIHTVYKAGSPDRSGIYDSSVPSSELSPLMEGL 661
 Db 623 QHGLDQDGEARPDGSAALQPLIHTVYKAGSPDRSGIYDSSVPSSELSPLMEGL 682
 QY 662 STDQETSLTSSVSSGLGEEPPALPSKLLSSGCKADIGCRSYTDELHAPV 717
 Db 683 STDQETSLTSSVSSGLGEEPPALPSKLLSSGCKADIGCRSYTDELHAPV 738

RESULT 12
 AAU04958
 ID AAU04958 standard; Protein; 728 AA.
 AC AAU04958;
 DT 24-OCT-2001 (first entry)
 DE Human Interleukin 17 receptor, IL-17RH4.
 KW Human; Interleukin-17 receptor; IL-17RH4; agonist; antagonist;
 KW PRO20026; DNA 154095-2998; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; diabetes mellitus;
 KW allergic disease; asthma; demyelinating disease;
 KW degenerative cartilaginous disorder; transplantation associated disease.
 OS Homo sapiens.
 FH Key
 FT Region
 FT 19..24 /note- "N-myristoylation site"
 FT Modified-site 31..34 /note- "Asn is N-glycosylated"
 FT Modified-site 38..41 /note- "Asn is N-glycosylated"
 FT Modified-site 56..59 /note- "Asn is N-glycosylated"
 FT Modified-site 113..116 /note- "Asn is N-glycosylated"
 FT Modified-site 147..150 /note- "Asn is N-glycosylated"
 FT Modified-site 182..185 /note- "Asn is N-glycosylated"
 FT Region 232..235 /note- "cAMP/GMP-dependent protein kinase phosphorylation site"
 FT Modified-site 266..269 /note- "Asn is N-glycosylated"

FT Domain 283..307 /note- "Transmembrane domain"
 FT Region 312..319 /note- "Tyrosine kinase phosphorylation site"
 FT Region 375..380 /note- "N-myristoylation site"
 FT Region 416..424 /note- "Tyrosine kinase phosphorylation site"
 FT Region 428..433 /note- "N-myristoylation site"
 FT Region 429..434 /note- "N-myristoylation site"
 FT Region 432..437 /note- "N-myristoylation site"
 FT Region 433..436 /note- "Glycosaminoglycan attachment site"
 FT Region 517..522 /note- "N-myristoylation site"
 FT Region 574..579 /note- "N-myristoylation site"
 FT Region 652..657 /note- "N-myristoylation site"
 FT Region 707..712 /note- "N-myristoylation site"
 XX
 PN WO200146420-A2.
 PD 28-JUN-2001.
 XX
 PF 20-DEC-2000; 2000WO-US34956.
 XX
 PR 23-DEC-1999; 99US-0172096.
 PR 30-DEC-1999; 99WO-US31274.
 PR 11-JAN-2000; 2000US-0175461.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 21-MAR-2000; 2000US-0191007.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 22-JUN-2000; 2000US-0213087.
 PR 22-AUG-2000; 2000US-0644848.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 24-OCT-2000; 2000US-0242837.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 28-NOV-2000; 2000US-0253646.
 PR 01-DEC-2000; 2000WO-US32678.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ;
 PI Gurney AL, Li H, Hillan KJ, Tamas D, Van Lookeren M, Vandlen RL;
 PI Watanabe CK, Williams PM, Wood WI, Yansura DG;
 XX
 WI WI: 2001-451708/48.
 DR N-PSDB; AAS09517.
 XX
 PT Novel PRO polypeptides homologous to interleukin-17, useful for the
 PT diagnosis and treatment of immune related disease e.g. rheumatoid
 PT arthritis and diabetes
 XX
 PS Claim 10; Fig 18; 188pp; English.
 CC
 CC The sequence is PRO20026 which is the human Interleukin 17 receptor,
 CC IL-17RH4, encoded by DNA 154095-2998. A composition
 CC containing ant/agonists to the PRO polypeptides or individual components
 CC are useful for treating a mammal with an immune related disease, e.g.
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthritis, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease, an autoimmune or immune-mediated skin
 CC disease, contact dermatitis, an allergic disease e.g. food

CC hypersensitivity, asthma, a transplantation associated disease, or a
 CC chronic inflammatory demyelinating polyneuropathy. Treating a
 CC degenerative cartilaginous disorder comprises administering a PRO1031 or
 CC PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous
 CC examples of the diseases and disorders are given in the specification.
 XX
 SQ Sequence 728 AA:

Query Match 96.7%; Score 3703; DB 22; Length 728;
 Best Local Similarity 96.7%; Pred. No. 0;
 Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

QY 7 RKMAARPLCVAKE-CVGPASNSGLNITFKYDNCITTYLNPVGRHVIADQAQNTISQY 65
 DB 3 RASASGVPAIFVSGEGVGPASNSGLNITFKYDNCITTYLNPVGRHVIADQAQNTISQY 62
 QY 66 ACHDOVAVTILWSPALGIEFLAGFVILEELKSGRCOCQOLILKDPKOLNSFKRTGME 125
 DB 63 ACHDOVAVTILWSPALGIEFLAGFVILEELKSGRCOCQOLILKDPKOLNSFKRTGME 122
 QY 126 SQPLFMKFFDYFKVVPSPSKNESNTHFFETFRACDLLOPONLACKFPFMRPLN 185
 DB 123 SQPLFMKFFDYFKVVPSPSKNESNTHFFETFRACDLLOPONLACKFPFMRPLN 182
 QY 186 ISQ-----BGSDMOVSDHAPHNFGFRFFLYHLKKGHPFKRTCKOBOTT 232
 DB 183 ISQSGSDMOVSDHAPHNFGSDMOVSDHAPHNFGFRFFLYHLKKGHPFKRTCKOBOTT 242
 QY 233 ETTSCILQNVSPGDIYIELVDNTNTRKVMYALKPVHSPWAGPIRAVAITPLVVISAP 292
 DB 243 ETTSCILQNVSPGDIYIELVDNTNTRKVMYALKPVHSPWAGPIRAVAITPLVVISAF 302
 QY 293 ATLFTVCKRKQENIYSHLDESSSTYTAALPRERLRPRKPVFLCYSSKDGQENNV 352
 DB 303 ATLFTVCKRKQENIYSHLDESSSTYTAALPRERLRPRKPVFLCYSSKDGQENNV 362
 QY 353 VOCFAIFLDPCGCEVALDWEFSLCREGQENVYOKIESOFILVCSKGYFVDKK 412
 DB 363 VOCFAIFLDPCGCEVALDWEFSLCREGQENVYOKIESOFILVCSKGYFVDKK 422
 QY 413 NTKHGGGSGGKGEFLVAVSAIAEKLQAKQSSAALSKFIATVFDYSCSDVPGILD 472
 DB 423 NTKHGGGSGGKGEFLVAVSAIAEKLQAKQSSAALSKFIATVFDYSCSDVPGILD 482
 QY 473 LSTKRLMDNLPLQCSHLHSRDLGLQEPQOHTROGSRNRYFRKSGRSYVAICNNHOFI 532
 DB 483 LSTKRLMDNLPLQCSHLHSRDLGLQEPQOHTROGSRNRYFRKSGRSYVAICNNHOFI 542
 QY 533 DEEDPWFKQVPPHPPPLRYEPVLEKFDPSGLVINDVCKPSPESDFCLKVEAAVLGAT 592
 DB 543 DEEDPWFKQVPPHPPPLRYEPVLEKFDPSGLVINDVCKPSPESDFCLKVEAAVLGAT 602
 QY 593 GPASQSHESORGGILDGGEARPALDGSAAALPLHTYKAGSPDMPRDSGIYDSSVPSSE 652
 DB 603 GPASQSHESORGGILDGGEARPALDGSAAALPLHTYKAGSPDMPRDSGIYDSSVPSSE 662
 QY 653 LSLPLMCLSTDTQETSSSITESVSSSGLGEETPPALPSKLLSGGCKADLCGRSYTDEL 712
 DB 663 LSLPLMCLSTDTQETSSSITESVSSSGLGEETPPALPSKLLSGGCKADLCGRSYTDEL 722
 QY 713 HAVAPL 718
 DB 723 HAVAPL 728

RESULT 13

AAU10602

ID AAU10602 standard; Protein; 739 AA.

XX AC

XX AAU10602;

DT 14-FEB-2002 (first entry)

XX

DE Human interleukin 17 (hIL-17) receptor-like protein version 2.
 XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone disease; vascular disorder; eye disorder; cancer; human.
 XX Homo sapiens.
 OS WO200168859-A2.
 XX 20-SEP-2001.
 XX 15-MAR-2001; 2001WO-0508678.
 XX 16-MAR-2000; 2000US-189816P.
 PR 28-NOV-2000; 2000US-0724460.
 XX (AMGE-) AMGEN INC.
 PI Jlog S;
 XX WPI: 2001-611392/70.
 DR N-PSDB; AAS16201.
 XX Nucleic acids encoding interleukin 17 receptor like polypeptides,
 useful for preventing, diagnosing and treating, e.g. leukaemia, asthma,
 diabetes, psoriasis and glaucoma -
 Claim 2; Fig 1; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-leukemic, dermatological, osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17r) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis, cancers (e.g. leukaemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also be used as diagnostic probes to detect and quantify the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17r may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-IL17r antibodies and antagonists may also be used to down regulate expression and activity. This is the amino acid sequence of human interleukin 17 (IL-17) receptor like protein described in the method of the invention.
 CC Note: Residues 1-288 of this sequence correspond to residues 8-296 of the sequence shown in AAU10601 which is incomplete in the specification.

Sequence 739 AA;

Query Match 96.6%; Score 3700; DB 22; Length 739;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 695; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 21 EGVGPASNSGLNITFKYDNCITTYLNPVGRHVIADQAQNTISQYACHQVAVTILWSPG 80

Db 42 QGVGASRSGLYNITFKYDNCITLNPVGHVIAQAQNTISQYACHDQAVAVILWSPG 101
 QY 81 ALGIEFLKGFVILEELKSGROCOQILKDPKLNSSFKRTGMSQPLNKFETDIFV 140
 Db 102 ALGIEFLKGFVILEELKSGROCOQILKDPKLNSSFKRTGMSQPLNKFETDIFV 161
 QY 141 KVPFPIKSNENYPPFFRTRACDILLQPDNLACKPFWKPNLNISQSGDMQVSDHA 200
 Db 162 KVPFPIKSNENYPPFFRTRACDILLQPDNLACKPFWKPNLNISQSGDMQVSDHA 221
 QY 201 PHNFGFRFYLYKLGHEGPKRTCKEQTTETTSCLQNSPGDYIIELVDVNTNRK 260
 Db 222 PHNFGFRFYLYKLGHEGPKRTCKEQTTETTSCLQNSPGDYIIELVDVNTNRK 281
 QY 261 VHYALKPVHSPWAGPIRAVAITPVNIVISAFATLTVVGRKQENIYSHLDESSS 320
 Db 282 VHYALKPVHSPWAGPIRAVAITPVNIVISAFATLTVVGRKQENIYSHLDESSS 341
 QY 321 TTYAALPRERLRPRKPVFLCYSSKQGNHNNVVOCFAYFLQDFCCCEVALDLWEDFSLCR 380
 Db 342 TTYAALPRERLRPRKPVFLCYSSKQGNHNNVVOCFAYFLQDFCCCEVALDLWEDFSLCR 401
 QY 381 EGOREWVIOKIHESQFIIVVCSKGMKYFVDKKNYKHKGGSGGKGLFVAVSAEKL 440
 Db 402 EGOREWVIOKIHESQFIIVVCSKGMKYFVDKKNYKHKGGSGGKGLFVAVSAEKL 461
 QY 441 RQAKSSAALSFKFIATVDFYSCGDPVPGILDLSTKRYLMDLQPCSHLSRDBGLQEP 500
 Db 462 RQAKSSAALSFKFIATVDFYSCGDPVPGILDLSTKRYLMDLQPCSHLSRDBGLQEP 521
 QY 501 GQTRQGRNRTFRSKGRSLYVAICNMHOFIDEDPDMFEKQFVFPFPPPLRYREPVLK 560
 Db 522 GQTRQGRNRTFRSKGRSLYVAICNMHOFIDEDPDMFEKQFVFPFPPPLRYREPVLK 581
 QY 561 FDSGLVINDVCKPQSPEDFCLKVEAVLGNATGNGPADSQHSGHGLQDGEARPDGSA 620
 Db 582 FDSGLVINDVCKPQSPEDFCLKVEAVLGNATGNGPADSQHSGHGLQDGEARPDGSA 641
 QY 621 ALQPLHTYKAGSPDMPSDGIYDSVPSSLSLPLMEGLSTDTQTTSSITSVSSSSG 680
 Db 642 ALQPLHTYKAGSPDMPSDGIYDSVPSSLSLPLMEGLSTDTQTTSSITSVSSSSG 701
 QY 681 LGEEPPALPSKLLSSGSKADLGCRSYTDELHVAAPL 718
 Db 702 LGEEPPALPSKLLSSGSKADLGCRSYTDELHVAAPL 739
 RESULT 14
 ID AAU11355
 AC AAU11355; standard; Protein; 738 AA.
 XX AAU11355;
 AC AAU11355;
 DT 26-MAR-2002 (first entry)
 XX Human DNAX cytokine receptor subunit 8 (DCRS8) polypeptide.
 DE Human; DNAX cytokine receptor subunit 8; DCRS8; phosphate labelling;
 KW gene therapy; protein therapy; immunological disorder.
 KW Homo sapiens.
 OS Homo sapiens.
 XX Key
 FH Location/Qualifiers
 FT Misc-difference 25
 FT /label= Val
 FT /note= "Encoded by GTN"
 XX W0200190358-A2.
 PN 29-NOV-2001.
 XX 23-MAY-2001; 2001WO-US16767.
 XX

PR 24-MAY-2000; 2000US-206862P.
 XX (SCHE) SCHERING CORP.
 PA
 XX
 PI Gorman DM;
 XX WPI; 2002-106198/14.
 DR N-PSDB; AAS18134.
 XX Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in response to presence of increased protein levels or immunological disorders -
 PT
 PT
 PT
 PT
 PS Claim 1; Page 25; 148pp; English.
 XX
 CC The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polynucleotides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents the human DCRS8 polypeptide.
 CC
 CC
 XX Sequence 738 AA;
 Query Match 95.5%; Score 3657.5; DB 23; Length 738;
 Best Local Similarity 96.4%; Pred. No. 0;
 Matches 692; Conservative 2; Mismatches 9; Indels 15; Gaps 2;
 QY 1 AUTCGWRMAAARPLCAVNEGVGASRSGLYNITFKYDNCITLNPVGHVIAQAQNI 60
 Db 36 AUTCSW-----XGVGASRSGLYNITFKYDNCITLNPVGHVIAQAQNI 81
 QY 61 TISQYACHDQAVAVILWSPGALGIEFLKGFVILEELKSGROCOQILKDPKLNSSFK 120
 Db 82 TISQYACHDQAVAVILWSPGALGIEFLKGFVILEELKSGROCOQILKDPKLNSSFK 141
 QY 121 RTGMSQPLNKFETDIFVYKVVPPPIKSNENYPPFFRTRACDILLQPDNLACKPFWK 180
 Db 142 RTGMSQPLNKFETDIFVYKVVPPPIKSNENYPPFFRTRACDILLQPDNLACKPFWK 200
 QY 181 PRNLNISQSGDMQVSDHAPHNFGFRFYLYKLGHEGPKRTCKEQTTETTSCLQ 240
 Db 201 PRNLNISQSGDMQVSDHAPHNFGFRFYLYKLGHEGPKRTCKEQTTETTSCLQ 260
 QY 241 NVSPGDYIIELVDVNTNRKVMETALKPVHSPWAGPIRAVAITPVNIVISAFATLTVV 300
 Db 261 NVSPGDYIIELVDVNTNRKVMETALKPVHSPWAGPIRAVAITPVNIVISAFATLTVV 320
 QY 301 RKQQENIYSHLDESSSSTYTAALPRERLRPRKPVFLCYSSKQGNHNNVVOCFAYFL 360
 Db 321 RKQQENIYSHLDESSSSTYTAALPRERLRPRKPVFLCYSSKQGNHNNVVOCFAYFL 380
 QY 361 QDFCCCEVALDLWEDFSLCRBQREWVIOKIHESQFIIVVCSKGMKYFVDKKNYKHKGG 420
 Db 381 QDFCCCEVALDLWEDFSLCRBQREWVIOKIHESQFIIVVCSKGMKYFVDKKNYKHKGG 440
 QY 421 RGSNGELFLVAVSAIAEKLQAKSSAALSFKFIATVDFYSCGDPVPGILDLSTKRYLM 480
 Db 441 RGSNGELFLVAVSAIAEKLQAKSSAALSFKFIATVDFYSCGDPVPGILDLSTKRYLM 500
 QY 481 DNLQPCSHLSRDBGLQEPQTRQGRNRTFRSKGRSLYVAICNMHOFIDEDPDMFE 540
 Db 501 DNLQPCSHLSRDBGLQEPQTRQGRNRTFRSKGRSLYVAICNMHOFIDEDPDMFE 560
 QY 541 KQFVFPFPPPLRYREPVLKFGSLVINDVCKPQSPEDFCLKVEAVLGNATGNGPADSQH 600

DD 561 KQVFPHPPLRYREPVLKFDGLVNDVCKPGPSDFCLKVYAAVATGATGADSDQHE 620
 QY 601 SOHGLODQGEARPDGSAALQPLHTVYKAGSPDMRDSGIYDSSVFSSELSLPLMEG 660
 DB 621 SOHGLODQGEARPDGSAALQPLHTVYKAGSPDMRDSGIYDSSVFSSELSLPLMEG 680
 QY 661 LSTDQTSSTLSTSSVSSGSGEPPALPSKLLSSGCKRADLGCSTYDELHVAVL 718
 DB 681 LSTDQTSSTLSTSSVSSGSGEPPALPSKLLSSGCKRADLGCSTYDELHVAVL 738

RESULT 15.

ABB07630

ID ABB07630: standard; Protein; 739 AA.

XX AC

XX AC

XX AC

DT 20-MAY-2002 (first entry)

XX DE Murine cytokine receptor, Zcytor18.

XX DE

KW Cytokine receptor; Zcytor18; cell proliferation; antiproliferative; antiproliferative; human;
 KW pulmonary alveolar proteinosis; familial periodic fever; antitumor;
 KW erythroleukemia; chromosome 3p14.3; gene therapy; mouse.

XX OS

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Claim 1; Page 111-115; 119pp; English.

The invention relates to an isolated cytokine receptor polypeptide designated Zcytor18. The Zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumor growth. The encoding nucleic acids are useful for providing Zcytor18 in vivo by gene therapy techniques. Zcytor18 oligonucleotide probes are useful for in vivo diagnosis, and the Zcytor18 probes and primers can be used to detect and localize Zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a murine Zcytor18 amino acid sequence.

Sequence 739 AA;

Query Match.

Best Local Similarity 83.8%; Score 3208; DB 23; Length 739;

Matches 611; Conservative 37; Mismatches 52; Indels 22; Gaps 6;

QY 1 ADTCGWRKAAAPRLCVANEGVGPASRNSGLNITFYDNCYTYLNP-VGKHVIAQAQN 59

DB 36 ADTCGWR-----GVGPASRNSGLNITFYDNCYTYLNPVGGKHAIAQAQN 81

Search completed: May 19, 2003, 09:20:01
 Job time: 58.0074 secs.

QY 60 ITTSQACHDOAVATILNSPGALGIEFLKGFVILEELASERQCOQIILKDPKOLNSSF 119
 DB 82 ITTSQACHDOAVATILNSPGALGIEFLKGFVILEELASERQCOQIILKDPKOLNSSF 141
 QY 120 KRTGMSQPLANKETFDYFVYVPPFSIKNESNYHPPFRACDILLQDNLACPFH 179
 DB 142 RYCHESQPLANKETFDYFVYVPPFSIKNESNYHPPFRACDILLQDNLACPFH 201
 QY 180 KPRNLISQBGSDMVQSFHAPHNFGFRFFLYLKLHGHGPFKRTCKOBTETTSCLL 239
 DB 202 KPRNLISQBGSDMVQSFHAPHNFGFRFFLYLKLHGHGPFKRTCKOBTETTSCLL 261
 QY 240 QNVSQDITIELVDNTTRKVMYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVM 299
 DB 262 QNVSQDITIELVDNTTRKVMYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVM 321
 QY 300 CRKQDQENIYSHLDSESSSTYTAALPRELPRKPVFLCYSSKQGNHNVVOCFAIF 359
 DB 322 CRKQDQENIYSHLDSESSSTYTAALPRELPRKPVFLCYSSKQGNHNVVOCFAIF 381
 QY 360 LQDFCCEVALDIEDFSLCREGQRENVIOKIHESQFIIVVC-SKGNKYFVDKKNYKHGG 419
 DB 382 LQDFCCEVALDIEDFSLCREGQRENVIOKIHESQFIIVVC-SKGNKYFVDKKNYKHGG 441
 QY 420 GRSGGELFLVAVSAIAKLRQAKSSAALSKEFTAVTFDYSCEBDVPGILDISTKYL 479
 DB 442 SREAGQEFFLVAVSAIAKLRQAKSSAALSKEFTAVTFDYSCEBDVPGILDISTKYL 501
 QY 480 MDMLPOLCSHLSRDEGLQEP-GQHTQSGRRNYFRSKSRLTYAICNMHOFIDEEPDW 538
 DB 502 MDMLPOLCSHLSRDEGLQEP-GQHTQSGRRNYFRSKSRLTYAICNMHOFIDEEPDW 558
 QY 539 FEKQFVPPPPVLYREPVLKFDGLVNDVCKPGPSDFCLKVYAAVATGATGADSDQ 598
 DB 559 FEKQFVPPPPVLYREPVLKFDGLVNDVCKPGPSDFCLKVYAAVATGATGADSDQ 618
 QY 599 H--ESQHGILDQGEARPDGSAALQPLHTVYKAGSPDMRDSGIYDSSVFSSELSLP 656
 DB 619 STYLESQHVGLDQDTEAQFSCDSAPALQPLHVAVKAGSPDMRDSGIYDSSVFSSELSLP 678
 QY 657 LMBGLSTDQTSSTLSTSSVSSGSGEPPALPSKLLSSGCKRADLGCSTYDELHVA 716
 DB 679 LMBGLSTDQTSSTLSTSSVSSGSGEPPALPSKLLSSGCKRADLGCSTYDELHVA 737
 QY 717 PL 718
 DB 738 PL 739

GenCore version 5.1.4.p5.4578
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OM protein - protein search using sw model

Run on: May 19, 2003, 09:16:08 ; Search time 26.5067 Seconds
(without alignments)
2604.041 Million cell updates/sec

Title: US-09-912-157-2_copy_36_753

Perfect score: 3829

Sequence: 1 ADTCGWRKAAARPRICVAN.....CKADLCGRSTYDELHAPVL 718

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1.*

2: p1r2.*

3: p1r3.*

4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3005	78.5	564	2 T42695	hypothetical prote
2	170.5	4.5	846	2 T27282	hypothetical prote
3	126.5	3.3	718	2 T30113	hypothetical prote
4	117	3.1	757	2 T09081	telomere-associate
5	116.5	3.0	901	2 F83781	transposase (08) /
6	110	2.9	535	2 T17212	hypothetical prote
7	110	2.9	592	2 T49239	vesicle transport
8	110	2.9	917	2 T04661	hypothetical prote
9	109	2.8	998	2 S37627	protein-tyrosine k
10	107.5	2.8	938	2 T49071	protein kinase - m
11	107.5	2.8	3788	2 T13960	beige protein homo
12	107.5	2.8	3942	2 T42730	Bassoon protein -
13	106.5	2.8	638	2 D86477	protein F1504.27 (
14	106	2.8	3788	2 T30851	lysosomal traffic
15	105	2.7	901	2 JC6093	dead ringer nuclea
16	105	2.7	1571	2 T14155	zinc finger protei
17	104	2.7	1462	1 B36182	protein-tyrosine-p
18	103.5	2.7	663	2 A39897	Grpase-activating
19	103.5	2.7	930	2 A84668	Argonaute (AGO1)-1
20	102	2.7	813	2 B47485	ABR protein 2 - hu
21	102	2.7	859	2 A49307	98K GTPase-activat
22	102	2.7	1448	2 A12007	Subtilase family p
23	101.5	2.7	822	2 A47485	ABR protein 1 - hu
24	101.5	2.7	1639	2 T50119	probable sensory t
25	101	2.6	641	2 T50497	hypothetical prote
26	101	2.6	664	2 T51247	ARR2 protein limpo
27	101	2.6	1275	2 A38985	nucleotide exchang
28	100.5	2.6	1007	2 T24643	hypothetical prote
29	99.5	2.6	657	2 E96949	serine/threonine p

30	99.5	2.6	794	2 S59069	213 protein - mous
31	99.5	2.6	981	1 F0MVGM	gag-abl polyprotei
32	99	2.6	341	2 H71716	190 kd antigen pre
33	99	2.6	783	2 A31491	sex-determining re
34	99	2.6	970	2 S63059	hypothetical prote
35	98.5	2.6	353	2 T33782	hypothetical prote
36	98.5	2.6	963	2 AD2381	type 1 site-specif
37	98.5	2.6	1050	2 G86582	exodeoxyribonuclea
38	98.5	2.6	1050	2 H70441	exodeoxyribonuclea
39	98.5	2.6	1050	2 C81624	exodeoxyribonuclea
40	98	2.6	820	2 S33794	hypothetical prote
41	98	2.6	1023	2 T48997	epsin-like protein
42	97.5	2.5	291	2 F86451	protein F6N18.2 (1
43	97.5	2.5	589	2 F96599	protein F14J16.6 (
44	97.5	2.5	1121	2 T25715	hypothetical prote
45	97	2.5	984	2 A39753	protein-tyrosine k

ALIGNMENTS

RESULT 1

T42695

hypothetical protein DKFZp434N1928.1 - human (fragment)

C: Species: Homo sapiens (man)

C: Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000 ~

R: Bloeker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, November 1999

A: Reference number: T22230

A: Accession: T42695

A: Status: preliminary

A: Molecule type: mRNA

A: Residues: 1-564 <AAA>

A: Cross-references: EMBL:AL133097

A: Experimental source: adult testis; clone DKFZp434N1928

C: Genetics:

A: Note: DKFZp434N1928.1

Query Match 78.5%; Score 3005; DB 2; Length 564;

Best Local Similarity 99.8%; Pred. No. 4.7e-231;

Matches 563; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 155 HFFFTTRACDLLOPONLACKFFWPRNLNSQHGSDMQVSPDHAPHNGFFFTLHK 214

Db 1 HFFFTTRACDLLOPONLACKFFWPRNLNSQHGSDMQVSPDHAPHNGFFFTLHK 60

QY 215 LKHGPPFRKTKCKQRTTETSCLLQNVSPGDYIIELVDDTNTTKVMHYALAPVSPWA 274

Db 61 LKHGPPFRKTKCKQRTTETSCLLQNVSPGDYIIELVDDTNTTKVMHYALAPVSPWA 120

QY 275 GPRAVATVPLVVISAPILFTVNCRRKKQENIYSHLDESSSTYTAALPRELRPR 334

Db 121 GPRAVATVPLVVISAPILFTVNCRRKKQENIYSHLDESSSTYTAALPRELRPR 180

QY 335 PVFLCYSSKQDNHNVVOCFAFLQDCGCEVALDWEFSLCRGQREWIQIHES 394

Db 181 PVFLCYSSKQDNHNVVOCFAFLQDCGCEVALDWEFSLCRGQREWIQIHES 240

QY 395 QFTIIVCSKGMKYFDKNTKHKGGGSGKGFELVAVSAIAKLKQKSSAALSKF 454

Db 241 QFTIIVCSKGMKYFDKNTKHKGGGSGKGFELVAVSAIAKLKQKSSAALSKF 300

QY 455 IAVFDYSCGDPVGLDSTKYRLMDNLPLQCSLHLSRDHGLQEPQGHTRQGSRRNYR 514

Db 301 IAVFDYSCGDPVGLDSTKYRLMDNLPLQCSLHLSRDHGLQEPQGHTRQGSRRNYR 360

QY 515 SKSGSLYVACNNHQFIDEPPWFKEQVFPPEPPLRYREPVLEKFGSLVNDVCKP 574

Db 361 SKSGSLYVACNNHQFIDEPPWFKEQVFPPEPPLRYREPVLEKFGSLVNDVCKP 420

QY 575 GPESDFCLKVAENVLGTGADGADSOHESQHGGLDQDGEARPALDGSAAQLPFLHTVKGSP 634

A:Reference number: 216557; MUID:98198830; PMID:9539423

A:Accession: T09081

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-757; <SAS>

A:Cross-references: EMBL:AF030885; NID:g2642221; PID:g2642222

A:Experimental source: strain FB2

C:Genetics:

A:Gene: UTAS-recQ

C:Keywords: DNA binding

Query Match 3.13; Score 117; DB 2; Length 757;

Best Local Similarity 20.13; Pred. No. 0.64;

Matches 111; Conservative 56; Mismatches 187; Indels 190; Gaps 27;

QY 233 ETTSCLLQNVSPGDIYIELVDVNTYKVMYHATAPVSPWAGPIRAV-----AITVPL--286

Db 77 ETTILPTVALRANLAKLDVN-----IRYVMPQ-GSKAAPIVSTEAATLAFKE 131

QY 287 -----VVISAFATLFTVMCKKQENIYSHLDEESSESTYTAALP-----327

Db 132 YANRLQOQRLDRIVIDCHLTLTARSYRSNMQLAWRVDETOTVLTATLPPIFEDA 191

QY 328 -----RERLRPPKVF-----LCYSSKDGQNMNVVOCF-AYFQDFCGCEVALDWEDE 376

Db 192 FISHKLKPLIVRESTRNLSICYSVTAHRNSGTCIDAVRYD--ECRARTDN--246

QY 377 SLCRBQREWVQKIHESOFIIVVCSKGMKIFYDK-----KNYKKGGRGS-----423

Db 247 -----NGQED-----RIIVVCTS--KELVARLAEMLCMAYSSESSEADKAATIT 290

QY 424 -----GGGELFVAVSAIAKLRQAKOSSNALSKEFIATVYQSCGQVPGIL--DLSTKY 477

Db 291 DWICGSGPVIARSA-----LVGVDFPHVRVFIHLGPDLLTDF 331

QY 478 -----RMLNLPOLCSHLSDHGLQBPQGTROGSRNRYFRS 515

Db 332 SOESGRAGRDGMPAESILLAGPOLDDRAP--ASGKASSAEKGVAPG--ADKEAMQLYRS 387

QY 516 KGRSLYVAICNMHOFIDESPWFEXQFVFPFPPPLRYREPVLKEDSGVLVANDVMCKPG 575

Db 388 RK-----YCLRGVLSQLLDQSDM-----RWCMESGDLCSVC 419

QY 576 PSDFCLVAVAVGATGPADSOH-----ESQHGLODGEARAPALDGAALOPILFTVKG 632

Db 420 PGHHF-----QARGPGDOFHFTAPAQAGDPSTQGRHPSMGSS--HPSMH-----463

QY 633 SPSPDPRSGIYDSVPSSE--LSLPLMEGLSTDQETSLTESYSSS--SGLGEPEPPA 688

Db 464 -----GSSHPSSGSHSPSHSGSHPSHSGSS--HPSIHSGSGHGGQRRKQPD 510

QY 689 LPSK 692

Db 511 PFSE 514

RESULT 5

F83781

C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C:Accession: F83781

R: Takai, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: F83781

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-901 <STO>

A:Cross-references: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BA804773.1; GSPDB:GNOC

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH1054

Query Match 3.03; Score 116.5; DB 2; Length 901;

Best Local Similarity 19.63; Pred. No. 0.9;

Matches 112; Conservative 76; Mismatches 169; Indels 215; Gaps 27;

QY 26 ASRNSGLNITFKYDNCNTYINLVGVKHYIADQNTITISQY-ACHDQAVVITLWSPALGI 84

Db 333 ALKESGL-----PLPKTLIADAGISGSNTYVNADELFTFLIPS-----371

QY 85 EFLKGFVRVLELSEGR-----OCQOL--ILKDPKOLNSFKRTGMSOPFLANKF 134

Db 372 ---EFER--QOKESPAKKEPHFNWRCDETDVTWCENQKVSFKRYKRTDPY---CY 423

QY 135 ETDYFV-----KVVPF-PSI-----KNESNHPFFTRACDLLQPDMLACKPWRPR 182

Db 424 ARDFKVCESCGCPKPECTKARGNRQVHNPVY-----EELKAKOQKILK 471

QY 183 NLNLSQHG-----SDMQVSFDHAPNFGFRPFYLYHKLKHEGPFKRTCKQEQTTET 234

Db 472 ---SEEGRTLYQKRKTDESVEFGVKQNLGPRRLHGRK-----507

QY 235 TSCLLQNVSPGDIYIELVDVNTYKVMYHATAPVSPWAGPIRAVAITVPLVVIS-AFA 293

Db 508 -----ESVHIEGLVLAHNLR 524

QY 294 TLTVMCKKQENIYSHLDEESSESTYTAALPRERLRPRKPVFLCYSSKDGQNMNVY 353

Db 525 KRATVDRESKPKNTNQHKNREN-----RIKRF-----SRFVYL 558

QY 354 QCF---AYFLQDFCGCEVALDWEDESLCRQOREWV---IOKIHESQFIIVVCSKGMK 406

Db 559 RCFWDSPPFIKSDGQKQFASPLFD--KLREGGENNIEVIDLSKTYNRQVV---KGIN 612

QY 407 YFVDKNTYKKGGRSGGKELFVAVSAI-----AEKLRQAKOSSSALSK 453

Db 613 PFIEKGENVGLGPNAGAKSTTSMISLIQPTSGDVLKGGSIHKQSKAIRSILGVVPQ 672

QY 454 FIATVDFYSCF-----GDVPGILDLSKTYRLMDNLPOLCSHLSDHGLQBPQGTROG 507

Db 673 EIAVYHDLTARENLAFFGKIYGLAGELAHR-MESTLQLV-----GLEE-----RON 718

QY 508 SRNRTFSKSGRSUTVAICNMHQ---FIDEEP 536

Db 719 DRVHTFGSGMKRRLLNTIAVALLHEPELIDEP 750

RESULT 6

T17212

C:Species: Homo sapiens (man)

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T17212

R: Poustka, A.; Klein, M.; Nemes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, September 1999

A:Reference number: Z18723

A:Accession: T17212

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-488;489-535 <POD>

A:Cross-references: EMBL:AL117401

A:Experimental source: adult testis; clone DKFZp434P211

C:Genetics:

A:Note: the cDNA sequence contains a -1 frameshift near codon 488

A:Note: DKFZp434P211.1

Query Match 2.98; Score 110; DB 2; Length 535;

Best Local Similarity 23.53; Pred. No. 1.4;

Matches 70; Conservative 42; Mismatches 108; Indels 78; Gaps 17;

QY 439 KLRQAKOSS-SAALKSFIAVDFYSCGQVPGI-----LDLSKTYRLMDNLPQ 485

Db 103 RYNQTSQTSWTSSTCTNNRNLSSYSTGLGPKLRKRRGPASSHCQLTSLSSKTVSEDRPQ 162

QY 486 LCSEHLSRDLGLOE--PGQTRGSRNRYFRSKGRSLYVAICNMHQTDEPWFQK 543
DB 163 AVSSGHTQCAKADIAPGQTLT--LRNDSSTSEASRP-----STKFK---PLPERRG 210
QY 544 VFPH-PPPL-----RYREPVELEKFDGLVNDVY---CKPGESDFCLKVAEA 587
DB 211 EPLMLPPLEIGYVTVVDDLDREKKAAPORINSALQVEDKAIKSDCRPSRSH---TLSSL 267
QY 588 VLGATG-PADQSHQSGGLDQGEARPALDGSALQALPLHTVAKGSPDMP-----RD 640
DB 268 ATGASGLPAVSKAPS-----NDACQETHKSDQCLGLDPLASA--AGVPSTAPMSGKKRHP 321
QY 641 SG-IDYSSVPSSELSLPLMEGLSTQDTETSSITSSVSSSGLEGEPPALPSKLLSSG 697
DB 322 PGPLFSSSDP-----LPATSSDSQSAQVTSILI-----PAPPEAASNDAG 361

RESULT 7
149239
vesicle transport protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I49239
R:Tellam, J.T.; McIntosh, S.; James, D.E.
A:Title: Molecular identification of two novel Munc-18 isoforms expressed in non-neurons
A:Reference number: I49238; MUID:95197608; PMID:7890715
A:Accession: I49239
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-592 <RES>
A:Cross-references: EMBL:U19521; NID:9642027; PIDN:AA69913.1; PID:9642028
C:Genetics:
A:Gene: munc-18c

Query Match 2.9%; Score 110; DB 2; Length 592;
Best Local Similarity 18.5%; Pred. No. 1.6;
Matches 93; Conservative 64; Mismatches 157; Indels 188; Gaps 22;

QY 286 LVVISAPATLVNCRKQKQ-----ENYSHLDESESESTYTAALPRERLRPRK 336
DB 34 IMLEDFTKLLSCCKTKDLEEGITVNIENYKRPVROMKALYF-----ISPTPK 86
QY 337 VFCLYSGKDGQNMVYVQCFAYFLODFC-----GCE----- 367
DB 87 SVDCFLRDFGSKSEKKYKAAIYFTDCPDSLNFKNKASCSKSRCKEINISFIPQESQ 146
QY 368 -VALDLWEDSLC-----REGQREWYQKTHESQFIIVC-----SKNKY----- 407
DB 147 VTLVDVPAFYCYSPDPSNARKEVMEAAEQ--IVTCATLDENPGVYKSKPLDNA 204
QY 408 -----FVDDK--NYK--HGGGSGSGKGLFLV-----AVSAEAKLRQAKQSSAALS 452
DB 205 SKLAQVLEKLEDDYKIDRGLKGTQSQLLIDRGFDPPVSVLHEL----- 252
QY 453 KEIAYVED-----ISCEG-DVPGIL-----DLSTKTR-----LMDNLPOLCSHLH 491
DB 253 TFOAMAYDLLPIENDYTKYKTDGKEAIVLEDDDLAVRVRHRHIAVLEETPKLKEIS 312
QY 492 SRDHGLQPGFQTRGSRNRYFRSKGRSLYVAICNMHQTDEPWFQKQVFPHPPL 551
DB 313 STK-----KATEGTSLSALTQLKMKPHFRKQISKOVV-----HL 348
QY 552 RYREPVELEK-----DSGLVNDVYVCKKPGSPDCLKVE 585
DB 349 NLAEDCMNKKFLNTEKLTCTEODLAGTDAEQGRVKDSMLVLPVLL--KNHEDNCKIR 406
QY 586 AAVLGATPADQSHQSGGLDQGEARPALDGSALQALPLHTVAKGSPDMPRO--SGTY 644
DB 407 AVLLYIFGINTTEEN-----LDRLHNKVIDEEDSDMIRNWSHLG 446
QY 645 DSSVPSSELSLPLMEGLSTQDT 666

DB 447 VPVPPSQAKPLKRSAREET 468

RESULT 8

hypothetical protein F8D20.70 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 24-Nov-1999

C:Accession: T04661

R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Jesse, P.; Heijnen, L.; Vos, P.; Mew

submitted to the Protein Sequence Database, July 1998

A:Reference number: Z15381

A:Molecule type: DNA

A:Accession: T04661

A:Residues: 1-917 <REV>

A:Cross-references: EMBL:AL031135

A:Experimental source: cultivar Columbia; BAC clone F8D20

C:Genetics:

A:Map position: 4

A:Introns: 13/3; 58/2; 93/1; 274/3; 340/3; 373/3; 395/1; 437/3; 536/1; 624/2; 665/3;

A:Note: F8D20.70

C:Superfamily: Arabidopsis thaliana hypothetical protein F8D20.70

Query Match 2.9%; Score 110; DB 2; Length 917;

Best Local Similarity 18.1%; Pred. No. 3;

Matches 154; Conservative 124; Mismatches 281; Indels 292; Gaps 37;

QY 24 GPASR-----NSGLYNITFYKDYCTYLPVGVKEV---LADAQNI--TISQYACHDOVA 72

DB 148 GKASRVTVVSSSSQVLLVNEQTETRMKIGLVSEPCADMEMLIADVRSKHKQDP 207

QY 73 VTLWSPGALGI--BELAGFRVILEELKSGROQQLILADPQKLNNSFKRTGMESOP-- 128

DB 208 LFLVLSGRVYADDDYMIETKYLQSQSKSPSLPKETVTKLPFSDSSITVTKELTNPSH 267

QY 129 FLNKKPTDY-----FVKVVPFSPSIKESN---YUPFF-----FTRACDILLQDPNL 173

DB 268 LLNLSDY-DYLAQKANDVPFPPFTVPKESRSNAHPGTVKKNVYITTCGDIISWDM 326

QY 174 ACK-----PFWKPR-NLNTSQHG-----SDMQVSDHAPHNFGFRFFLYTKL 215

DB 327 TCSFPILVLFLKBDIDQDVSSRGNALTAHYDSNRLVSGDHNGWVLYRFRPEPILT 386

QY 216 KH-----EGPFRK-----KTCQKQPTTETTSILQNVSP-----GDYIELVDD 254

DB 387 ENSFIPQGSLLKGNHIVQSVKIKLTGTSITCIQKSONSKHLAIGSGQGBHSLVEID- 445

QY 255 TMTTRKVMYALKPVSPWAGPIRAVAITVPLVVISAFATLFT----- 297

DB 446 -----ALTPVY-----LOVSLVDIEANVLTHTKHLASDIPCGLISLOFE 484

QY 298 -----VMCRKKQENIYSHLDESESESTYTAALPRERLRPRKRVFCYSSKDGQ 347

DB 485 SCIVQGFKNVLVWVARESSVFA-LDSGTGMNIGTNMIRPK-----KPKVLMQLDQK 538

QY 348 NNMVVOCTFAFLQDCGCEVALDLWEDFSLCRGQREWYQKTHESQFIIVCS----- 402

DB 539 -----QDTSG-----NGFOTSR-----TVFEISITRQPSVLWCSEKAIY 573

QY 403 -----KGMKYFVDKKNYKHG-----GGRSGKGLFLVAVSAIAE-----KLR 441

DB 574 IYSLAHVGVQKVLKHKFKFSSSPICSASTFYGTSGVG---LTLVFTDGTVEIRSLPELS 630

QY 442 QAKQS-----SSAALSKFIATVFDYSCGD-----VPCILDSTKFLMDNL 483

DB 631 QLAQTSIRGTYTSSPKNPSLPEITISASWDGDLVWNGDDLVSSVLPQKETFALVESH 690

QY 484 POLCSHLSDHGLQPGFQTRGSR-----NYFRSKGRSLYVAICNMHQTDEP 537

DB 691 -----NRVYKDNVCEGIIITSSSPREKKSFMFGSVFKTKRTTDTPESSKETIELSK 746

QY 538 WFEKQVFP-----HPPPLRYREPVELEK 565

Db 747 IFSTANFPMNNVNSREINTRYVEDEELDIDDIDHHPNQQQKPKQGLSGL 806
 QY 566 ----VLNDVCKKPPSPDCLVEAAVLGATGADPSOHSOHLG-----DO 608
 Db 807 SKQMANFNFNGKLGKQAAANEKSV-----TNDKEHKGNTVDQIKKYGTSDE 862
 QY 609 DGEARPDGSAALQPLHTVRAGSPDMPRDSGIYDSSVPSSELSPLMEGLSDTOTET 668
 Db 863 MGAARMA-----OSKLOD-----NLKLOGISLRTTEM 890
 QY 669 SSLTESVSSSS 679
 Db 891 EDTAKSPSSTA 901

RESULT 9

837627

protein-tyrosine kinase (EC 2.7.1.112), receptor-type - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence_revision 03-Aug-1995 #text_change 04-Feb-2000

C:Accession: S37627

R:Boehme, B.; Holtrich, U.; Wolf, G.; Luxius, H.; Grzeschik, K.H.; Strechardt, K.; Ruebs

Oncogene 8: 2857-2862, 1993

A:Title: PCR mediated detection of a new human receptor-tyrosine-kinase, HEK 2.

A:Reference number: S37627; MUID:93390963; PMID:8397371

A:Accession: S37627

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-998 <90>

A:Cross-references: EMBL:X75208; NID:Q406867; PIDN:CAA53021.1; PID:Q406868

C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat

C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein ki

F:631-899/Domain: protein kinase homology <KIN>

F:639-847/Region: protein kinase ATP-binding motif

F:922-988/Domain: SAM homology <SAM>

Query Match 2.8%; Score 109; DB 2; Length 998;

Best Local Similarity 18.9%; Pred. No. 4.1;

Matches 157; Conservative 122; Mismatches 301; Indels 250; Gaps 42;

QY 1 ADTCGRMKAAARPLC-----VANEGVGA-----SRNSG-----LYNITFY 39
 Db 268 ACTCATGHEPAAKESQCRPCPGSKAKQGGPCPLCPNPNRTTSPAAICTHNNFYA 327
 QY 40 DN-----CTTYLNPVGRHVIAADQNTITISQYACHDQVAVTILWS-PGALGIEFLKGRV 92
 Db 328 DSDSADSACTVFPSP-PRGVISN-----NETSILEWSEPRDLGVRODLLYNV 375
 QY 93 ILEELKSEG-----ROCOOLILKDPKQLNSSFRTGMSQPLNNKFETDYFKVVPSPS 147
 Db 376 ICKKCHGAGGASACSDNDNVEFVRQLGLSEPRVHS-----HLIAHRTYFEQAVNG 430
 QY 148 IKNSNTHPFFTRACDILLQPDMLACKPFWKPRNLNISQHGSDNQVSDHAPNFR 207
 Db 431 VSGSKPLPPRYAAVNITTNQAAPSEV-----PTLRHSSGSSITLSWAPERPNG-- 481
 QY 208 FFYLHLKHEGPF-KRCKCKEQBTETTSCLLQNVSP-GDYIIELVDQNTTRKWHYA 265
 Db 482 -VILDYEMKY--FESEGIASVTISOMNSVOLGLAPDARYVQV-----RARTVAGYG 532
 QY 266 -LKPVH-----SPWAGPIRAVAITPLVVISAFATL-----FTVCKKQKQNIYSH 311
 Db 533 QYSPAFEFETTSERGSQAQLOEQPLIVGSAAGLVFVAVVIAIVCLRKQRH----- 587
 QY 312 LDESSSSYVTAALPRERLRPRKVFLLCTSSKDGQNMVWQCFAYFLQDFC-CCEVAL 370
 Db 588 -----GSDSEYTEL-QQYIAGMKVYIDPTIEDPN--BAVREFAKEIDVSCVLEIVI 639
 QY 371 DLWEDFSLCRGREGNVIQKIHESOFITVCSKGMKYTFVCKKMKHKGGRSGSGELFL 430
 Db 640 GAGEFGVCR-----GRKQFGREVF-- 661

QY 431 VAVSAI---AEKLRQAKQSSAALSKFIATVDFYSCGDVPGILDLS---TKYR--- 478
 Db 662 VALTKLVGTYTERQREDYLSAINGOF-----DHENIIRLGVTGVTSRPVMIL 710
 QY 479 --LMDNLPOLCSHLHSRDHGLQEPQBT-----ROGSRNY-FRSKSGS 520
 Db 711 -TEPMENC-ALDSFLKLD-----GOFTVQLVGMRLGTAAGMKYLSMNTVHRDLAARN 763
 QY 521 LTY---AIC-----NMHQFIDEEPDMFEKQFVPFHP-----PLRYKEP---VLKRFDS 563
 Db 764 ILVNSNLVKVSDFLSRFLEDDPS-----DPTTSSLGKIPIRWTAPEAIYRKFTS 817
 QY 564-----GLVNDVCKKPPSPDCLVEAAVLGATGADPSOHSOHLGSDOGEARPAL 616
 Db 818 ASDVWSYIGVMVEVNS-----YGERPTWMSNQDVIINAVQDRLPFP 861
 QY 617 DGSAALOPLHTVRAGSPDMPRDSGIYDSSVPSSELSPLMEGLS 662
 Db 862 DCPALBOLMLDCWVRDNLKPKFSQIVNTDLKIRNAASLKVIAASQSGNSQPLDRTV 921
 QY 663 TDQTTSSITTESVSSSSGLGEEPPALPSPKLLSSGSKADLGCRSTTDEL 712
 Db 922 PDITFTTVDMLDAIK-MGRYK-----ESFVSAGFASFDLVQAQTAEDL 965

RESULT 10

I49071

protein kinase - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999

C:Accession: I49071

R:Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.

Mech. Dev. 46: 153-164, 1994

A:Title: Identification of novel protein kinases expressed in the myocardium of the d

A:Reference number: I49071; MUID:95200798; PMID:7893599

A:Accession: I49071

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-938 <9>

A:Cross-references: EMBL:U11493; NID:Q595418; PIDN:AAAG7925.1; PID:Q595419

C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea

C:Keywords: ATP; transmembrane protein

F:571-839/Domain: protein kinase homology <KIN>

F:579-587/Region: protein kinase ATP-binding motif

F:862-928/Domain: SAM homology <SAM>

Query Match 2.8%; Score 107.5; DB 2; Length 938;

Best Local Similarity 19.3%; Pred. No. 5;

Matches 152; Conservative 115; Mismatches 271; Indels 251; Gaps 42;

QY 1 ADTCGRMKAAARPLC-----VANEGVGA-----SRNSG-----LYNITFY 39
 Db 205 ACTCATGHEPAAKESQCRPCPGSKAKQGGPCPLCPNPNRTTSPAAICTHNNFYA 264
 QY 40 DN-----CTTYLNPVGRHVIAADQNTITISQYACHDQVAVTILWS-PGALGIEFLKGRV 92
 Db 265 DSDSADSACTVFPSP-PRGVISN-----NETSILEWSEPRDLGVRODLLYNV 312
 QY 93 ILEELKSEG-----ROCOOLILKDPKQLNSSFRTGMSQPLNNKFETDYFKVVP 144
 Db 313 ICKKCHGAGGASACSDNDNVEFVRQLGLSEPRVHS-----HLIAHRTYFEQAVNG 367
 QY 145 FPSIKNESNTHPFFTRACDILLQPDMLACKPFWKPRNLNISQHGSDNQVSDHAPN 204
 Db 368 VNGVSKSPLPPRYAAVNITTNQAAPSEV-----PTLRHSSGSSITLSWAPERP 420
 QY 205 GFREFFLHYLKLKHEGPF-KRCKCKEQBTETTSCLLQNVSP-GDYIIELVDQNTTRK 261
 Db 421 G-----VILDYEMKY--FESEGIASVTISOMNSVOLGLAPDARYVQV-----RAKTYA 469
 QY 262 -----MHTALKPVHSPWAGPIRAVAITPLVVISAFATL-----FTVCKKQKQNI 308
 Db 470 GYGYTHPAEFETTSERGSQAQLOEQPLIVGSAAGLVFVAVVIAIVCLRKQRH-- 527

QY 309 YSHLDSESESTYTAALPRERLRPRKPVLCYSSKOGONHNVVQCFAYFLQDFC-GCE 367
 Db 528 -----GPDAXTEKL-QQYIAPGKVIYIDPFTEDPN-EAVREFAKEIDVSCVKIE 576
 QY 368 VALDWEFSLRCBQREWVIOKIHESOFIIVVCSKGMKIFVCKNKYKHGGGSGKGE 427
 Db 577 EVIGAGEFCEVR-----GRLLKLPGRGE 599
 QY 428 LELVAYSAT-----AEKLRQAKSSAALSKFIATVDFSCBQVPGILDLS---TKYR--- 478
 Db 600 VF-VAIKTLVGYTERQRDFLSEASNMGO-----DPTNIIRLEGVYVTKSRV 647
 QY 479 -----LMDNLPCSLHSHRDLQEPQHT-----ROGSRNY-FRKS 517
 Db 648 MILTEPMENC-ALDSFLKND-----GOFTVTLVGMKLGJAGMKYLSMNVHDLA 700
 QY 518 GRLSYV---AIC-----NMHOFIDEPDMFEKOF-----VPEH---PPLRYREPVLE 559
 Db 701 ARNLVSNLVCYSDFGLSRFLDDPS---DPTYSLLGGKIPINWTAPEPIATYR----- 753
 QY 560 KFDG-----GLVNDVCKPGPESDFCLKVEAAVYLGATGPADSHQSHGGGLDQGEA 612
 Db 754 KFDASDVNSYIGVNEVMS-----YGEQPTWNNMSQDDINAVEQDYRL 797
 QY 613 RPALDGSAAOLPLATVVKAGSPDMPDSDGIYD-----SSVPSSELSLPL 657
 Db 798 PPMDCPTALHOLMASCHVRDNLRPKFSQIVNTLKLIRNAASLKVTASAPSG-MSQPL 856
 QY 658 MEGLSTDQT 666
 Db 857 LDRVDPDYT 865

RESULT 11

T13960

beige protein homolog - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T13960

Submitted to the EMBL Data Library, November 1998

A:Description: Deletion in the beige gene of the beige rat due to recombination between

A:Reference number: Z17837

A:Accession: T13960

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-3788 <MOR>

A:Cross-references: EMBL:AB020019; NID:dl1241953; PID:dl035670; PIDN:BAA34688.1

A:Experimental source: strain DA; spleen

C:Genetics:

A:Gene: beige

Query Match 2.8%; Score 107.5; DB 2; Length 3788;

Best Local Similarity 19.7%; Pred No. 39;

Matches 142; Conservative 93; Mismatches 258; Indels 229; Gaps 38;

QY 16 LVANEGVG---PASR-----NSGLYNTFFKYNCTTYLNPVGHVIAQAQNTTISQYA 66

Db 658 LCGAGSCGLPSPFRFGILPSSGSEDFLWKWDALAEYQNFIFQE--DRLHNTQIASHI 715

QY 67 CH--DQVAVTILWSPGALGIEFLAGFRVILEELKSEG-----RQCOOLILKDPKQLNSFK 120

Db 716 CNLIQKGNVIVQ-----KLYNIENPVLRQVGVHVCQLSLI-----TSA 757

QY 121 RTCHESQPLNKKFET-DYFKVVP-----FPSIKN-----ESNT-----HPF 157

Db 758 QTHSSQLKQYLPQVLYQYILKLPILLKSRVIRDLFSCGNVHIELNLTLOGIRSHSL 817

QY 158 -FFRTACDLILQPNLACKPFWKPRNLNISQBSQDMQVDFDAPNPFGRFFFLYHLK 216

Db 818 KAFETLIVSLGRQKRAAPVGV---DGLDILQELSLSV----- 853

QY 217 HEGPFKTKCKQRTTETTSCLLQNVSPGDIYIELVDVDTNTRKVMHYALAKVPSFWNAP 276
 Db 854 --GFSLEK-----QOASTDPCSLRK-----FYASLRDTDPKPKTKVHQ----- 890
 QY 277 IRVAIVTVPVWISAPATILFVCKRKQKQNIYSHLDESESESTY--TAALPRERLRPR 334
 Db 891 -DAHINTINFLCVAF-----LCVSKADSRESAN-ESEDTSYDSTVASEPLSHMLPR 942
 QY 335 PNYFLCYSSKDGONHNVV-----OCFAYFLQDFCCEVALDLWEDSLRCBQREWV---I 388
 Db 943 LSL-----ENVLPSPFELCH-----AADIN---SMCR-----WITNL 972
 QY 389 OKIHESOFI-----IVVCSKGMKIFVCKNKYKHGGGSGKGEF-----IVAVSAIAE 438
 Db 973 NSVFOKOFHRLGGFQVCH-E-LIFMTIQLFRSHTEQDQROGEMSVNKNQGLMRISQEM 1031
 QY 439 KLRQAKSSAALSKFIATVDFYSCBQVPGILD-----LSTK----- 476
 Db 1032 ILKEDVSSSTAPERGFLKASADRVSLESHQMLPTSAQILATKSPGEAKTFNNQESET 1091
 QY 477 -----YRLMDNLPOLCSH-----LHSRDLQEPQHTROGSRNTRFRSGRSILYVIAICMH 529
 Db 1092 CIGSTRILLESLLAICLSASARASQKMELEPQ-----SLSLENTILCELR 1136
 QY 530 OFIDEEP-----DWFEKQVPPPPPLRYRPPVLEKFDGSLVNDVCKPGPES 578
 Db 1137 DRLSQSVATELAKPLFDALLRVALGNHSADLPDGTVTTEKSHPS---EEVLSQPGDPS 1193
 QY 579 DEFLKVEANVLGATG-----PADSQHESQHGGLDQGEARPALDG-SAAALQP--LLHTRV 630
 Db 1194 EEAEDSQCSKLIGSEEGYEADSENPDGTDQDQVLEPFAEGFSGSIVPNNLESIT 1253
 QY 631 AG 632
 Db 1254 HG 1255

RESULT 12

T42730

Bassoon protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000

C:Accession: T42730

J:Dieck, S.; Sammarti-Villa, L.; Langnaese, K.; Richter, K.; Soyke, A.; W

J:Cell Biol. 142, 499-509, 1998

A:Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively local

A:Reference number: Z22249; NID:98345363; PMID:9679447

A:Accession: T42730

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-3942 <DIE>

A:Cross-references: EMBL:Y17034; NID:g3413809; PIDN:CAA76598.1; PID:g3413810

A:Experimental source: strain 129 SVJ

C:Genetics:

A:Map position: 9p1

A:Introns: 72/2; 208/3; 505/3; 675/3; 2889/3; 3582/1; 3851/3; 3886/1; 3930/1

A:Note: Bassoon

C:Function:

A:Description: may be involved in cytomatrix organization at the site of neurotransmi

A:Note: component of the presynaptic cytoskeleton

C:Keywords: coiled coil; zinc finger

Query Match 2.8%; Score 107.5; DB 2; Length 3942;

Best Local Similarity 19.1%; Pred No. 41;

Matches 58; Conservative 29; Mismatches 99; Indels 117; Gaps 11;

QY 481 DMLPOLCSLHSHRDLQEPQHTROGSRNTRFRSGRSILYVIAIC-----NMHOFIDEE 535

Db 3535 DTCPOFC-----SHSNPVDQVEHVKDGPRAHAYKEEGTMDLSDHCVSDSEAYHLGOEE 3589

QY 536 PMWFEKQVPPPPPLRYR-----PVLEKF-----DSGLVNDVCKPG 575

Db 3590 TDWFK---PDARSDFRHHGHTVSSQKNGPARHSYHDYDEPPEGLWPHD---BSG 3643

QY 576 PESDFCLVEMAVTGNATGAPDSQHSQHG-----GLDQDG-----EAPR- 614
Db 3644 PGRH-----TSAKEHRHSDGHRSGRHAGEPGRRAAKPAARDMGHREARPH 3691
QY 615 -----ALDGSAAQPLILHTV 629
Db 3692 PQASPAPAKKGGQPGTSSADYSQSRAPSAVHASESKKGSROAHTGPSLOPRADTQ 3751
QY 630 KAGSPDMRDSGIYDSSVPSSELSLPLMEGLSTDTQTTSSLSVSSSGCLCEPPAL 689
Db 3752 AQPMQGRQAPGPOOSPSSRGT-----PSGTASRQPTGQOQOQOQOQOGLGQAPQQA 3808
QY 690 PSK 692
Db 3809 PSQ 3811

RESULT 13

Protein F1504.27 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D86477
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, T.H.; Dwyer, K.;
anssen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khatkin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mafti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D86477
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-638 <STO>
A:Cross-references: GB:AE005172; MID:g8778345; PIDN:AAF79353.1; GSPDB:GN00141
C:Genetics:
A:Gene: F1504.27
A:Map position: 1

Query Match 2.8%; Score 106.5; DB 2; Length 638;
Best Local Similarity 19.4%; Pred. No. 3.4;
Matches 94; Conservative 63; Mismatches 175; Indels 153; Gaps 24;

QY 59 NITISOTACHDOVAVTILWSPGALGIEFLAGFVILELKSRCQCOQLILKPKQLNSS 118
Db 275 DIKGYTISCHLQDCHYVHS-----KCAHENWVGKELEWIESDTEIDISP 322
QY 119 FKRTGESQFLMMKFEDYFVKVPPP-----SIKSNYHPPFFTRACDILLOPNLAC 175
Db 323 FRMLG-----DGIKFKCHKRLKLNKDAGAROTKOCAC-----IYV-IVS 364
QY 176 KPMKPRNLNISOHG--SDMQVSPDHAPHNGFFFLHYLKLKEGP--FKRTCKOBT 231
Db 365 HQYFCKKKNYSLHVCAGLSKRLDHALN-----HTLSFSPKCCSACREST 416
QY 232 TETTSCLQNVSPGYITIELVDDNTTRKVMYALPVHSPWAGPIRAVAITVPLVISA 291
Db 417 GFSTIC--SNKQDQFVLVD-----RCISVLEYFIHRSHEH-----PIFSTS 457
QY 292 FATLFTVMCKKQENIYSHLDESSE--SSTYTA--LPRE-----RLRPRKVFCLYCSKOG 346
Db 458 YNKDILKVCCKKCLAHLOCTLCFTCTCTCAIIPDIHYKFDKHLPLTSCGESAD- 516
QY 347 QNHNVVQCFATVLDQFCGEVALDMEFSLCRQGEWVQKIHESQFIIVVCSGKMK 406
Db 517 -----NTYCEV-----CEKQDLPKEWFTYCNK-----CCITIH-----LHCIFGSS 553
QY 407 YFVDKKNYHKGGRSGKGLFVAVSAIAEKLRQAKOSSAALSKEFIATVDFSCGD 466

Db 554 VFM-----KPG-----SIFDYTGKVO 570
QY 467 VFGILDLSKYRLMDNLPQICSLHSDRGHQEPQOHTROGSRN--YFRSKSGRSLY-V 523
Db 571 V-----FRNNSNTRQICYNCHNCTGL-----IFTEGTRNATYYTNHSNRSTHER 616
QY 524 AICNM 528
Db 617 IFCSL 621

RESULT 14

T30851
lysosomal trafficking regulator, long splice form - mouse
N:Alternate names: beige protein homolog
C:Species: Mus musculus (house mouse)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 24-Nov-1999
C:Accession: T30851
R:Barbosa, M.D.P.S.; Tchernev, V.T.; Kingsmore, S.F.
submitted to the EMBL data library, September 1996
A:Description: Two bg or not two bg? Longest isoform of mouse Lyst (beige) gene.
A:Reference number: Z20903
A:Accession: T30851
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-3788 <BAR>
A:Cross-references: EMBL:U70015; MID:g1813541; PID:g1813542; PIDN:AAC53011.1
A:Experimental source: strain C57BL/6J
C:Genetics:
A:Gene: Lyst
A:Map position: 1
C:Keywords: alternative splicing

Query Match 2.8%; Score 106; DB 2; Length 3788;
Best Local Similarity 19.6%; Pred. No. 51;
Matches 154; Conservative 99; Mismatches 275; Indels 256; Gaps 44;

QY 16 LCVANEGVGPA-----RNSLYNITPKYDNCCTTILNVPVGRVIADQNIPI 62
Db 658 LC-----GAGPTSGILPSPSYRFPQILSPSSSEDLKRWDALEYQSFVQE--DLRLNIQI 711
QY 63 SOYACH--DQVAVTILWSPGALGIEFLKGRFVILELKESEG-----RQOQLILKDPKQLN 116
Db 712 ANHICNLQKNGVYVQV-----KLYTFNPVLQGVLEVHBCOOLSTPS----- 756
QY 117 SSFKRTGMSQPFLLNMKFET-DYFVKVVP-----PFSIKN-----ESNY----- 154
Db 757 ---AETHMCSQLKQYLQEVLYIYKTLPLVLSKSRVIRDLFLSCNGVNHIELYLDGIR 813
QY 155 -HPP-FFTRACDILLOPNLACKPKWPRNLNISOHSDMQVSPDHAPHNGFREFYILH 212
Db 814 SLSLAKFETLIVSGEOCKDAVLDV--DGLDIOQELPSLSV----- 853
QY 213 YKLKEGEPFKTKCQQTETTSCILQNVSPGYITIELVDDNTTRKVMYALKPVHSP 272
Db 854 -----GFSLHK-----QOASDSDSPCLRK-----FVASLRPPDKPKKTIH--QDVH-- 893
QY 273 WAGPIRAVAITVPLVISAFAITFTWCKKQENIYSHLDESSESTYTAALPRERLR 332
Db 894 -----INTINIFLCVAF-----LCVSKADS-----DRESANESDTSYDPSPE 934
QY 333 PRPKVFLCYSSKQOQNMNVV--QCFAIFLQDFCGCEVALDMEFSLCRQGEWV- 387
Db 935 PLSEMLPCLSLD-----VVLSPCLLH-----AADIW--SMCR-----WIY 970
QY 388 -TQKHESQFI-----IYVCSKGMKYFDKNTKHKGGSGSKGELF-----LVAVSAI 436
Db 971 MLNSVFOKQFHLRGVGVCHL-LIFMIIOKLFRTSTEDQGRGQGMENQELIRIS-- 1027
QY 437 AEKLRQAKOSSAALSKEFIATVDFSCGDVPGIL--DLSTKYLMDN-----LPQ 485
Db 1028 -----YPELTLKGDVSSATAPDLGLFKRSADSVRGFSQPVLP 1066

QY 486 LCSEHSHDHGQLQPGQHTROGSRNRYFSKSGSLYVAICNHOFTDEPWFQKQVP 545
DB 1067 SAEQIVATE---SVPGE-----RKAFNSQOSETSLQSKILLESILD-----IC 1106
QY 546 FHPPLRYREVPLEKFDGSLVNDVCK-----PGPESDCLKVAALVG 590
DB 1107 LESARACQRMELPQGLSVENILCELREHLSOSKVAETELAKPLDALLVALGHS 1166
QY 591 A-TGADS---QESHGGLDQGEARPDGSAALQPLLTHTKAGSPSDM---PROSG 642
DB 1167 ADLPGDVAITEKSPSEELISQDGFSEAECSQCSLKILGEEGYEADSESNPEVD 1226
QY 643 IYDSVPSELSPLMGLSTDTSTSTESVSSSGLOE---EPPALPSKLLSSGSC 699
DB 1227 TQDDGV---ELN-PEASFS-GSIVSNLENLTH---GHIYPEICMLGLNLSASKA 1277
QY 700 KADL 703
DB 1278 KLDV 1281

RESULT 15

JC6093

dead ringer nuclear protein - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 13-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000

C:Accession: JC6093

R:Gregory, S.L.; Kortschak, R.D.; Kallionis, B.; Saint, R.

Mol. Cell. Biol. 16, 792-799, 1996

A:Title: Characterization of the dead ringer gene identifies a novel, highly conserved

A:Reference number: JC6093; MUID:96182081; PMID:8622680

A:Accession: JC6093

A:Molecule type: mRNA

A:Residues: 1-901 <GRE>

A:Cross-references: GB:U62542; NID:91480739; PID:NAB05771.1; PID:91480740

A:Experimental source: embryo

C:Genetics:

C:Keywords: DNA binding; embryo

Query Match 2.7%; Score 105; DB 2; Length 901;
Best Local Similarity 20.4%; Pred. No. 7.4;
Matches 96; Conservative 56; Mismatches 157; Indels 162; Gaps 23;

QY 370 LDLWEDFSL--CREG-----QREW--VIQIHESQFI-----IVCSKGMYF---VDK 411
DB 313 LDLELYNLVTARGLVVDVINKLMQEIINGLHLPSSITSAFTLTQYMKLYPYCEK 372
QY 412 KNYK-----HKGGRSGKGE-----LFLVAV 433
DB 373 KNLSTPAELQAAIDGNREGRRSSYGOYEAMHNMPTPIRPSLPGGMOQSPALVTH 432
QY 434 SAIEKLA-QAKOSSAALSKEFTAVFDYSCGVPGLDLSKYRLMDNLQIC-----487
DB 433 AAVANNOQAQAAAAAHHRLAGA----PAFGQPNLVQETESRMETL-OLIQAKE 487
QY 488 -----SHLSRDRHGLQEPQH-----TRQSRNRYFRKSGR-----SL 521
DB 488 QGMPPVLGGNHPOQHSSQOQHQQHQQOQQOQQOQHQQOQQOQQOQQOQQOQQOQQO 547
QY 522 YVACNMQ-----FIDEEDWFEKQFPVPPPL-----RYREPVLEKFD-----562
DB 548 QVALMHTNNNSPPGSAHTSPQOALNLSPPNLTNKREREPTEPVPDQDDKRV 607
QY 563 -----SGLVNDVMCKPGPESDFCLAYE--AAVLGATPADSQHESQHGGLDQDG 610
DB 608 QQPPPAKRVGSGLL-----PPGFANFYLNPHNNAVAAAAG---FHPHSMGHQDDAAS 658
QY 611 EARPALDGSAAALQPLLTHTKAGSPDMPDSCGYDVSVPSELPLMEG-----660
DB 659 EGEPEDD-----YAGEHTNTGSSNMDIDSEPOQ-----MNGHHHHTHLD 701

QY 661 LSTDQTETSLTESVSSSGLGEEEPALPSKLLSSGCKADLGCKRSTYDE 711
DB 702 KSODSAIENSPTTSTTGGSVGHRHSSPVSTK--KKGAKPOSGGKDLFTE 750

Search completed: May 19, 2003, 09:25:25
Job time: 38:5067 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 19, 2003, 09:08:53 ; Search time 14.5787 Seconds
(without alignments)
2042.709 Million cell updates/sec

Title: US-09-912-157-2_COPY_36_753.

Perfect score: 3829

Sequence: 1 ADTCGNKAAARPLCVAN.....CADLGRSYTDELHVAFL 718

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	310	8.1	866	1 I17R_HUMAN	Q96f46 homo sapien
2	306	8.0	864	1 I17R_MOUSE	Q60943 mus musculus
3	135.5	3.5	502	1 I17S_HUMAN	Q9nm6 homo sapien
4	126.5	3.3	718	1 YSO2_CAEEL	Q10128 caenorhabdi
5	110.5	2.9	499	1 I17S_MOUSE	Q91ip3 mus musculus
6	110	2.9	592	1 STB3_MOUSE	Q60770 mus musculus
7	109	2.8	998	1 EPB3_HUMAN	P54753 homo sapien
8	104	2.7	1462	1 PTP6_DROME	P16620 drosophila
9	103.5	2.7	663	1 RGP2_HUMAN	P47736 homo sapien
10	102	2.7	859	1 ABR_HUMAN	Q12979 homo sapien
11	101	2.6	1275	1 GNRP_HUMAN	Q13972 homo sapien
12	99.5	2.6	794	1 E151_MOUSE	Q60821 mus musculus
13	99	2.6	783	1 ZFY2_MOUSE	P20662 mus musculus
14	98.5	2.6	970	1 PSU1_YEAST	P53550 saccharomyc
15	98.5	2.6	1050	1 EK5B_CHLPN	Q92797 chlamydia p
16	98	2.6	820	1 CTNB_TRIGR	P35223 tripneustes
17	97.5	2.5	1845	1 Z236_HUMAN	Q9ul36 homo sapien
18	97	2.5	984	1 EPB1_RAT	P09759 rattus norv
19	96.5	2.5	746	1 ABL_MLVAB	P00521 abelson mur
20	96	2.5	424	1 MK09_HUMAN	P45984 homo sapien
21	96	2.5	660	1 HT31_ARATH	Q04936 arabidopsi
22	96	2.5	902	1 EPBB_XENLA	Q91736 xenopus lae
23	96	2.5	984	1 EPB1_CHICK	Q07494 gallus gall
24	96	2.5	1114	1 E2K3_MOUSE	Q92285 mus musculus
25	95	2.5	828	1 CAN_DROME	Q11002 drosophila
26	95	2.5	933	1 PRGR_HUMAN	P06401 homo sapien
27	95	2.5	1036	1 AXOL_CHICK	P28685 gallus gall
28	94.5	2.5	351	1 RM14_CAEEL	P20271 caenorhabdi
29	94.5	2.5	770	1 GITI_RAT	Q92272 rattus norv
30	94.5	2.5	841	1 IE63_MCNVS	Q69154 murine cyto
31	94.5	2.5	1011	1 M3K6_HUMAN	Q95382 homo sapien
32	94	2.5	984	1 EPB1_HUMAN	P54762 homo sapien
33	94	2.5	2044	1 SIF2_DROME	P91620 drosophila

34	94	2.5	2064	1 SIFL_DROME	P91621 drosophila
35	93.5	2.4	806	1 RMIL_CHICK	Q04982 gallus gall
36	93.5	2.4	807	1 RMIL_COTJA	P34308 coturnix co
37	93.5	2.4	901	1 A180_MOUSE	Q61348 mus musculus
38	93.5	2.4	915	1 A180_MOUSE	Q05140 rattus norv
39	93	2.4	429	1 EPC_RAT	P01855 rattus norv
40	92.5	2.4	347	1 SH33_MOUSE	P01855 rattus norv
41	92.5	2.4	548	1 IDD_MOUSE	P98154 mus musculus
42	92.5	2.4	684	1 FBL1_CHICK	Q73775 gallus gall
43	92.5	2.4	830	1 JIP2_MOUSE	Q9ere9 mus musculus
44	92.5	2.4	993	1 EPB3_MOUSE	P54754 mus musculus
45	92.5	2.4	2314	1 PTP2_HUMAN	P23471 homo sapien

ALIGNMENTS

RESULT 1					
I17R_HUMAN					
ID	I17R_HUMAN	STANDARD	PRT	866 AA	
AC	Q96f46:Q03844				
DT	15-JUN-2002 (Rel. 41, Created)				
DT	15-JUN-2002 (Rel. 41, Last sequence update)				
DE	Interleukin-17 receptor precursor (IL-17 receptor).				
GN	I117R				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RA	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=R-cell;				
RX	MEDLINE=98035683; PubMed=9367539;				
RA	Yao Z., Spriggs M.K., Derry J.M.J., Strockbine L., Park L.S.,				
RA	VandenBos T., Zappone J., Painter S.L., Armitage R.J.;				
RT	Molecular characterization of the human interleukin (IL)-17				
RT	receptor.				
RL	Cytokine 9:794-800(1997).				
RP	[2]				
RA	SEQUENCE FROM N.A.				
RC	TISSUE=uterus;				
RA	Strausberg R.;				
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.				
CC	-!- FUNCTION: Receptor for IL17. Binds its ligand with low affinity,				
CC	suggesting that additional components are involved in IL17-induced				
CC	signaling.				
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).				
CC	-!- TISSUE-SPECIFICITY: Widely expressed.				
CC	-!- PTM: Glycosylated.				

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or send an email to license@isb-sib.ch).					

EMBL; U58917; AAB99730.1;					
DR EMBL; BC011624; AAB11624.1;					
Genew; HGNC:5985; I117R.					
DR MIM; 605461;					
DR KX	Receptor; Transmembrane; Signal; Glycoprotein.				
FT SIGNAL	1	31	POTENTIAL.		
FT CHAIN	32	866	INTERLEUKIN-17 RECEPTOR.		
FT DOMAIN	32	320	EXTRACELLULAR (POTENTIAL).		
FT TRANSMEM	321	341	POTENTIAL.		
FT DOMAIN	342	866	CYTOPLASMIC (POTENTIAL).		
FT DOMAIN	810	818	POLY-GLU.		
FT DOMAIN	49	49	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT CARBOHYD	54	54	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT CARBOHYD	206	206	N-LINKED (GLCNAC. . .) (POTENTIAL).		

FT CARBOHYD 225 N-LINKED (GLCNAC. . .) (POTENTIAL)
 FT CARBOHYD 242 N-LINKED (GLCNAC. . .) (POTENTIAL)
 FT CARBOHYD 265 N-LINKED (GLCNAC. . .) (POTENTIAL)
 FT CONFLICT 367 V -> A (IN REF. 1)
 FT CONFLICT 580 H -> R (IN REF. 1)
 SQ SEQUENCE 866 AA; 28330BED2303B0C9 CRC64;
 Query Match 8.1%; Score 310; DB 1; Length 866;
 Best Local Similarity 23.1%; Pred. No. 6.4e-16;
 Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;
 QY 34 NITFKYDNC--TYTLPNPKGVKVIADQNTIT-----ISOTACHDQ-----VAVTILMS 78
 Db 49 NCTVKNSTCLDSDWHP-----RNLTSPSPKDLQIQCFHARTOQDGLFPAVLEWT 99
 QY 79 -PGALGIEFLKGFVILEELKSGROCOOLILKDPKLNLSFKTKGMSOPFLNMPED 137
 Db 100 LQTDASILYLEGAELSVLQNTWNLQVR--FEFLSKLHHRWRRTFFSHV-VDPDQE 156
 QY 138 IFYKV--VPPFSIKNESYHFFTRACDQLLOPDNLACK---PFWKPRNL-----184
 Db 157 YEYVHLGPKIPDGDPHNOSKPLVDPDEHAKMVTTPCMSGSLNDP-NITVETLEAH 215
 QY 185 -----NLSQSGDMQVSOFAHNFNGFRFFYLHYKLKHEGPFKRTCKOQOTETT 235
 Db 216 QLRVSTLWNESTHVQILLTSPFMENHSCFEHR-HIPAPRPEEFHORSNVTLLRNLK 274
 QY 236 SCLLQVSPGDYIIEVDVT---NTRKVMHYALFVSPHAGIPRAVATVPLVVISAP 292
 Db 275 GCRQVQIQFFSSCLNCLRLRSATVSCPEMPDPPEIPDYNLWYVITGISILVG 334
 QY 293 ATLFTVCKKQOENIYSHLDESSSTYTAALPRERLRP-----KVELCSKSDGON 348
 Db 335 SVILLTVMTRLAGPSG---EKYSOTYTKDGLPDLPLPKPRKWIYSA-DHPL 390
 QY 349 ENNVOCFAIFLODPCCEVALDWEFSLCREGQENV---LQTHESQFLLVCSRG 404
 Db 391 YDVVLKFAQLFACTEVALDLLEQALISAGVWYWGKQKQENVESKSLVLCVCSRG 450
 QY 405 MYFVDKMYKHGGG-----RSGKGELFVAVSAIAEKLRQAKQSSAALSKFTA 456
 Db 451 TR-----AKWQALLGKAPVRLCRDHGKPGVDLFTAAHMLPDKR-----PACFGTYV 501
 QY 457 VTF-DYSCGQVPGTDLSTKYRLMDNLPLQCSLHSDHGLQFPGQHTROG---SRRTVF 513
 Db 502 CYFSEVSCDGVDPDLFGAAPRYPLNDREFV--YFRIDLEMTQPGRMHVRGELSGDNL 559
 QY 514 RSKGSLYVAICNKHQFIDEEPDWFE-----KQVPPHPPPLRYEPVLEKFDGSL 565
 Db 560 RSPGGRQLAALDRFQVHCDFMFCENLYSADDQAPSLDEEV-FEFLPLPP-GTGI 617
 QY 566 VLNDVCKPGPESDFCLKVAAYLGAATGAPDSQHE-----SOHGG 605
 Db 618 VKRAPLVRE-PSQACLAIDPLVGEAGAAVAKLEPHLQPGQAPQPLFTVLAAECA 676
 QY 606 LQDCEAPALDGA---ALQ-----PLLETVKAGSDMPDPSGIYDSVPSSELSLP 656
 Db 677 LVANVEPLADGAURLAAGEACPLIGSGAG-----RNSVLF-----LPVDPEDSP 727
 QY 657 LMBSLSTQOTETSSLSVSSSGSLGEEPPALPSKLLSSGSKADLGC 705
 Db 728 L-GSSTPMSPDILLPEVDR-----EHLEGLMLSLFEOSLSCQAQGC 768

RESULT 2

IL17R_MOUSE
 ID IL17R_MOUSE
 AC 060943;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-17 receptor precursor (IL-17 receptor).
 GN IL17R.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymic lymphoma;
 RX MEDLINE=3611968; PubMed=877726;
 RA Yao Z., Fanslow W.C., Seidlin M.F., Rousseau A.M., Painter S.L.,
 RA Comeau M.R., Cohen J.I., Spriggs M.K.;
 RT "Herpesvirus Saimiri encodes a new cytokine, IL-17, which binds to a
 RT novel cytokine receptor".
 RL Immunity 3:811-821(1995).
 CC !- FUNCTION: Receptor for IL17. Binds its ligand with low affinity,
 CC suggesting that additional components are involved in IL17-induced
 CC signaling (By similarity).
 CC !- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC
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 CC
 CC EMBL; U31993; AAC52357.1;
 DR MGD; MGI:107399; IL17r.
 KW Receptor; Transmembrane; Signal; Glycoprotein.
 FT SIGNAL 1 31 POTENTIAL.
 FT CHAIN 32 864 INTERLEUKIN-17 RECEPTOR.
 FT DOMAIN 32 332 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 323 343 POTENTIAL.
 FT DOMAIN 344 864 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 809 814 POLY-GLY.
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 206 206 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 225 225 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 308 308 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 864 AA; 97807 MW; 343FD51AA687DA31 CRC64;
 Query Match 8.0%; Score 306; DB 1; Length 864;
 Best Local Similarity 22.5%; Pred. No. 1.3e-15;
 Matches 189; Conservative 129; Mismatches 326; Indels 207; Gaps 42;
 QY 5 GWRM-----KAAARPL-----CVANSGVGPASRNSGLNITFKYDNCYTYLNPVKR 51
 Db 17 GWLLLLNLVAPGRASPRLLDFFAPVCAQEGLSGRVNSKSLDSDSWIHPNTPSPKNI 76
 QY 52 VIADAQNTISOTACHDOVAVT-ILWS-PCALGIEFLKGFVILEELKSGROCOQ---106
 Db 77 YI-----NLSVSTQGBELVPLVLENTLQTDASILYLEGAELSVLQNTWNLQVR 131
 QY 107 --LILKDPKOLNSGSPRTGMSQPFNLMKFTDYFVVPFPPSKIKESYHFFTRAC 164
 Db 132 LSLQHKRKMRFSEF-----SEFVVDPGQBYETVYVHLPKPIPDGDPNPKIIFVDP 185
 QY 165 D-----LLQPDNLACKPFWKPRNLNI-----SQH-----GSDMQV 195
 Db 186 EDSKMKMTSCVSSGSLNDP-NITVETLDTQHLAVDTFLANESTPYOVLESFSDSEHS 244
 QY 196 SFD-----HAPNFGFRFFYLHKLKHE---GPFRTCKOQOTETTSCIL 239
 Db 245 CFDVVKQIPAPROEERQANVTFTLSKFRHCCHEHVVQVQPF-FSSCLND-----CLR 296
 QY 240 QNVSPGDYIIEVDVTNTRKVMHYALFV--HSP-WA-GPRAVATVPLVVISAPATL 295
 Db 297 HAVYVPCFVI-----SNTI-----VPRVADYIPLVWYGLIILAI-----LLVGSVIL 341
 QY 296 FTVCKRKKQOENIYSHLDESSSTYTAALPRERLRPFRKVELCSKSDGONENNVOC 355

Db 342 IICMWRSLGADQKHGDSKINGILPVLADLPPPLPR-KVAVITSA-DHPLVVEVLK 399
QY 356 FAYLQDFGCEVALDHEDESICRBOREWIQK-----IHESQIIVWCCKGKHYVDK 411
Db 400 FAQLITAGTCEVALDHEDESICRBOREWIQK-----IHESQIIVWCCKGKHYVDK 411
QY 412 KTKKHKGG-----GRSGKGEFLVAVSAIAELKRAKQSSAALSKEIAVIFYDI 461
Db 455 AKKALILWAEPVAVLGRCDHMKPAGDLFTAAAMMILPDKR-----PACFTVVCYFSG 509
QY 462 SC-EGDVGILDLSTKYELMDNLPOLCSHLSDHGLQERGO--HTQSGSRMYTFKSG 518
Db 510 ICSEVDLPDLNIRYPLMDREEV--YFRQDLEMFEGSMHVRHETGDMPLQSPSG 567
QY 519 RSLVIAICNMHGFIDEEPWFKEQFVFPHP-----PPLR---YREPVLEKFDGSLVNDVM 571
Db 568 ROLKEAVLRFQWQCPDPERENCLADQDPLSDIEVEFEDPLPP-GGGIVKQOPL 626
QY 572 CKGPESDPLAVAAVLGANGPADSOHSGGLDOD-----GEAR 613
Db 627 VRELPSDGLVVDVY-----SEESRMALDPLQVRELVAHTLQSNVLPABQV 677
QY 614 PALDGSAAOLPLHVVKAGSPDMP--ROS-----GIYDSV--PSSELSLPL----- 657
Db 678 PA---ARVPEPLPDGGAALPMTDESEACPLGVQRNSILCLPVDSDPLPACSTPM 734
QY 658 -----MEGLSTQDTSTSLTESVSSSGGEEEP-----ALPSKLLSSGSKADLG 704
Db 735 MSPDLQDAREQLSIALSVLQSLSGOPLESMPREVLGCTPSEERQSGVSDQG 794

RESULT 3
ID 117S HUMAN STANDARD; PRT: 502 AA.
AC Q9NR66; Q9NP20; Q9NRL4; Q9NR55;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Interleukin-17B receptor precursor (IL-17B receptor) (IL-17 receptor homolog 1) (IL-17Rhl) (IL17Rhl) (Cytokine receptor CRL4).
GN IL17B OR EVI27.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=20273223; PubMed=10815801;
RA Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A., Copeland N.G., Shalhoub J.D. Jr.;
RT "Evi27 encodes a novel membrane protein with homology to the IL17 receptor."
RL Oncogene 19:2098-2109(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF N-TERMINUS.
RX TISSUE=Lung;
RC MEDLINE=20317118; PubMed=10749887;
RA Shi Y., Ulrich S.J., Zhang J., Connolly K., Grzeszczewski K.J., Barber M.C., Wang W., Mathen K., Hodge V., Fisher C.L., Olsen H., Ruben S.M., Kuyavev I., Cho Y.H., Rao V., Wilkinson K.A., Carrell J.A., Ebner R.;
RT "A novel cytokine receptor-ligand pair. Identification, molecular characterization, and in vivo immunomodulatory activity."
RL J. Biol. Chem. 275:19167-19176(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Zhang W., Cao X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC Tissue=Cervix;
RA Strausberg R.;

Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
[5]
RN FUNCTION.
RX PubMed=11058597;
RA Lee J., Ho W.H., Maruoka M., Corpuz R.T., Baldwin D.T., Foster J.S., Goddard A.D., Vansura D.G., Vandien R.L., Wood W.I., Gurney A.L.;
RT "IL-17E, a novel proinflammatory ligand for the IL-17 receptor homolog IL-17Rhl."
RL J. Biol. Chem. 276:1660-1664(2001).
CC -1- FUNCTION: Receptor for the proinflammatory cytokines IL17B and IL17E. May play a role in controlling the growth and/or differentiation of hematopoietic cells.
CC -2- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1). Secreted (isoform 2).
CC -3- ALTERNATIVE PRODUCTS: 2 isoforms: 1 (shown here), and 2; are produced by alternative splicing.
CC -4- TISSUE SPECIFICITY: Expressed in several endocrine tissues, mostly in fetal and adult liver, kidney, pancreas, testis, colon, brain and small intestine; not detected in peripheral blood leukocytes, lymphoid organs, and most cell lines.
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CC
CC EMBL: AF208110; AAF86051.1;
CC EMBL: AF208111; AAF86052.1;
CC EMBL: AF212365; AAF87876.1;
CC EMBL: AF250309; AAK37428.1;
CC EMBL: BC000980; AAH00980.1;
CC GenBank: U00000; IL17B.
CC MIM: 605458;
KW Receptor; Transmembrane; Signal; Glycoprotein; Alternative splicing.
FT SIGNAL 1 17
FT CHAIN 18 502 INTERLEUKIN-17B RECEPTOR.
FT DOMAIN 18 292 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 293 313 POTENTIAL.
FT DOMAIN 314 502 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 67 67 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 103 103 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 283 283 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARSPLIC 250 288 LTPYPTGSGDCIRHKGTVVLCPTGVPPPLDNKSKPG
FT -> VKFSELGGHGRHLEFHHLSLLRNLSNALLPADT
FT S (IN ISOFORM 2).
FT VARSPLIC 289 502 MISSING (IN ISOFORM 2).
FT CONFLICT 6 6 L -> I (IN REF. 1).
FT CONFLICT 422 426 LFPLA -> SSPCL (IN REF. 2).
FT CONFLICT 427 502 MISSING (IN REF. 2).
FT CONFLICT 468 468 L -> F (IN REF. 1).
SQ SEQUENCE 502 AA; 55884 MW; CDB87586FAAE49CC CRC64;

Query Match 3.5%; Score 135.5; DB 1; Length 502;
Best Local Similarity 20.1%; Pred No. 0.008;
Matches 76; Conservative 49; Mismatches 141; Indels 113; Gaps 14;
QY 183 NLNISOGRSDMOVSF-----DHAPNFGFRFYLYLKHEGPFKRTK-----226
Db 143 NANNEDGPGSMVNFPTSPGCLDH-----INRYK-----KKCYAGSLWDPN 183
QY 227 -----KQOTTE-----TSCLLQNVSPGDYIELVDVNTTRKVMHYALKPVHSGFAGPIR 278
Db 184 IFACKNKEVEVNFPTPL-----GNRYMALIQHSYI-----IGSQVFPEHKKOT 231
QY 279 AVAITVPLVISAFATL-----FTVNCRKQKQENIYSHLDESSSS 320
Db 232 RASVIVPTGDSGATVLTPTFTGSGDCIRHKGTVVLC-----POTGVPPPLDNKSKPG 288

QY 321 TTAAAL-----PRELR-----PRPKVLCYSSKQGNHN 351
 DB 289 GHLPLLLSLVATVAVVAGIYLMWRHERIKKTSFTTLPLPKVLVVPSEICPH-- 346
 QY 352 VVQCFAYFLQPCCEVALDWFELSCREGORENVIOKIHESOFILVWCKGMKVFYDK 411
 DB 347 TICYTEFLQNECHSEVILEKWKKKIAENGVPWLAOKAAKDVVILSDNSVCDG 406
 QY 412 KYKKGGRSGGKGLFVLVAVSAIAEKLRQAKSSAALSFKFIATVTFDSCGSDVGL 471
 DB 407 TCGKSGSPSENQ-DLFFLAFLNFCSDLR-----SQIHLKHYVYVTFREIDTKDYNAL 460
 QY 472 DLSTYRLMDNLPCLSHL 490
 DB 461 SVCPRYHLMDATACAE 479

RESULT 4

XS02_CABEL STANDARD; PRT; 718 AA.
 ID XS02_CABEL
 AC Q10128;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Hypothetical 81.6 kDa protein F56D1.2 in chromosome II precursor.
 GN F56D1.2
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;
 OC Rhabditidae; Telodermidae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Chisoe S., Wilson R.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
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 CC
 CC EMBL; U39997; AAA81100.1;
 DR WormPep; F56D1.2; CE01970.
 KW Hypothetical protein; Transmembrane; Signal.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 718 HYPOTHETICAL PROTEIN F56D1.2.
 FT TRANSMEM 373 393 POTENTIAL.
 SQ SEQUENCE 718 AA; 81622 MW; 4289E056288417AA CRC64;

Query Match 3.3%; Score 126.5; DB 1; Length 718;
 Best Local Similarity 20.6%; Pred. No. 0.065;

Matches 89; Conservative. 68; Mismatches 165; Indels 111; Gaps 20;

QY 280 VAITPLVVISAF-----TLTVWCKKQENIYSHLDESSSESTYTAALPRERLRP 333
 DB 375 IAVVLLILLIIVLAVTGFVLMRDKVRGVRNI-----ALTE 413
 QY 334 RKPKVLCYSSKQGNHNHVQCFAYFLQPCCEVALDWFELSCREGORENVIOKIH 393
 DB 414 FVKVMIVYAD-DNDLFTDCKVLKLVENLRNCASCDPVFDEKLITAEIVPSRLVDQISS 472
 QY 394 SFIIVVCKGMKVFYDKKKYKKGGRSGGKGLFVLVAVSAIAEKLRQAKSSAALS 453
 DB 473 LAKFIIVVSDCAEKILDTASETHQLVQARPFADLFGPAMENI---IRDTATHNFPPEAR 529
 QY 454 FIATVFDSCGSDVP-----GILDSTYRLMDNLPCLSHLSDHSDHGLQPCQTRGSR 510
 DB 530 YAVVRENTS--PHVPPNLAAILNLPT-FILPEQPAQLTAFLNVEH-----TERA 575

QY 511 NYFRSKSGRSLY---VAICNNHQFIDEEDWFKQFVP-----PHPPRLRYREPVLEKF 561
 DB 576 NVTONTSEAGIHEWNLCASSNNMSFFVRNPWMLSTRKPKDELAAALF---LKRQSPVIVPI 632
 QY 562 DSGVLNDVWCKPGPSDFCLAVAAVLGATGPADSOHESOHGGLDODGEARPLDGSAA 621
 DB 633 QT-----EED---RIASIKYLVPPQALVDS-----DED-----DVD 663
 QY 622 LQPLLVKAGSPDM--PROSGIYDVSPPSELSELSPLMEGLSTQDTQTSSTESVSSSS 679
 DB 664 LQP---HASHQNPILLPPQCG-----PDS-----SDSESSSESESDNE 706
 QY 680 GLGEEPPALPSK 692
 DB 707 G---EDPKTIWK 716

RESULT 5

IL17_MOUSE STANDARD; PRT; 499 AA.
 ID IL17_MOUSE
 AC Q9JIP3; Q9JIP2;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-17B receptor precursor (IL-17B receptor) (IL-17 receptor
 DE homolog 1) (IL-17Rh1) (IL17Rh1) (IL-17ER).
 GN IL17BR OR EVI27.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC MEDLINE-2073223; PubMed-10815801;
 RA Tian E., Sawyer J.R., Largespada D.A., Jenkins N.A., Copeland N.G.,
 RA Shaughnessy J.D. Jr.;
 FT *EVI27 encodes a novel membrane protein with homology to the IL17
 FT receptor.
 RL Oncogene 19:2098-2109(2000).
 CC -1- FUNCTION: Receptor for the proinflammatory cytokines IL17B and
 CC IL17E. May play a role in controlling the growth and/or
 CC differentiation of hematopoietic cells.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
 CC Secreted (isoform 2).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Liver and testis. Expressed at lower level in
 CC kidney and lung. Expressed in selected T-cell, B-cell and myeloid
 CC cell lines.
 CC -1- MISCELLANEOUS: EVI27 is a common site of retroviral integration in
 CC BXH2 murine myeloid leukemias, localized near the IL17BR gene.
 CC Proviral integrations result in increased expression of IL17BR on
 CC the cell surface.
 CC
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 CC
 CC EMBL; AF708108; AAF86049.1;
 DR EMBL; AF708109; AAF86050.1;
 DR MGD; MGI:1355292; IL17Br.
 KW Receptor; Transmembrane; Signal; Glycoprotein; Alternative splicing.
 FT SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 499 INTERLEUKIN-17B RECEPTOR.
 FT DOMAIN 18 286 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 287 307 POTENTIAL.
 FT DOMAIN 308 499 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 67 67 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 103 103 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 156 156 N-LINKED (GLCNAC...) (POTENTIAL)
 FT CARBOHYD 197 197 N-LINKED (GLCNAC...) (POTENTIAL)
 FT VARSPLIC 163 218 LNEWMYKQCTEAGSLMDPDITACKKEMVENVETTPPL
 FT GNYTILIDQNTILG -> TRENTETVSGVFPKAKGQALRI
 FT SAPPILOFPGGPDSVILPPQPLASLEHDFVKLT (IN
 FT ISOFORM 2)
 FT VARSPLIC 219 499 MISSING (IN ISOFORM 2)
 SQ SEQUENCE 499 AA: 55617 MW: 66440430E3C31F3 CRC64;

Query Match 2.98; Score 110.5; DB 1; Length 499;
 Best Local Similarity 24.18; Pred No 0.67;
 Matches 40; Conservative 27; Mismatches 82; Indels 17; Gaps 4;

QY 320 STTALPRERLRPRKPVLYCYSSKQGNENNVYQCFVPLQDFGCVVALDMEFSLC 379
 DB 314 STATSPITMLLPKIRLVLYPSEICFHH--TVCRFTDFLQNYCRSEVILKQKKIA 371
 QY 380 REGQREWVQKTHESOFIIVVCSKGMFYVDKKNYKHGSGKSGELFLVAVSALAEK 439
 DB 372 EMPGVQWATQKQADKVVELLPDSVPLCDSDAGHNEGSAENSO-DLFLAFLNLCSD 430
 QY 440 LRQAKOSSSNAISKEIATVDEYSGEDVPGILDLSTKYRLMDNLPO 485
 DB 431 F-----SSQTHLKLIVL-----GGADLGDYNALSYCPO 462

RESULT 6
 ID STB3_MOUSE STANDARD; PRT; 592 AA.
 AC 060770;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Syntaxin binding protein 3 (UNC-18 homolog 3) (UNC-18C) (MUNC-18-3).
 GN STXB3 OR UNC18C.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95197608; PubMed=7890715;
 RA Teliam J.T., McIntosh S., James D.E.;
 RT "Molecular identification of two novel Munc-18 isoforms expressed in
 non-neuronal tissues";
 RL J. Biol. Chem. 270:5857-5863(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE=Brain;
 RX MEDLINE=96421662; PubMed=8824310;
 RA Gengyo-Ando K., Kitayama H., Mukaida M., Ikawa Y.;
 RT "A murine neural-specific homology corrects cholinergic defects in
 Cenorhabditis elegans unc-18 mutants";
 RL J. Neurosci. 16:6695-6702(1996).
 CC -1- TISSUE SPECIFICITY: DBIQUITOUSLY EXPRESSED.
 CC -1- SIMILARITY: BELONGS TO THE STXB/UNC-18/SEC1 FAMILY.
 CC
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 or send an email to license@sib-sib.ch).
 CC
 CC ENBL: U19521; AAA69913.1;
 DR ENBL: D30798; BAA19478.1;
 DR MED: MG1:107362; Stxbp3.
 DR InterPro: IPR001619; Sec1-like.
 DR Pfam: PF00995; Sec1; 1.
 RW Protein transport.
 SQ SEQUENCE 592 AA: 67942 MW: 7874871DE107871A CRC64;

Query Match 2.98; Score 110; DB 1; Length 592;
 Best Local Similarity 18.58; Pred No 0.92;
 Matches 93; Conservative 64; Mismatches 157; Indels 188; Gaps 22;

QY 286 LVVISAFATLFTVCRKQKQ-----ENYSHLDRESSSTYTAALPRRLRPRK 336
 DB 34 IMLDEFTKLSSCKMTLLEGGITVIENYKRNREPVRQMKALYF-----ISPTK 86
 QY 337 VFLCYSSKQGNENNVYQCFVPLQDFC-----GCE----- 367
 DB 87 SVDCFLRDFGSKSEKTKAAIYFTDCPDLSFNKIKASCSIRCKEINISFIQESQ 146
 QY 368 -VALDMEFSLC-----REGQREWVQKTHESOFIIVV-----SKGMK 407
 DB 147 VTTLDVDPAFYCYSPDSNASRKYVMEAMAQ--IVTVCATLDENGVRYKSKPLDNA 204
 QY 408 -----FVQKK--NYK--HKGGRGSGKGEFLV-----AVSALAEKLRQAKOSSSAA 452
 DB 205 SKLAQLVEKLEDYKIDKGLKNGTOSQLIIDRGDPVSTVLEH----- 252
 QY 453 KETATVFD-----YSCGG-DYVPGIL-----DLSTKYR-----LMDNLPLQCSL 491
 DB 253 TQAMAYDLPIENDTYKTDGKEKENVLEDDDLVVRHRHNAVLEIFPKMKES 312
 QY 492 SRDHGLQEPGQTRGSGRRNYFRSKGRSLYVAICNMHOFIDEEPDMFEKQVFFHPPL 551
 DB 313 STK-----KATEGTSLSALTQAKKMPHFQKQISKQV-----HL 348
 QY 552 RYREPVLKFP-----DSGLVNDVMCKPGSPDCLKVE 585
 DB 349 NLAEDCMKFKLNIETKCTEODLAUGTDAEGORVDSMLVLLPVLL--KNHEDNCKIR 406
 QY 586 AAVLGATGADSDQSHSGGLDGDGEARFALOGSAAALPPLLETVAAGSPDMPD-SGIY 644
 DB 407 AVLLYIFGNGTTEEN-----LDRLTHNVKIEDSDMRNWSHLG 446
 QY 645 DSVSPSSLSPLMEGLSTQDT 666
 DB 447 VPIVPPSQAKPLRKRSABET 468

RESULT 7
 ID EPB3_HUMAN STANDARD; PRT; 998 AA.
 AC P54753;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ephrin type-B receptor 3 precursor (BC 2.7.1.112) (Tyrosine-protein
 kinase receptor HEK-2).
 DE EPB3 OR ETK2 OR HEK2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=93390963; PubMed=8397371;
 RA Boehme B., Holtrich U., Wolf G., Luzius H., Grzeschik K.-H.,
 Striebhardt K., Ruesamen-Waigmann H.;
 RT "PCR mediated detection of a new human receptor-tyrosine-kinase, HEK
 2";
 RL Oncogene 8:2857-2862(1993).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. BINDS TO
 EPHRIN-B1 AND -B2.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 tyrosine phosphate;
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN

RECEPTOR SUBFAMILY

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EMBL: X75208; CAAS3021.1;
 BSSP: P29223; I94F;
 Genew: HGNC:3394; EPHB3
 KIM: 601839;
 InterPro: IPR001090; Ephrin_receptor.
 InterPro: IPR000719; Euk_pkinase.
 InterPro: IPR003961; FNIII.
 InterPro: IPR003962; FNIII_repeat.
 InterPro: IPR001660; SAM.
 InterPro: IPR001245; Tyr_pkinase.
 InterPro: IPR001426; Tykase_receptor.
 Pfam: PF00041; fn3; 2.
 Pfam: PF00069; pkinase; 1.
 Pfam: PF00536; SAM; 1.
 Pfam: PF01404; EPH_Ibd; 1.
 PRINTS: PR00014; FNTYPEIII.
 PRINTS: PR00109; TYRKINASE.
 ProDom: PD000001; Euk_pkinase; 1.
 ProDom: PD001495; Ephrin_receptor; 1.
 SMART: SM00060; FN3; 2.
 SMART: SM00454; SAM; 1.
 SMART: SM00219; TYKIC; 1.
 PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 PROSITE: PS00102; SAM_DOMAIN; 1.
 Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 33
 FT CHAIN 34 998
 FT DOMAIN 34 559
 FT TRANSMEM 560 580
 FT DOMAIN 581 998
 FT DOMAIN 199 336
 FT DOMAIN 337 448
 FT DOMAIN 449 544
 FT DOMAIN 633 896
 FT DOMAIN 925 989
 FT SITE 996 998
 FT NP_BIND 639 647
 FT BINDING 665 665
 FT ACT_SITE 758 758
 FT MOD_RES 608 608
 FT MOD_RES 614 614
 FT MOD_RES 792 792
 FT MOD_RES 942 942
 FT CARBOHYD 351 351
 FT CARBOHYD 445 445
 SQ SEQUENCE 998 AA; 57C82C397CC61103 CRC64;
 Query Match 2.8%; Score 109; DB 1; Length 998;
 Best Local Similarity 18.9%; Pred. No. 2.3;
 Matches 157; Conservative 122; Mismatches 301; Indels 250; Gaps 42;
 QY 1 ADTCGRWKAARPRIC-----VANEGVGA-----SRNSG-----LYNITERY 39
 DB 268 ACTCATGHEPAKESQCPGPGYKAGQGPCLPCPPNSRTTSPASICTCHNNEYRA 327
 QY 40 DN-----CTTLPNPKVGHVIAQNTISQYACHQDVNTILMS-PGALGIEFLKGRV 92
 DB 328 DSDSADSACTVPSF-PRGVSNV-----NETSLILENSEPRDUGVRDILLNV 375

QY 93 ILEELASEG-----ROCOOLILKDPKQLNSFKRTGHSQPLNKKFDTFVKKVFPFS 147
 DB 376 ICKKCHGAGASACSDNDNVEFVPRGLSEPRVTS-----HLLATRTTFFVQVANG 430
 QY 148 IKNESYHPPFTRACDILLQPNLACKPFWKPRNLNLSOHSQDMOVSFDAHPENGF 207
 DB 431 VSGKSLPPRYAANVTITNOARPEV-----PTLEHSSGSGSLTISWAPPRNG-- 481
 QY 208 FFLYHKLKHEGF-KRTCKOQETTTSCLLQNVSP-GDYIIELVDVDTTTRVRYHYA 265
 DB 482 VILDYEMK--FEKSEGIATSTVSQNSVOLDGLRDPARIYVQV-----RARTVAGIG 532
 QY 266 -LKPVH---SPWAGPIRAVAITVPLVVISATNL-----FTVMCRKQCOENIYSH 311
 DB 533 QYSEPAFEFTTSESGACQLOEOLPLIVGSATAGLVFVAVVIAIVCLRKQRH----- 587
 QY 312 LDESSSESTYTAALPRELRPRPVFLCYSSKDGQNNHNVQCFAYFLQDFC-GCEVAL 370
 DB 588 -----GSDSEYTEKL-QQYIAPGMKVIIDFTYEDPN--EAVREFAKEIDVSCVKIEVI 639
 QY 371 DLWEDFSLCREGQREWVIOKIHESQFIIVVCSKGMKFFVKKNYKHKGSGSGKGELEL 430
 DB 640 GAGEGEVCR-----GRLKQPGRRVEF- 661
 QY 431 VAVSAI-----AEKLKQKSSSNAISLFIAYVYDSCGDVPGILDLS-----TKYR----- 478
 DB 662 VAIKTLKVGTYERQRDFLSEASINGQF-----DHPNIIRLEGVTKRPRVAIL 710
 QY 479 --LADNLPQLCSHLHSRDRGLQEPQGT-----RQSSRNT-FRKSGRS 520
 DB 711 TEFMENC-ALDSFLRND-----GQFTVQLVCLMGLGIAAGMKVLSMNTVHRDLAARN 763
 QY 521 LYV---AIC-----NMHOFIDEEPWFQKQVPPHP-----PLRYREP---VLEKFD 563
 DB 764 ILVNSNLVCKVDFGLSRLEDDPS-----DPTYSISLGGKIPINWAPAIATFAS 817
 QY 564 -----GLVINDVCKPGPESDFCLKVEAVLGATGADPADSOHSGHGLDGDGEARPAL 616
 DB 818 ASDVNSYGIYVMEVNS-----YGERPYNDMSQDVINAVQDRLPPLPPM 861
 QY 617 DGSAAQLPILHTKAGSPDMPDSGIYDS-----SVPSSELSLPLMGLS 662
 DB 862 DCPALHQLMLDCWVEDRNLKPKESQIVNTLDKLIRNAASLVASQSGSQPILORTV 921
 QY 663 TDQTESSLSYSSSSGGLGEEPPALPSKLSGSGCKADLCGRSTDEL 712
 DB 922 PDYITFTTVDGLDAIK-MGRYK-----ESFVSAGFASFDLVAQMTAEDL 965
 RESULT 8
 ID PTP6_DROME STANDARD; PRT: 1462 AA.
 AC P15620;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protein-tyrosine phosphatase DTP precursor (EC 3.1.3.48) (Protein-tyrosine-phosphate phosphohydrolase).
 GN PTP9D OR DPTP
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid:7221;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE-90046860; PubMed-2554325;
 RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;
 FT "A family of receptor-linked protein tyrosine phosphatases in humans and Drosophila."
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).
 CC -!- FUNCTION: IT IS POSSIBLE THAT DTPP IS A CELL ADHESION RECEPTOR.

CC - SUBCELLULAR LOCATION: Associated with Golgi membranes
 CC - TISSUE SPECIFICITY: Significant expression seen in the brain,
 CC kidney and pancreas. Abundant in the cerebral cortex and expressed
 CC at much lower levels in the spinal cord. Not detected in the
 CC lymphoid tissues.
 CC - INDUCTION: By 12-O-tetradecanoylphorbol-13-acetate (TPA) in
 CC promyelocytic HL-60 cells.
 CC - SIMILARITY: CONTAINS 1 RAP/RAN-GAP DOMAIN.
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: M64788; AAA60252.1;
 CC Genbank: HGNC:9858; RAPICAL.
 CC MIM: 600278;
 CC InterPro: IPR003109; GTPase_LGN.
 CC InterPro: IPR000331; Rap_GAP.
 CC Pfam: PF02145; Rap_GAP; 1.
 CC Pfam: PF02188; Goloco; 1.
 CC SMART: SM00390; Goloco; 1.
 CC GTPase activation; Membrane.
 CC FT DOMAIN 210 397
 CC RAP/RAN-GAP.
 CC SEQUENCE 663 AA; 73391 MW; 3703B7CC603404DA CRC64;
 CC
 CC Query Match
 CC Best Local Similarity 2.7%; Score 103.5; DB 1; Length 663;
 CC Matches 143; Conservative 80; Mismatches 262; Indels 247; Gaps 33;
 CC
 CC 132 MFPEYDFYKVPSPKSNESNHPFFTRACDILLQPD----- 171
 CC 21 LATEEDY-----IPFSP-----HEVIGREGPFLLPQGGWIGSTNHTSIPETE 70
 CC
 CC 172 -----NLACKP-----FWKPRNLNISQHSQDMQVSDHAPHNFGFFYLHYK 214
 CC 71 PQSPPTTKVKLECNPTARIYKHFLEKHEFN-----YYSLOTA-----LGLVFLSKYD 119
 CC 215 L-----KHGPFKRTKQEQTTTSCLLQNSPGDIIEIWDNDTNRKVMYALKPVH 270
 CC 120 VIGDQELHLLKRYEDYVIPSCLTEFPNVQMAKLYCEDVYDR-----FYPVL 173
 CC 271 SPWAGPIRAVITPLVVIS---AFATLFTVMCRKKQENIYSHLDESSSESTYTAALP 327
 CC 174 YPKAS---RLIVTFDEHVISNNFKGVYQKLGOTSEB-----LFTNEESPAFYEFLE 225
 CC 328 RERLRPRKRVFLCYSSKDGQNNHNVQCEAYFLQDFCEVALDLWE-----DFSLCR-- 380
 CC 226 -----FLQKVR-----LQDFKGRGLDVTGOTGVTSVCNFR 260
 CC 381 -----EGRENVQKTHESQFIIVCSKGMFYVDK-----KNYK 415
 CC 261 NKEIMFHVSTKLPTEDDAQOLKRRHIGNIVAV-----VFQDENTFPVPMIASNPL 314
 CC 416 H-----KGGRGSGGELFLVAVSAIAE-----KLKQAKSSSAALESKFTA 456
 CC 315 HAVVVVQAEQGG---PDGPLYKVSITARDVFPFGPPLDPDAVFKGPEQFEFLKLLN 371
 CC 457 VTFDFSC-EGDVFGILDSLYKRLMDNLQCLSHLSRD-HGLQEPQGHTRQGRNRYF- 513
 CC 372 A-ETACYKAERFAKLEERTRALLETLYEEL-HHSQSMGLGGEDKMGSGGGGFF 428
 CC 514 -----RSKSGSL-----YVACNMQHFDSEPWFE-----KQFVFPFPPPLR 552
 CC 429 ESKRVIRSRQSDAMGLSNKKPNTVSTSHSGSPAPNPNPLAKAAGISLIVPGKSPTRK 488
 CC 553 YREPVLERFDSGLVLDVCKPFGPESDFCLKVEAVILGATGPADSOHESQHGILDQGEA 612
 CC 489 KSGPFGSRSSAIGIENI-----QEVQKRESPPAGKQTP-DSGHVSOEPKSE----- 535

QY 613 RPALDSSAALQPLHTVTRKAGSPDMRDSGIYDSSVPSSELS-----LPLMEGLSTQOTE 667
 DB 536 ---NSTOSSPMPPTTKNRATTAQRAEALKDFSRSSSSASSFASVVEYETEGVDGTG 591
 QY 668 TSS-----LTSVSSSSG-----LGEPEPALPSKL 693
 DB 592 LESVSSGTPPHKDSFIKSTWLEDSVYITGSGSPGSPSPHDPACKLGDPAPEIKQL 651
 QY 694 LSGSCCKADLGC 705
 DB 652 EASQHPQLGC 663
 RESULT 10
 ABR_HUMAN STANDARD; PRT; 859 AA.
 AC Q12979; Q13693; Q13694;
 DT 15-JUL-1999; (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Active breakpoint cluster region-related protein.
 GN ABR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Hippocampus;
 RX MEDLINE-94086546; PubMed-8262969;
 RA Tan E.-C., Leung T., Manser E., Lim L.;
 RT "The human active breakpoint cluster region-related gene encodes a
 RT brain protein with homology to guanine nucleotide exchange proteins
 RT and GTPase-activating proteins."
 RL J. Biol. Chem. 268:27291-27298(1993).
 RN [2]
 RP SEQUENCE OF 39-859 FROM N.A. (LONG AND SHORT FORMS).
 RC TISSUE-Fibroblast;
 RX MEDLINE-93352461; PubMed-8349582;
 RA Heisterkamp N., Kaartinen V., van Soest S., Bokoch G.M., Groffen J.;
 RT "Human ABR encodes a protein with GAPrac activity and homology to the
 RT DBL nucleotide exchange factor domain."
 RL J. Biol. Chem. 268:16903-16906(1993).
 RN [3]
 RP SEQUENCE OF 436-597 FROM N.A.
 RX MEDLINE-90067847; PubMed-2587217;
 RA Heisterkamp N., Morris C., Groffen J.;
 RT "ABR, an active BCR-related gene."
 RL Nucleic Acids Res. 17:8821-8831(1989).
 CC - FUNCTION: GTPASE-ACTIVATING PROTEIN FOR RAC AND CDC42. PROMOTES
 CC THE EXCHANGE OF RAC OR CDC42-BOUND GDP BY GTP, THEREBY ACTIVATING
 CC THEM.
 CC - ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM. ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC - TISSUE SPECIFICITY: HIGHLY ENRICHED IN THE BRAIN. MUCH WEAKER
 CC EXPRESSION IN HEART, LONG-AND-MUSCLE.
 CC - SIMILARITY: CONTAINS 1 DBL-HOMOLOGY (DH) DOMAIN.
 CC - SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC - SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC - SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.
 CC - SIMILARITY: STRONG. TO HUMAN BCR.
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 CC
 CC EMBL: U01147; AAC50063.1;
 CC EMBL: L19704; AAC37519.1;
 CC EMBL: L19705; AAC37518.1; ALT_INIT.

DR Genew: HGNC:81; ABR.
 DR MIN: 600365;
 DR InterPro: IPR000008; C2;
 DR InterPro: IPR001331; GDS_CDC24.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR000198; RhoGEF.
 DR InterPro: IPR000219; RhoGEF.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00169; PH; 1.
 DR Pfam: PF00620; RhoGAP; 1.
 DR Pfam: PF00621; RhoGEF; 1.
 DR SMART: SM00233; C2; 1.
 DR SMART: SM00233; PH; 1.
 DR SMART: SM00324; RhoGAP; 1.
 DR SMART: SM00325; RhoGEF; 1.
 DR PROSITE: PS00004; C2_DOMAIN_2; 1.
 DR PROSITE: PS00010; DL2; 1.
 DR PROSITE: PS00741; DL1; 1.
 DR PROSITE: PS50003; PH_DOMAIN; 1.
 DR Guanine-nucleotide releasing factor; Alternative splicing.
 KW DOMAIN 91 284
 FT DOMAIN 301 459
 FT DOMAIN 463 595
 FT DOMAIN 661 805
 FT DOMAIN 417 420
 FT VARSPLIC 1 82

DR CONFLICT 67 67
 DR CONFLICT 657 660
 DR CONFLICT 761 761
 DR SEQUENCE 859 AA; 97696 MW; 9FD50CD54FA99483 CRC64;
 SQ

Query Match 2.7%; Score 102; DB 1; Length 859;
 Best Local Similarity 20.5%; Pred. No. 6.4;
 Matches 117; Conservative 57; Mismatches 190; Indels 208; Gaps 25;

QY 81 ALGIEFLGPR---VILELSEKSGRQCOOL--ILKDPKOLNSFSKRTGMSQPLNM-K 133
 DB 80 APGVAGAGLEMRKLVLGSLGFLASEEYIINLEALLPMKPL---KATATTSPQVLTIQ 135

QY 134 PTDYFVYVPPFPIKSNESYHPFFRFRACDLLOPDNLACKPFWKPRNLNISQSGDM 193
 DB 136 IETIFY-----KIDIVIEHKFY-----DNLCPK-----VQOM--DS 166

QY 194 QVSFDHAPHNFG-----FRFFYLHYK-----LKHGEPFKRKC 226
 DB 167 QVTMGLPQLKASQLGVYKAFVDNRYKVALEAKESQSNNQPKISEELKVRGP---KDS 223

QY 227 KQBTETTSCLLQNSPGDYIIELYDDTNTKRVHYALKPVHSPWAGP----- 276
 DB 224 KDSHTSVTNEALL-----YKPIDRVTRSTLVLDHLA--HTPVDHPTPLQDALR 272

QY 277 -----IRAVAITVP-----LVVISAFAT-----LFT--VMCRK 302
 DB 273 ISONELSLNEDIDPRATVTPKGETOLVDGFLVEVSSESKLRHVEFLTDVLCAK 332

QY 303 KOENIYSHL-----DEESSESTYTAALPRELRPRKPVFLCYSSKDG 346
 DB 333 LKNTSAGRHQYQCKNTWPIADLVFPSPSEASQVPPFDHELEDMKMKISALKSEIQ 392

QY 347 QNEMNVQCFAYFLQDFCCGEVALDLWEDFSICREGQREWIYQIKHESQFIIVVCSKGMK 406
 DB 393 KEKANKGQSAI-----ERLKKMFENEFLILANSPTIP 426

QY 407 YFVDKKNTKKGGRSGSGKGEFLV-----AVSATAEKLROAKOSSAALSKEFI 455
 DB 427 FRIHNRN-----GKYLFLSSDYERSEWREAIQKLRKDLQAFVLSSEVQLVT 476

QY 456 AVTFDYCEGVDPGILDSTKYRLMDNLPQLCSHLHSRDLGLOPFGQH-----TROGSR 510
 DB 477 GSCFKRLRVTHNIP-----VTSNKDDDESPLYGFLFVIVHSAKGFQKSANLYCTLEVDSEF 531

QY 511 NYFRSGRSLVAICNNHQFID-EEDPDWEK 541
 DB 532 GYFVSA-----KTRVTRDAEPKWEDE 554

RESULT 11
 GNRP_HUMAN
 ID GNRP_HUMAN STANDARD; PRT; 1275 AA.
 AC Q13972;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Guanine-nucleotide-releasing protein (GNRP). (Ras-specific nucleotide
 DE exchange factor CDC25).
 GN RASGRF1. OR: CDC25.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-95129875; PubMed-7828890;
 RA Wei W., Das B., Park W., Broek D.,
 RT Cloning and analysis of human cDNAs encoding a 140-kDa brain guanine
 RT nucleotide-exchange factor, Cdc25GEF, which regulates the function of
 RT Ras.;
 RL Gene:151:279-284(1994).
 CC -1- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP.
 CC -1- SIMILARITY: CONTAINS 2 PH DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY (DH) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 RAS-GEF DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IQ DOMAIN.
 CC

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 or send an email to license@isb-sib.ch).
 EMBL; L26584; AA58417.1;
 Genew: HGNC:9875; RASGRF1.
 DR InterPro: IPR001331; GDS_CDC24.
 DR InterPro: IPR000048; IQ_region.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR000651; RasGEFN.
 DR InterPro: IPR001895; RasGRF_CDC25.
 DR InterPro: IPR000219; RhoGEF.
 DR Pfam: PF00169; PH; 2.
 DR Pfam: PF00612; IQ; 1.
 DR Pfam: PF00617; RasGEF; 1.
 DR Pfam: PF00618; RasGEFN; 1.
 DR Pfam: PF00621; RhoGEF; 1.
 DR SMART: SM00015; IQ; 1.
 DR SMART: SM00233; PH; 2.
 DR SMART: SM00147; RasGEF; 1.
 DR SMART: SM00229; RasGEFN; 2.
 DR SMART: SM00325; RhoGEF; 1.
 DR PROSITE: PS00010; DL2; 1.
 DR PROSITE: PS00741; DL1; 1.
 DR PROSITE: PS00720; GDS_CDC25; 1.
 DR PROSITE: PS50006; IQ; 1.
 DR PROSITE: PS50003; PH_DOMAIN; 2.
 KW Guanine-nucleotide-releasing factor; Repeat.
 FT DOMAIN 22 129
 FT DOMAIN 204 229
 FT DOMAIN 240 426
 FT DOMAIN 467 584
 FT DOMAIN 1038 1272
 FT SEQUENCE 1275 AA; 145381 MW; 86C6F54AA1E451F1 CRC64;

Query Match: 2.6%; Score 101; DB 1; Length 1275;
 Best Local Similarity 19.2%; Pred. No. 13;
 Matches: 98; Conservative 66; Mismatches: 144; Indels 202; Gaps: 24;

QY 91 RVILELKEGROCOOL-ILAD-----PKOLNSSEKRTGNE-----SOPPLANKKPTDYFVK 141
 Db 243 QVFSMLEAEAYVOLHILNNEPLRLMAASSKKPTTHDVSIFLNS--ETIMFLH 300
 QY 142 VVFPSSIKNESYHFFTRACDILLQDNLACAPFWKPNLNISQ-----HGSDMQVS 196
 Db 301 QIFYOGLKARISNPTVLADLLILP-----MLNIQEFYRNEHQISLOI- 346
 QY 197 FDIAPNFGFRFFYLHYKHEGPFKKTKCKOBOTETTSCILLQNVSPGYIITLVD-- 253
 Db 347 LAECKNQRFDFLLKHYEAKPD-----C-EERTLETFYYPNFOIP-RYILTLHDVLA 397
 QY 254 ---DWTTRKVMHYALAPVHSPWAGPIRAVATVPLVVISAPALFTVVCRRKQOENIYS 310
 Db 398 HTPHEVENSLOYA-----KSKLEELSR 421
 QY 311 HLPDEESSESTTAALPRERLRPRKVFICYSSKQDNHNVVQCFAYFLQDFCGCEVAL 370
 Db 422 IMDEVSETEINRKNLATERN-----IIE-----GCEILL 451
 QY 371 DLWEDS-----SICREGRENVIOKIHESQFIIVVCSKGN 405
 Db 452 DTSQTVROGSLIQVPSSEKKTIRGLSLSLEKEGRCQFLSKH-----LIITRGS 506
 QY 406 --RYFDVKNY-----RHKGKG-----RSGKGELFLVA 432
 Db 507 GGLHLTKNGVISLIDCTLLEPESTEERAKSGQDIDHLDKIGKVFDPSPPTVILVA 566
 QY 433 VSAIAELKQAKQSSAALSFIAYDYSCGDVPGILDSTKYRLMDLNPOLCSLHLS 492
 Db 567 SS-----ROEKAANTSQDQVD---NIRCNGLMNAFEENSKV---IVPQNI----- 608
 QY 493 RDHGLQEPQHTROGSRNRYFRSKSGSLY 522
 Db 609 -----KRTREGTRENEM-SRSDASLY 628

RESULT 12
 ID Z151_MOUSE STANDARD; PRT; 794 AA.
 AC Q60821; Q60699;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Zinc finger protein 151 (Polyomavirus late initiator promoter binding protein) (LP-1) (zinc finger protein Z13).
 GN ZNF151 OR ZFP100.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rapp L., Carmichael G.G.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBA; TISSUE=Kidney;
 RX MEDLINE=96003919; PubMed=7575457;
 RA Schulz T.C., Hopwood B., Rathjen P.D., Wells J.R.B.;
 RT "An unusual arrangement of 13 zinc fingers in the vertebrate gene Z13".
 RL Biochem. J. 311:219-224(1995).
 CC -1- FUNCTION: MAY FUNCTION AS A HOUSEKEEPING DNA-BINDING PROTEIN THAT REGULATES THE EXPRESSION OF SPECIFIC GENES.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -1- TISSUE SPECIFICITY: FOUND IN ALL THE EMBRYONIC AND ADULT TISSUES EXAMINED.
 CC -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-

CC FINGER PROTEINS.
 CC -1- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
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 CC EMBL; U22396; AAA64848.1;
 CC EMBL; U14556; AAA85493.1;
 CC HSSP; P08046; 1A1H.
 CC MGD; MGI:107410; Zfp100.
 CC InterPro; IPR000210; BTB_POZ.
 CC InterPro; IPR000822; ZnF_C2H2.
 CC Pfam; PF00096; zf-C2H2; 13.
 CC Pfam; PF00651; BTB; 1.
 CC PRINTS; PR00048; ZINC_FINGER.
 CC ProDom; PD000003; ZnF_C2H2; 1.
 CC SMART; SM00225; BTB; 1.
 CC SMART; SM00355; ZnF_C2H2; 13.
 CC PROSITE; PS50097; BTB; 1.
 CC PROSITE; PS00028; ZINC_FINGER_C2H2_1; 13.
 CC PROSITE; PS00157; ZINC_FINGER_C2H2_2; 13.
 KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
 KW Nuclear protein; Repeat.
 FT DOMAIN 1 104
 FT BTB.
 FT ZINC FINGERS.
 FT C2H2-TYPE.
 FT ZN_FING 297 730
 FT ZN_FING 325 347
 FT ZN_FING 353 375
 FT ZN_FING 381 403
 FT ZN_FING 409 431
 FT ZN_FING 437 459
 FT ZN_FING 465 487
 FT ZN_FING 493 515
 FT ZN_FING 519 543
 FT ZN_FING 549 571
 FT ZN_FING 577 599
 FT ZN_FING 605 628
 FT ZN_FING 708 730
 FT ZN_FING 507 507
 FT CONFLICT 507 507 G -> A (IN REF. 2).
 FT CONFLICT 573 573 N -> K (IN REF. 2).
 SQ SEQUENCE 794 AA; 86664 MW; FFF8E56DEBFFED CRC64;
 Query Match: 2.6%; Score 99.5; DB 1; Length 794;
 Best Local Similarity 20.6%; Pred. No. 8.9;
 Matches 71; Conservative 41; Mismatches 146; Indels 87; Gaps 15;

QY 364 CGCEVALDWDSESLCREGRENVIOKIHESQFIIVVCSKGMK-YFVDKNTKHKGGRG 422
 Db 24 CDCTFVDV-GVDF-----KAKKA-VLAACSEYFMLEFVQDQVWVLDISNA 67
 QY 423 SGKGLFLVAVSAIAELKQAKQSSS-----AALSKFIATVFDYSCGDVPGILDST 475
 Db 68 AGLGQ-----VLEFMTAKLSLSPENVDDVLAVASFQMQ-----DIVT 106
 QY 476 KYRLMDNLPOLCSHL-HSRDRGLQEPQH-----TROGSRNRYFRSKSGSLY 522
 Db 107 ACHTLKSLAEPSSSTTGESADASAVEGDKRAKDEKAAATMLSLGQARSSSTGPGRELK 166
 QY 523 VAICMHOQFDEEPPDWFQKQVFFPHPPPLRYREPVLKFDGLVNDVMCKKPGPSDFCL 582
 Db 167 EERGOAESASSGAQETEKADAPREPPP-----VELKPDPTSSMA- 206
 QY 583 KYEAALVATGAPDASHESQHGQLQDGEARPALDGSAAQLPILRTVKAGSPSPMDPSG 642
 Db 207 AAEALSESSESEMEVEPASKG--EDGEEGAGPATVKEGMH-LDNGEPEENESA 263
 QY 643 IYDSSVPSSELSLP---LMEGISTQDTETSSLSYSSSSGSGLEE 684

Db 264 GTDS---GQELGNEQNLRSYTGDRTESKAYGSIHHCEDGKE 305

RESULT 13

XY2_MOUSE STANDARD; PRT; 783 AA.

AC P00662

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE zinc finger, Y-chromosomal protein 2.

GN XY2 OR ZFY-2

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89168416; PubMed=2493989;

RA Mardon G., Page D.C.;

RT "The sex-determining region of the mouse Y chromosome encodes a

RT protein with a highly acidic domain and 13 zinc fingers.*";

RL Cell 56:765-770(1989).

CC -1- FUNCTION: PROBABLE TRANSCRIPTIONAL ACTIVATOR.

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- SIMILARITY: BELONGS TO THE KROPPDEL FAMILY OF C2H2-TYPE ZINC-

CC FINGER PROTEINS. ZFY/ZFY SUBFAMILY.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

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CC or send an email to license@sib.ch).

CC -----

DR EMBL; M24401; AAM56845.1;

DR PIR; A31491; A31491.

DR HSP; P08048; 5ZNF.

DR MGD; MGI:99213; Zfy2.

DR InterPro: IPR000822; Znf_C2H2.

DR Pfam: PF00096; zf-C2H2; 13.

DR PRINTS; P00048; ZINCFINGER.

DR PRODOM; PD000003; Znf_C2H2; 1.

DR SMART; SM00355; Znf_C2H2; 13.

DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.

DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 10.

DR KW Transcription regulation; Activator; Zinc-finger; Metal-binding;

FT DNA-binding; Repeat; Nuclear protein.

FT DOMAIN 372 382 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT DOMAIN 403 777

FT ZN_FING 403 425

FT ZN_FING 434 456

FT ZN_FING 466 488

FT ZN_FING 497 520

FT ZN_FING 526 548

FT ZN_FING 554 577

FT ZN_FING 583 605

FT ZN_FING 611 634

FT ZN_FING 640 662

FT ZN_FING 668 691

FT ZN_FING 697 719

FT ZN_FING 725 748

FT ZN_FING 754 777

SQ SEQUENCE 783 AA; 88856 MW; 1722D1C23F019DF8 CRC64;

Query Match 2.68; Score 99; DB 1; Length 783;

Best Local Similarity 19.28; Pred.No. 9.5; Mismatches 207; Gaps 34;

Matches 117; Conservative 74;

OY 36 TFFYDCTYLPVGVKHYADQNTISQYACHQDVAVTILNSPGALGIEFLKGRVILE 95

Db 339 TAYDNNDSBEI-----EVONATASAMLRHDESG-----GLD-----RVPKQ 374

OY 96 ELKS-----EGROCOQLILADPKOLNSSFKRTGMSQP---FLNNKFETDYFVKVVPFPPSIK 149

Db 375 KSKKKRPDESQKQSAIPVAPDQT-----LRVYPCMGCKKFKTKRFLK-----RHLK 423

OY 150 NESNTHPFFTRACDILLOPWLACKPFWKPNLNISOGSDMQVSDPBNPFGPFF 209

Db 424 N-----HPEYLANKKY-----HCTEDYSTNKKIS----- 448

OY 210 YLHYKLKEGPFKRKTQKQTTETTSCLQNVSPGDYIILVDVDTNTRKVMHTALAPV 269

Db 449 -LHNEMESH-----KLTIKTEKTECCDC-RKNLSHA-----GTLCTEKTMYTE----- 490

OY 270 HSPWAGPPIRAVATVPLVVI---SAPATLFT---VCCRKKQENIYSHLDRESSSTY 322

Db 491 -----KGVNCKCKCFCDYETAEQTLNHLHLVVERK-----PPHICGCGKGFH 537

OY 323 TAALPRE-RLRPRKVELC-----YSSKQGN---HMNVVQCFAYFLQDFGCEVALDME 374

Db 538 PSALAKHIVRTGKPYECYCYEKSADSSNLKTHIKSHKSEIPLK-----CDICL---L 590

OY 375 DESLCREQREWI---OKIHESQFIIVVCSKGMKYFVDKANKYKGGGSGKGEFLV 431

Db 591 TSDTKEAQQAHLVHQSRTHQ-----CS-----HCNHSNSSLARHILSV 633

OY 432 AVSAIAELKRAQOS---SSAALSKEFIANTFYDS-----CEGDPVG-----ILDSTK 476

Db 634 HTKATPHKCDMSKGFHPSLAKRVATHKSKKHQCHRCDFNSPDPFLSHHLSAHTK 693

OY 477 YRLMDNLPLCSHLSDHGLQEPGQTRGSRNRYFRSKSRSLYVAICNMHOFIDEEP 536

Db 694 -----NVDFCKRCKK-----EFQOCELOTHKTHESRKYQ---CEYCEYSTIDA 737

OY 537 DMFEKQFVFPFPPPLRTREPVLEKFDGLVLDVNMCKPSPDCLKVEANVGATGPAD 596

Db 738 SGFKRHVISITKDYPH-----CDPCKK-----GFRPSE 768

OY 597 -SOHESQH 603

Db 769 KNOHIMRH 776

RESULT 14

PSUL_YEAST STANDARD; PRT; 970 AA.

AC P53550;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE mRNA decapping protein 2 (PSUL protein).

GN DCP2 OR PSUL OR YNL118C OR M1917.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=D273-10B;

RA Tzagoloff A.A.;

RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.

RN [2]

RN SEQUENCE FROM N.A.

RX MEDLINE=97245296; PubMed=9090055;

RA de Antoni A., D'Angelo M., Dal Pero F., Sartorello F., Pandolfo D.,

RA Pallavicini A., Lanfranchi G., Valle G.;

RT "The DNA sequence of cosmid 14-13b from chromosome XIV of

RT Saccharomyces cerevisiae reveals an unusually high number of

RT overlapping open reading frames.*";

RL Yeast 13:461-466(1997).

RN [3]

RP INTERACTION WITH DCP1.

RX MEDLINE=99438017; PubMed=10508173;

RA Duncley T., Parker R.;

RT "The DCP2 protein is required for mRNA decapping in Saccharomyces cerevisiae and contains a functional, mult motif."

RL EMBL: J. 18:5411-5422(1999).

CC -1- FUNCTION: REQUIRED FOR THE PRODUCTION OF ACTIVE DECAPPING ENZYME, PERHAPS IN A PROCESS REQUIRING THE HYDROLYSIS OF A PYROPHOSPHATE BOND. DECAPPING IS A THE MAJOR PATHWAY OF MRNA DEGRADATION IN YEAST. IT OCCURS THROUGH DEACETYLATION, DECAPPING AND SUBSEQUENT 5' TO 3' EXONUCLEOTIC DECAP OF THE TRANSCRIPT BODY.

CC -1- SUBUNIT: INTERACTS WITH DCP1.

CC -1- SIMILARITY: BELONGS TO THE NUDIX HYDROLASE FAMILY. STRONG, TO S. POMBE SPAC19A8.12.

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CC EMBL: L43065; AAA68866.1;

DR EMBL: 269382; CAA93389.1;

DR EMBL: 271394; CAA95998.1;

DR SGD: S0005062; DCP2.

DR InterPro: IPR000086; NUDIX_hydrolase.

DR Pfam: PF00293; NUDIX. 1.

DR PRINTS: PR00502; NUDIXFAMILY.

DR PROSITE: PS00893; NUDIX. 1.

KW Hydrolase.

FT DOMAIN 134 155 NUDIX BOX.

FT DOMAIN 436 439 POLY-SER.

FT CONFLICT 425 425 P -> L (IN REF. 1).

FT SEQUENCE 970 AA; 108667 MW; D53CA2C5A546FAA CRC64;

Query Match 2.6%; Score 99; DB 1; Length 970;

Best Local Similarity 17.9%; Pred. No. 13; Indels 218; Gaps 26;

Matches 106; Conservative 86; Mismatches 182;

QY 239 IONVSPGYIE--LV-----DQNTTKYMHYALPKVHSPN--AGPIRAVAITVP 285

DB 9 LENTSVDRILEDLLVFIINCPNEDLSVERELFEFEE--EASFYTFDKLANPTLP 64

QY 286 LVVTSATLFTVCKKQOENIYSHDESSSESTVTAALP-----RELR----- 332

DB 65 SLAKTSFALLIKLPLVKNWDL--RVDEALQOFKSKYKSIPIVGAIAFENLSILVQ 122

QY 333 -----PRPVFTCYSKQGNHNVOCFAFYFDGCGCEVALDWDFSLCRGQ 383

DB 123 QTESDWSFPRGKI-----SKD-----ENDIDCIREVKE-----EIGFDLTD 160

QY 384 REWVTKIHESQFTIVVCSKGMKIFVDKKNYKHKGCGSGKGEFLVA-VSAI----- 436

DB 161 -----YIDNQFI-----ERNLOGKNYK-----IFLISGVSEVNEKRPQ 194

QY 437 -----AKLR--QAKQSSSALSFKFIATVDFYS-----CSGD 466

DB 195 VNEIDKIEVDFPKKISKYTKYKINSKYLINSWAPLSMLRHQRKEDOLKSYAEQ 254

QY 467 VPGILDLSYRLMDNLPLCSHLHSR-----DHGLQEPQUTR 505

DB 255 LALLGI--TREQIDPGRELLNMLTAVQANNNVNGVPSQQLHLKQSGEENQ 313

QY 506 QGSRNRTFRSKSGSLVAICN-----HQFDIDEPWFE-----KQFVFP- 546

DB 314 QKQOQSSFSQQQPSIPPSLSEPFANNKVPPTMPMANVFNPNQPLFATNGQFAPFP 373

QY 547 -----BPPPLATREPVLEKTFDSGLVLDVNDVCKPQGESDFC 581

DB 374 FMLPLTNNSANPIPTPPVPPNAPPNEMAGVPMNLSGNVSPQSLPAPL----- 429

QY 582 LYEAVNLGATGADSDSHESQHG--LDQGEARPDLDGSAALQPLHVTWAGSGSDMPR 639

DB 430 -----PRDSGYSSSPGQLDLNLSKKPDSNVQSSKKPKIKLQIRGTDLSIK 477

QY 640 DSGIVDSSVPSSELSPLMGLSTDO-----TETSSLTGVSSSSGIGREE 685

DB 478 QNNNETAHSNSQALLDLKKPTSSQKIHASKPDYSFLPN--DSVSGIQDAE 527

RESULT 15

ID EX5B CHLPN STANDARD; PRT: 1050 AA.

AC Q927G7; Q9J5B1; Q9K2F2;

DT 30-MAY-2000 (Rel. 39, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE Exonuclease, v beta chain (EC 3.1.11.5).

GN RCB OR CPN0738 OR CP0007.

OS Chlamydia pneumoniae (Chlamydia pneumoniae).

OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

OX NCBI_TaxID=83558;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CW029;

RX MEDLINE=99206606; PubMed=10192388;

RA Kalman S., Mitchell W., Marathe R.W., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.;

RA "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";

RL Nat. Genet. 21:385-389(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=AR39;

RX MEDLINE=20150255; PubMed=10684935;

RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Liner K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwynn M., Nelson M., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;

RA "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";

RL Nucleic Acids Res. 28:1397-1406(2000).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=J138;

RX MEDLINE=20330349; PubMed=10871362;

RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kubara S., Nakazawa T.;

RA "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CW029 from USA.";

RL Nucleic Acids Res. 28:2311-2314(2000).

CC -1- FUNCTION: REQUIRED FOR EFFICIENT DNA REPAIR; IT CATALYZES THE UNWINDING OF DOUBLE-STRANDED DNA AND THE CLEAVAGE OF SINGLE-STRANDED DNA AND IT STIMULATES LOCAL GENETIC RECOMBINATION.

CC ALL OF THESE ACTIVITIES REQUIRE CONCOMITANT HYDROLYSIS OF ATP (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: Exonucleolytic cleavage (in the presence of ATP) in either 5' to 3' or 3' to 5' direction to yield 5'-phosphooligonucleotides.

CC -1- SUBUNIT: CONSIST OF THREE SUBUNITS; RECB, RECC AND RECD (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE HELICASE FAMILY. UVRD SUBFAMILY.

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CC EMBL: A5001655; AAD18877.1;

DR EMBL: AF002164; AAF37903.1;

DR EMBL: AF002547; BAA98945.1;

DR HSP; P09980; IUA.

DR TIGR; CP0007;

DR InterPro; IPR000212; UVRD-helicase.

1944-1945

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1944-1945

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OM protein - protein search, using sw model

Run on: May 19, 2003, 09:14:29 : Search time 56.3267 seconds
(without alignments)
2626.495 Million cell updates/sec

Title: US-09-912-157-2_COPY_36_753
Perfect score: 3829
Sequence: 1 AUTCGWRKAAARPLCVAN.....CAGDLGCRSTDELHNAVL 718

Scoring table: BLOSUM62
Gapop 10.0 : Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

SPTREMBL_21:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvrius:
16: sp_bacteriap:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3005	78.5	564	4 Q9UFA0	Q9UFA0 homo sapien
2	2616.5	68.3	582	11 Q8R5J8	Q8R5J8 mus musculus
3	1950.5	50.9	745	13 Q8QHJ9	Q8QHJ9 brachydanio
4	1941.5	50.7	745	13 Q8QHJ6	Q8QHJ6 brachydanio
5	170.5	4.5	846	5 Q9NAG4	Q9NAG4 caenorhabdi
6	117.5	3.1	562	4 Q99755	Q99755 homo sapien
7	117	3.1	757	3 Q13399	Q13399 ustilago ma
8	116.5	3.0	901	16 Q9KE04	Q9KE04 bacillus ha
9	112.5	2.9	549	4 Q99754	Q99754 homo sapien
10	111.5	2.9	348	4 Q9H460	Q9H460 homo sapien
11	111.5	2.9	370	4 Q9K8N9	Q9K8N9 homo sapien
12	110	2.9	428	4 Q9NTU6	Q9NTU6 homo sapien
13	110	2.9	917	10 Q81789	Q81789 arabidopsis
14	108	2.8	903	5 Q95WA7	Q95WA7 bulla gould
15	108	2.8	1058	10 Q9AVI0	Q9AVI0 oryza sativ
16	108	2.8	1962	11 Q9WUF3	Q9WUF3 mus musculus

17	107.5	2.8	938	11 Q60669	Q60669 mus musculus
18	107.5	2.8	3788	11 Q922X9	Q922X9 rattus norv
19	107.5	2.8	3942	11 Q88737	Q88737 mus musculus
20	107.5	2.8	1322	11 Q9QZP6	Q9QZP6 mus musculus
21	106.5	2.8	638	10 Q9LQF8	Q9LQF8 arabidopsis
22	106.5	2.8	1907	4 Q15017	Q15017 homo sapien
23	106	2.8	593	11 Q99PV2	Q99PV2 rattus norv
24	106	2.8	1516	4 Q9C0D2	Q9C0D2 homo sapien
25	106	2.8	1545	11 Q8VRS6	Q8VRS6 mus musculus
26	106	2.8	3788	11 P97412	P97412 mus musculus
27	105	2.7	901	5 Q24573	Q24573 drosophila
28	105	2.7	1545	5 Q9BHW7	Q9BHW7 leishmania
29	105	2.7	1571	11 Q54978	Q54978 mus musculus
30	105	2.7	2031	5 Q9N918	Q9N918 leishmania
31	104.5	2.7	707	4 Q9GSK7	Q9GSK7 homo sapien
32	104.5	2.7	806	5 Q9VQK5	Q9VQK5 drosophila
33	103.5	2.7	625	10 Q9FND7	Q9FND7 arabidopsis
34	103.5	2.7	924	10 Q9ZVD5	Q9ZVD5 arabidopsis
35	103.5	2.7	1289	11 Q9WTR2	Q9WTR2 mus musculus
36	103.5	2.7	1306	2 Q9L821	Q9L821 enterococu
37	103	2.7	549	5 Q19655	Q19655 caenorhabdi
38	103	2.7	1156	5 Q967X3	Q967X3 tribolium c
39	103	2.7	1428	5 Q9VU03	Q9VU03 drosophila
40	102	2.7	1448	16 Q8RWJ8	Q8RWJ8 anabaena sp
41	102	2.7	1654	5 Q9VC36	Q9VC36 drosophila
42	102	2.7	4169	4 Q8TCU4	Q8TCU4 homo sapien
43	101.5	2.7	341	6 Q9N0B3	Q9N0B3 macaca fasc
44	101.5	2.7	1639	3 Q9P7Q7	Q9P7Q7 schizosacch
45	101	2.6	539	5 Q9V490	Q9V490 drosophila

ALIGNMENTS

RESULT 1

Q9UFA0
ID Q9UFA0 PRELIMINARY; PRT; 564 AA.
AC Q9UFA0
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE Hypothetical 63.1 kDa protein (fragment).
GN DKFZP434N1928.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Rqgg.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Bloeker H., Boeher M., Brandt P., Mewes H.W., Gassenhuber J.,
RA Wiemann S.;
RL EMBL; AL133097; CAB61408.1;
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 564 AA: 63134 MW: 683AASBD4523E88C CRC64;

Query Match 78.5%; Score 3005; DB 4; Length 564;
Best Local Similarity 99.8%; Pred. No. 5e-268;
Matches 563; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 155 HPPFFETRADCLLQPNLACKPFWKPRNLINISQSGSDMOVSFOHAPHNFGFRFFLYLK 214

DB 1 HPPFFETRADCLLQPNLACKPFWKPRNLINISQSGSDMOVSFOHAPHNFGFRFFLYLK 60

QY 215 LKHEGPFKKTKCKQQTETTSCLLQNVSPGDIIELVDDTNTTKVMHTALPVPSPWA 274

DB 61 LKHEGPFKKTKCKQQTETTSCLLQNVSPGDIIELVDDTNTTKVMHTALPVPSPWA 120

QY 275 GPRAVAIVPLVWISAPATLFTVCKRKKQENIYSHLDEESSESTYALPRRLRPR 334

DB 121 GPRAVAIVPLVWISAPATLFTVCKRKKQENIYSHLDEESSESTYALPRRLRPR 180

QY 335 PRVFYCTSSKDGQNNHNVVOCFAIFLQDFCCCEVALDWMEDFSLCREGQRENVIOKIHES 394
 DB 181 PRVFYCTSSKDGQNNHNVVOCFAIFLQDFCCCEVALDWMEDFSLCREGQRENVIOKIHES 240
 QY 395 OFIIVVCSKGMKYPVDEKNTKHKGGSGGSGGELFLVAVSAIAEKLRQAKQSSAALSKF 454
 DB 241 OFIIVVCSKGMKYPVDEKNTKHKGGSGGSGGELFLVAVSAIAEKLRQAKQSSAALSKF 300
 QY 455 IAVFYDSCGDVPGILDSTKYRLMDNLPOLCSHLSRDBGLQEPQHTROGSRNRYFR 514
 DB 301 IAVFYDSCGDVPGILDSTKYRLMDNLPOLCSHLSRDBGLQEPQHTROGSRNRYFR 360
 QY 515 SSGSGLVAVICNNHQFIDEEPWFKEQFVFPHPPLRYEPVLEKFDGSLVNDVCKP 574
 DB 361 SSGSGLVAVICNNHQFIDEEPWFKEQFVFPHPPLRYEPVLEKFDGSLVNDVCKP 420
 QY 575 GPESDFCLVAVIAGATGAPDSQHSQGGGLDQDGEARPALDGSAAALPILTYKAGSP 634
 DB 421 GPESDFCLVAVIAGATGAPDSQHSQGGGLDQDGEARPALDGSAAALPILTYKAGSP 480
 QY 635 SDMPRDSGIYDSSVPSSELSPLMEGLSTDQTTSSLTSSVSSSGIGEEPPALPCKILL 694
 DB 481 SDMPRDSGIYDSSVPSSELSPLMEGLSTDQTTSSLTSSVSSSGIGEEPPALPCKILL 540
 QY 695 SSGCKADLGCRSYTDELHVAAPL 718
 DB 541 SSGCKADLGCRSYTDELHVAAPL 564

RESULT 2

Q8R5J8 PRELIMINARY; PRT: 582 AA.
 AC Q8R5J8;
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Similar expression to FGF protein (fragment).
 GN SEF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21824237; PubMed=11802165;
 RA Furchauer M., Lin W., Ang S.L., Thisse B., Thisse C.;
 RT "Seif is a feedback-induced antagonist of Ras/MAPK-mediated FGF
 signaling.";
 RL Nat. Cell Biol. 4:170-174(2002).
 DR EMBL; AF424804; AAL79530.1;
 FT NON_TER 1 1
 SQ SEQUENCE 582 AA; 65263 MW; 56663B2981C4268E CRC64;

Query Match 68.3%; Score 2616.5; DB 11; Length 582;
 Best Local Similarity 84.6%; Pred. No. 3.5e-232;
 Matches 496; Conservative 34; Mismatches 49; Indels 7; Gaps 4;

QY 136 TDYFVYVFPFSSIKNESNYHFFFRACDILLQPDNLACKPFWKPNLNISQSGSDMV 195
 DB 1 TDYFVYVFPFSSIKNESNYHFFFRACDILLQPDNLACKPFWKPNLNISQSGSDMV 60
 QY 196 SFDHAPHNFGFFFLYHLTKLHSGPFRKTCQEQTTTSCLLQNVSPGDYIIELVDT 255
 DB 61 SFDHAPHNFGFFFLYHLTKLHSGPFRKTCQEQTTTSCLLQNVSPGDYIIELVDT 120
 QY 256 NTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVCKKQENIYSHLDE 315
 DB 121 NTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVCKKQENIYSHLDE 180
 QY 316 SSESSTYTAALPRELPRKPVLCYSSKDGQNNHNVVOCFAIFLQDFCCCEVALDWMED 375
 DB 181 SSESSTYTAALPRELPRKPVLCYSSKDGQNNHNVVOCFAIFLQDFCCCEVALDWMED 240

QY 376 FSLCRGQRENVIOKIHESOFIIVVCSKGMKYPVDEKNTKHKGGSGGSGGELFLVAVSA 435
 DB 241 FSLCRGQRENVIOKIHESOFIIVVCSKGMKYPVDEKNTKHKGGSGGSGGELFLVAVSA 300
 QY 436 IAKLQKQKSSAALSKFIAVYDSCGDVPGILDSTKYRLMDNLPOLCSHLSRDB 495
 DB 301 IAKLQKQKSSAALSKFIAVYDSCGDVPGILDSTKYRLMDNLPOLCSHLSRDB 357
 QY 496 GLAEP-QHTROGSRNRYFRSKSGLSYVAICNNHQFIDEEPWFKEQFVFPHPPLRYFR 554
 DB 358 GEQEVLCQBPQHSRRNRYFRSKSGLSYVAICNNHQFIDEEPWFKEQFVFPHPPLRYFR 417
 QY 555 EPVLEKFDGSLVNDVCKPESDFCLVAVIAGATGAPDSQHSQGGGLDQDGEA 612
 DB 418 EPVLEKFDGSLVNDVCKPESDFCLVAVIAGATGAPDSQHSQGGGLDQDGEA 477
 QY 613 RPALDGSAAALPILTYKAGSPDMPRDSGIYDSSVPSSELSPLMEGLSTDQTTSSLT 672
 DB 478 QPSCDSAPALQALLAVKAGSPDMPRDSGIYDSSVPSSELSPLMEGLSTDQTTSSLT 537
 QY 673 ESYSSSSGIGEEPPALPCKILLSGCKADLGCRSYTDELHVAAPL 718
 DB 538 ESYSSSSGIGEEPPALPCKILLSGCKADLGCRSYTDELHVAAPL 582

RESULT 3

Q8QHU9 PRELIMINARY; PRT: 745 AA.
 AC Q8QHU9;
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Seif.
 GN SEF.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21824236; PubMed=11802164;
 RA Tsang M., Friesel R., Kudoh T., David I.;
 RT "Identification of Seif, a novel modulator of FGF signalling.";
 RL Nat. Cell Biol. 4:165-169(2002).
 DR EMBL; AF364103; AAL76112.1;
 SQ SEQUENCE 745 AA; 83431 MW; 56FELF089D98DDB4 CRC64;

Query Match 50.9%; Score 1950.5; DB 13; Length 745;
 Best Local Similarity 54.1%; Pred. No. 1.3e-170;
 Matches 383; Conservative 106; Mismatches 184; Indels 35; Gaps 8;

QY 17 CVANESGVPASRNSGL--YNITFKDNTYLLNPGVKEHLADANQITISQVACHQVAVT 74
 DB 35 CSYKQGTQSSMDGARKLGVTFRDNCVNMWPLGRKHAHEVNNITSHLSQCSQAAVV 94
 QY 75 ILSPGALGIEFLKFRVILELSEKSGCCQOLIKDPKLNSEFKRTGMSQPLNKKF 134
 DB 95 VHWASPLGIEHVKGFVLYEDKNPERKQCHLTKDQPLNLFYKTNMSSQPFSSLA 154
 QY 135 ETDYFVYVFPFSSIKNESNYHFFFRACDILLQPDNLACKPFWKPNLNISQSGSDMV 194
 DB 155 ETDYFVYVFPFSSIKNESNYHFFFRACDILLQPDNLACKPFWKPNLNISQSGSDMV 214
 QY 195 VSDHAPHNFGFFFLYHLTKLHSGPFRKTCQEQTTTSCLLQNVSPGDYIIELVDT 254
 DB 215 VSDHAPHNFGFFFLYHLTKLHSGPFRKTCQEQTTTSCLLQNVSPGDYIIELVDT 274
 QY 255 NTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVCKKQENIYSHLDE 314
 DB 275 NTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVCKKQENIYSHLDE 334

QY	195	YSTDAPHNFGFRFFLHYLTKLHGBPFKXCKQBQZTETTSCLLQNVSPGDIILVDD	254
Db	215	VYFDHAPSTYGFSGIYYLLKRLQEGFRLKRCQPEQNGPKTCVLQDVYPTGTAILEURD	274
QY	255	TNTTRKVMYIALKPVHSPWAGPTRAIVATVPLAWISAFATFLTVCRKKQOENIYSHLDE	314
Db	275	SNNTFRCTQYHVSQVHSPWAGPTRAIVATVPLWIKSAFATFLTVCRKKQOENIYSHLDE	334
QY	315	ESSESSYTAALPRELPPKPVLCYSSKQONHNVCCFAIFLQDFCCCEVALDLME	374
Db	335	ESSESSQVTLASDRPPRPKFICTSSDGAKEHLAVIOSFAFPLQDFCCCEVALDLME	394
QY	375	DFSICRGQREWYIOKTHESQYIYVCSGKMIFYDKNNTKHGGGR	435
Db	395	HLEICKEGQMSLRSRIDEAHEFTIYVCSXGLHFKVYKRRHKGKATSKENREPSADSSS	454
QY	424	CKGELFLVAVSAISKLRQAKQSSAALSKEFTAVTFQYCEGVDPIGLDLSKTKRLMDL	483
Db	455	SSRDLFIVASAIISEKLEVEKHSS-DLSRFPSTFYDSEHTDVPYLSLAPKFLMDQL	513
QY	484	POLCSHLHSDHGLQEPQOHTROGSRNATFRSKGSRSLYVACNMHOFIDEEPWFKEOF	543
Db	514	POLFAHLHQSLYDREPPQPNVSKRNTFCSKGSRSLYVATYNNHOFVDEPWLKEKL	573
QY	544	VPFHPPPLATRYEFLKEFDGLVLDVMCKPGPESDFCLKVEAVL	596
Db	574	M-----PPPLPKRNTIPEKYDGLVNEVYKLBHGESE-CPPVRSNVLILPOTPOGVGSLSL	639
QY	597	SOHESQBGGLDQGEARPALDGSAAQLPILHVVAKGSPDMPSDGIYDSSVPSSLSLP	656
Db	630	SREDLJREGSSQD-----ACSCRPVLFDGSASPEPMRPSGVIYDSSVPSSLSLP	680
QY	657	LWEGLSYDQYETTSSTESVSSSGSLGEEPPALPASKILLSGGS-CKADL	703
Db	681	LADGLSPDHADNSLADSVSSSGSLGDEPPAVVSLCETARTICKADL	728

RESULT 5	Q9NAG4	PRELIMINARY;	846 AA.
ID	Q9NAG4		
AC	Q9NAG4		
DT	01-OCT-2000 (TRMBLrel. 15, Created)		
DT	01-OCT-2000 (TRMBLrel. 15, Last sequence update)		
DT	01-DEC-2001 (TRMBLrel. 19, Last annotation update)		
DE	F64G10A.6 protein.		
DE	F64G10A.6		
GN	Cenorhabditis elegans.		
OS	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;		
OC	Rhabditidae; Peloderinae; Caenorhabditis.		
OX	NCBI_TaxID=6239;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RP	Ainscough R.;		
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.		
RL	[2]		
RP	SEQUENCE FROM N.A.		

RA	MEDLINE=99US96L3; PubMed=9831910;
KR	none;
RT	"Genome sequence of the nematode C.elegans: A platform for
RT	Investigating biology.";
RL	Science 282:2012-2018(1998).
EMBL:	ALL10498; CAB54470.1; ..
SQ	SEQUENCE 846 AA; 94052 MW; 613AEF55EBB89EAM CRC64;
Query Match	4.5%; Score 170.5; DB 5; Length:846;
Best Local Similarity	21.4%; Pred. NO. 2e-06;
Matches 141; Conservative 83; Mismatches 225; Indels 211; Gaps	
QY	64 QVACHDQVATILWSPGALGTETFLAGRVVELLSKRCQQQLIKDKPOLNSSFRTG 123 : : : : : : :
Dd	294 QY-CFEYEIVRLDS--GIVHLQSAILTKDELATE-----IINGRPVQGEF---- 338

DR InterPro: IPR001650; Helicase_C.
 DR Pfam: PF00270; DEAD; 1.
 DR Pfam: PF00271; Helicase_C; 1.
 DR SMART: SM00430; Helicase_C; 1.
 KW ATP-binding; Helicase_C
 FT NON_TER
 SQ SEQUENCE 757 AA; 84382 MW; 1AELE414435382A7.CRC64;
 Query Match 3.1%; Score 117; DB 3; Length 757;
 Best Local Similarity 20.4%; Pred. No. 0.15;
 Matches 111; Conservative 56; Mismatches 187; Indels 190; Gaps 27;
 QY 233 ETTSCLQWSPGVYIELVDYDNTTRKVMHYALAPVSPWAGPIRAV---AIVPL-- 286
 Db 77 ETYLLPTVALRANLAKLDVN---IRYHWQP-GSAAIVIVSTEAATITAPKE 131
 QY 287 ---VVSATLFTVMCRKKQENIYSHLDESSESTYTAALP----- 327
 Db 132 YANRLQOORLDRIVDECHLTATARSYRSMMOLANVROVETQVWLATLPIFEDA 191
 QY 328 ---RELRPRPKVF-----LCYSSKQONEMVVOCF-AVFLQDFCGCEVALDWEDF 376
 Db 192 FISHNKLKPLIVRETNRSNLCYSVTAERHSGMTCYDAVRVD---ECRATDILW--- 246
 QY 377 SLCRGOREWVIOKHESQFIIIVCSGKMKYFVDK-----KNYKHGGGRGS----- 423
 Db 247 ---NGORD-----RIIVYCTS--KELVARLAEMGCAIYSSGSEADRAA110 290
 QY 424 ---GRGELFVAVSAEKLROAKOSSAALSKEFIATVYFSCGDPVPGIL--DLSTKY 477
 Db 291 DWICGKSPVIVATSA-----LVGVEDYPHRVFVHLLGPDLLTDF 331
 QY 478 -----RLMDNLPOLCSHLSDHGLQEPQGHTRGSGRRNYFRS 515
 Db 332 SQESGRAGRGHPAESILLAGPOLDORAP-ASGKASSAEKGVAPG---ADKRAMGLYS 387
 QY 516 KSGRSIYVAICMHQFIDEPPDFEKFQFVFPFPPPLRYREVPLEKFSGLVLDVNVCKPG 575
 Db 388 RK---YCLRGVLSQLLDQRSW-----RWCMEGDLQCSVC 419
 QY 576 PESDFCLVAEAVLGATGADSOH---ESQHGGLDQGEARPALDGSANLQPLLETVKAG 632
 Db 420 PGHFP-----QARGPGDQHFYAPAGADPSTQSRHPSMHGSS--HPSNH----- 463
 QY 633 SPSPMDRSGYVDSVPSE--LSPLMEGLSTQDTETSLTESYSSS-----SGLGEPEPPA 688
 Db 464 -----GSHSPSSHSGSHPSHPSHSGSS-HPSHSGSGQGGQRRKQOPD 510
 QY 689 LPSPK 692
 Db 511 PPSK 514
 RESULT 8
 ID Q9KE04 PRELIMINARY; PRT; 901 AA.
 AC Q9KE04;
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Transposase (08)/ABC transporter (ATP-binding protein).
 GN BHI054.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125/JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirana C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;

RT Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis.
 RL Nucleic Acids Res. 28:4317-4331(2000).
 CC 1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
 CC (ABC TRANSPORTERS)
 CC EMBL; AP001510; BAB04773.1;
 DR InterPro: IPR003593; AAA_ATPase...
 DR InterPro: IPR003439; ABC_transport...
 DR InterPro: IPR002559; Transposase_1...
 DR Pfam: PF00005; ABC_tran; 1.
 DR Pfam: PF01609; Transposase_1; 1.
 DR ProDom: PD000006; ABC_transport; 1.
 DR SMART: SM00382; AAA; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
 KW ATP-binding; Transport; Complete proteome.
 SQ SEQUENCE 901 AA; 104585 MW; E519406650B2CBB.CRC64;
 Query Match 3.0%; Score 116.5; DB 16; Length 901;
 Best Local Similarity 19.6%; Pred. No. 0.21;
 Matches 112; Conservative 76; Mismatches 169; Indels 215; Gaps 27;
 QY 26 ASRNSGLNTERKYNCTYLNPGVKHVIADAQNTITISQY-ACHDOVAVTILWSPALGI 84
 Db 333 ALKESGL-----PLPTLIADNGYGSNTYVAMADELPETLIPS----- 371
 QY 85 EFLGKGVILLELKSGR-----QCOQL--TLKDPKOLNSFRKTGMSQPLNMF 134
 Db 372 ---HTFR--QEQKSPAKRFHFNWRCDEDDVYWCNQRKVSFKRYTKRDPY---GY 423
 QY 135 ETDYFV---KVVPF-PSI-----KNESYHPPFTRACDLLQDPNACKPFWKPR 182
 Db 424 ARDFVTECSGCGCFPECTKARGNQVYNPVY-----EELAKAQHQLK 471
 QY 183 MNLSQSG-----SDMVSFDHAPNPGFRFFLYHLKLAHEGPFKRTCKQQTET 234
 Db 472 ---SEGRTRYOKRKTDESVEFGVKQMGFLRHLRGK----- 507
 QY 235 TSCLLQWSPGVYIELVDYDNTTRKVMHYALAPVSPWAGPIRAVAVTIVLVVIS-AFA 293
 Db 508 -----ESVHIELGLVALAHLNR 524
 QY 294 TLFVWCKKQENIYSHLDESSESTYTAALPRERLRPRKPVFLCYLCKDQGNHNV 353
 Db 525 KRAIVDRSRKEPTNQHKNREN-----RIKRF-----SRFTVL 558
 QY 354 QCF---AYFLQDFCGCEVALDWEDFSLCRGQREWY---IQIHESQFIIIVCSGKMK 406
 Db 559 RCFWDSPPFIKSDGKQYASFALED--KLRRGEGENMIEVIDLSKTYRNRQVY---KGIN 612
 QY 407 YFVDKNTYKHGGSGRGSGKGLFVAVSAI-----AEKLQAKOSSAALS 453
 Db 613 MFEIEGEMVGLLPNGAGASTTISMISSLIQPTSGDVLIGGSIHQSIAISILGVVQP 672
 QY 454 FIATVYFYSCE-----GVPGILDSTNYRLMDNLPOLCSHLSDHGLQEPQGHTRGQ 507
 Db 673 FIATVHTLTARENLAFEGKIYGLKEELKHR-MESTLIQV-----GLEE-----RON 718
 QY 508 SRRNYFRSKSGRSILYVAICNMHO---FIDEEP 536
 Db 719 DRVHTFSGMKRRINIAVALLHEPELLIMDER 750
 RESULT 9
 ID Q99754 PRELIMINARY; PRT; 549 AA.
 AC Q99754;
 DT 01-MAY-1997 (TRENBLrel. 03, Created)
 DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE 68 kDa type I phosphatidylinositol-4-phosphate 5-kinase alpha (EC 2.7.1.68).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97115834; PubMed=8955136;
RA Toljens J.C., Anderson R.A.;
RT Type I phosphatidylinositol-4-phosphate 5-kinases are distinct
RT members of this novel lipid kinase family.
RL J. Biol. Chem. 271:32937-32943(1996).
DR EMBL: U78575; AAC50910.1;
DR InterPro: IPR002498; PIP5K.
DR SMART: SM00330; PIP5K; 1.
DR Pfam: PF01504; PIP5K; 1.
KW Kinase; Transferase.
SQ SEQUENCE 549 AA; 61186 MW; 7CD48BFE175564D CRC64;

Query Match 2.9%; Score 112.5; DB 4; Length 549;
Best Local Similarity 18.1%; Pred. No. 0.23;
Matches 121; Conservative 96; Mismatches 213; Indels 237; Gaps 32;

QY 79. PGLGIEFLK-GFRVLEELKSGRCQCOQILKDPKOLNSFKRTQMSQPLNKKFTO 137
DB 41 PYASGMPDKKIGHSVDSSTETTKTTSSALKAIGLITHTVGSLSLTKPERDLVMDQF 100
QY 138 YFVAVVFPSS-----INENYHPPFFTRACDLQLQDNLACPFKPRNLNISOHSDM 193
DB 101 IVESIEFFSGSNLTPAHYINDFRKTYA----- 130
QY 194 QVSDHAPHNFGFR---FTY-----LHYKHGEPFKRTCKOEQT 232
DB 131 PVAFRYRELFGRIPDYLISLCSEPLIELCSGASGLFY-VSSDEPIITVQKKEA 189
QY 233 ETTSCLLQVSPGDIIELVDDNTTRKVMYALKPVHSPWAGPIRAVAITVPLVVISAF 292
DB 190 -----FLOKLPGYIM-----NLQN-----PTLLPKP 213
QY 293 ATLTVMCRRKQ-----OENIYSHLDESESSSTYTAALPRERLRPRKVFCLYS 342
DB 214 YGLCYVAGGKNIYVNNLLPRSVKMHYIKLSTYKRRASQKEREKPLP-----T 267
QY 343 SKDQNMVNVQCFAYFLQDF-CGCEVALDLWDFSLCREGEWVIO---KHESOFII 398
DB 268 FED-----LFLQDIPDLGLDADN-ALCKTLQDCLVLOSFAINDYSILM 314
QY 399 VY-----CSKMKVFDKKNYKKGGRSGGELFLVAVSAIAEKLRQ-----442
DB 315 SIHNIDHAQREPLSSSTQSVDR-----RPAQKALYSTAMESIQGEARRGGTMET 366
QY 443 -----AKQSSAALSFIAYFYDSCGDVPGILDLSKTYRLMDNLPQLCSHL-HSR 493
DB 367 DDMGGIPARNKSGERLLAYI-----GIIDLOSTYFVKLHSHKALVHDG 413
QY 494 DE-GLQPGQHTQGRGRNFRKSGRSLYVAICMHOFTDEPDWFEKQVTFPPPLR 552
DB 414 DTVSVHPGPGYAEFROR-----FMCN-----TVFKK--IPLKPSFK 448
QY 553 TREPVLEKFGSLVMDVMCKPKPSDFCLAVEAALVATGAPDSQHSQHGGLQDGEA 612
DB 449 -----KFRSG---SSFSRRAGSGNSCITYQPSVSG-----EHKAQ-----481
QY 613 RPAIDGSAALQPLHTVAKGSDMPROSGIYD-----SVSPSELSLPLMEGLSTDQET 668
DB 482 ---VTTKAEVPGVH---LGRDVLPTQPPLEISEGPIPDPSFS-PLV-GETLQMLTT 533
QY 669 SSLAESV 675
DB 534 STLEKL 540

RESULT 10

Q9H460 PRELIMINARY; PRT; 348 AA.

ID Q9H460

AC Q9H460;

DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE BA425A6.2 (Similar to connexin) (Fragment)
GN BA425A6.2
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Heath P.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL121749; CAC10186.1;
DR InterPro: IPR000500; Connexin.
DR Pfam: PF00029; connexin; 1.
DR PRINTS: PRO0206; CONNEXIN.
DR SMART: SM00037; CNX; 1.
DR PROSITE: PS00407; CONNEXINS_1; 1.
DR PROSITE: PS00408; CONNEXINS_2; 1.
FT NON_TER 1
SQ SEQUENCE 348 AA; 37805 MW; 07EB6478067F8995 CRC64;

Query Match 2.9%; Score 111.5; DB 4; Length 348;
Best Local Similarity 28.9%; Pred. No. 0.14;
Matches 43; Conservative 25; Mismatches 56; Indels 25; Gaps 8;

QY 565 LVLDNYMC-----KPGPSDFCLAVEAALVATGAPDSQHSQHGGLDQGEARPAL 616
DB 189 LGLADLVCSLRMRMRPGPTSPSIRKOS---GASGHAEGRRDTEGGRGEG--APAP 243
QY 617 DGSAAQLPLETVKAGSPDPRSDGYDYSV---SSLSLPLMEGLSTDQETSSLTE 673
DB 244 PGARA-----GEGAGSPRSTRVSG--ETKIPDESEVTSSASEKLR-QPRGRPHRE 295
QY 674 SVSSSSGLG-EEPPALPSKLLSSGSKA 701
DB 296 AAQDPRGSGSEQPSAAPSRLAAPPSCSS 324

RESULT 11

Q96KN9 PRELIMINARY; PRT; 370 AA.

ID Q96KN9

AC Q96KN9;

DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)

DE Connexin40.1.
GN CX40.1.

OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Elberger J., Soehl G., Willecke K.;
RT "Structural and functional diversity of connexin genes in the mouse
RT and human genome."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ414564; CAC33846.1;
DR InterPro: IPR000500; Connexin.
DR Pfam: PF00029; connexin; 1.
DR PROSITE: PS00407; CONNEXINS_1; UNKNOWN_1.
DR PROSITE: PS00408; CONNEXINS_2; UNKNOWN_1.
SQ SEQUENCE 370 AA; 40140 MW; CD49F31743A7F7C2 CRC64;

Query Match 2.9%; Score 111.5; DB 4; Length 370;
Best Local Similarity 28.9%; Pred. No. 0.16;
Matches 43; Conservative 25; Mismatches 56; Indels 25; Gaps 8;

QY 565 LVLDNYMC-----KPGPSDFCLAVEAALVATGAPDSQHSQHGGLDQGEARPAL 616
DB 211 LGLADLVCSLRMRMRPGPTSPSIRKOS---GASGHAEGRRDTEGGRGEG--APAP 265

QY 617 DGAALQPLHLYKAGSDPRDSGYDSSVP---SSFLSLPLMEGLSYDQETSLE 673
 DB 266 PGARA-----GGGAGSPRTSRVSG--HTKIDDESEVSSASEKLR-QRGRPHRE 317
 QY 674 SYSSSSGLG-KEEPPALPSKILSSGCKA 701
 DB 318 AADPRGSGSEQPSAPSLAAPSCSS 346

RESULT 12
 Q9NTU6 PRELIMINARY; PRT; 428 AA;
 AC Q9NTU6;
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Hypothetical 45.4 kDa protein.
 GN DKFZ434P211
 OS Homo sapiens (Human)
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RX MEDLINE=21154917; PubMed=11230166;
 RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
 RA Ansong W., Boecker M., Bloeker H., Bauersachs S., Blum H.,
 RA Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,
 RA Meves H.W., Oosterhoeft B., Obermaier B., Tampe J., Heubner D.,
 RA Wambutt R., Korn B., Klein M., Poustka A.,
 RA "Towards a Catalog of Human Genes and Proteins: Sequencing and
 RT Analysis of 500 Novel Complete Protein Coding Human cDNAs";
 RL Genome Res. 11:422-435(2001).
 DR EMBL; AL117401; CAB55902.2;
 KW Hypothetical protein.
 SQ SEQUENCE 428 AA; 45443 MW; FA75BAC1A3FDB3EE CRC64;

Query Match 2.9%; Score 110; DB 4; Length 428;
 Best Local Similarity 23.5%; Pred. No. 0.27;
 Matches 70; Conservative 42; Mismatches 108; Indels 78; Gaps 17;

QY 439 KLRQAKQSS-SAALSKFIATVDFSCGVPGI-----LQSTKYLMDLNPQ 485
 DB 103 RYNQTSQTSCTNRNAISSYSTGGGLPKRRGPASSHCQLTSSSKTVSEDRPQ 162
 QY 486 LCHSLHSDHGLQE--PGQHTQGRNRNFRSKSGSLVAICNNHQIDREDPWFKQF 543
 DB 163 AVSSGHTQCEKAADIAPGQTLT--LRNDSSTSEASRP-----STHKP---PLPRRG 210
 QY 544 VPPE-PPPL-----RYREPVLKFDGSLVLDVYM---CKQPSDDFLCYEAA 587
 DB 211 EPLMLPPPLELYRYTVEDLREKFAAFQINSAQVEDKAISSDCRPSRSH-----TLSSL 267
 QY 588 VIGATG-PADQSHQSHGLDQDGEARPDALDGAALQPLHLYKAGSDMP-----RD 640
 DB 268 ATGAGLPAVSKAPS-----MDAQETHKSQDCLGLDPLASA--AGVPSTAPMSGKKHRP 321
 QY 641 SG-LYDSSVPSSELSLPLMEGLSYDQETSLSLTVSSSSGGLGEPEPALPSKILSSG 697
 DB 322 PGLFSSDP-----LPATSSDSQSAQVTSLI-----PAPFPAASNDAG 361

RESULT 13
 O81789 PRELIMINARY; PRT; 917 AA;
 AC O81789;
 DT 01-NOV-1998 (TRENBLrel. 08, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Hypothetical 101.6 kDa protein.
 GN F8D20.70 OR AT4G35560.

Arabidopsis thaliana (Mouse-ear cress).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsia
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Koettler P., Hempel S., Entian K.-D., Hohelsel J., Jesse T.,
 RA Reijnen L., Vos P., Meves H.W., Mayer K.F.X., Schueller C., Bevan M.,
 RN Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RA Rose M., Hempel S., Entian K.-D., Meves H.W., Kemcke K., Mayer K.F.X.,
 RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 3 WD REPEATS (TRF-ASP DOMAINS).
 DR EMBL; AL031135; CAA20026.1;
 DR EMBL; AL161587; CAB80272.1;
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 2.
 KW Hypothetical protein; Repeat; WD repeat.
 SQ SEQUENCE 917 AA; 101552 MW; 1809BDC42302C820 CRC64;

Query Match 2.9%; Score 110; DB 10; Length 917;
 Best Local Similarity 18.1%; Pred. No. 0.87;
 Matches 154; Conservative 124; Mismatches 281; Indels 292; Gaps 37;

QY 24 GPASR-----NSGLNITFKYDNCITLYNPVGRHV---TADAQNI--TISQYACHQOVA 72
 DB 148 GRASRVYIGSSNSQVLLNEQTETRAIKLGLVSEPCADMENIADVNSQSEKQDF 207
 QY 73 VTILMSPGALGI--EFLKGRVILELSEGRQCOQILKDPQLQSSSKFRGMSQSP-- 128
 DB 208 LFLVGLSGRVAYDDYDMIEKYLQSQSSPSLPKRTVVKLPFDSSSTVQKFLTNPSH 267
 QY 129 FLNKKFETDY-----FVKVPPPSIKNESN---YHPFF-----FTRACDLALQPNL 173
 DB 268 LLNLSDS-DYLAQLAKADAPPLPPTVPKSSSAHFPGFTKVKNYITGCDGTISWDM 326
 QY 174 ACK-----PFKPR-NLNISSQHG-----SDMVSFDBAPHNFGFFFLYHLKL 215
 DB 327 TCSFFILVFLKEIQDQDVSSRGNALTAHYDSNRLVSGDHNGKVRILFKPEPILT 386
 QY 216 KH-----EGPKR-----KTCQEQTTTSCILQVSP-----QDYIILVDD 254
 DB 387 ENSFTPFQGLKGNHIVQSVYIKLTGSIICQKQNSKHLAIGSDQGHSLVEVID- 445
 QY 255 TWTRKVMHYALKPVHSPWAGPIRAVAITVPLVTSAPATLET----- 297
 DB 446 -----ALTPVI-----IQSVLDIEANVLYTKHLSADICPGIISLQFE 484
 QY 298 -----VNCRRKQENIYSHLDESSSESTYTAALPRRLRPKRVFLCYSSKQDQ 347
 DB 485 SCIVQGEKKNVWVAMRDSVFA-LDSDTGNMIGTNMFKP-----KPKVLYTMQLDGR 538
 QY 348 NEMNVVOCFAVFLQDGCCEVALDWEDFLCREGOREWVLOKHESQFTIVVCS----- 402
 DB 539 -----QDTSG-----NGDTSRES-----IYVEELISIQPSVLYCSEKAI 573
 QY 403 -----KGMKYFVDKKNYKHG-----GGRGKGLFLVAVSAIAE-----KLR 441
 DB 574 IYSLARVVQGVKYLKHKFFSSPICSASTFTGTSGVG---LTLTFTDGTVEIRSLPELS 630
 QY 442 QAKQS-----SSAALSKEIAVFDYSCDG-----VPGILDSTKYLMDL 483
 DB 631 QLKQTSIRGFTYSSPKNSLPETISASWDGLVMVNGDDELIVSVLPKQETFLVESM 690
 QY 484 POLCSHLHSDHGLQEGQHTQGRSR-----NTRFSKSGSLVAICNNHQIDREDP 537
 DB 691 -----NRVTKDQNSVCHBGIIITSSSPREKSKMFGSVFKTKSKRTTDPESSEKTEIELSK 746

QY 538 WFERQVFPF-----HPPLRYREPVLEKFSGL 565
 DB 747 IFSTANFNWNNVNSREINTITRVEDEELDIDIDIDHHPNQQQKPEQGISGL 806
 QY 566 ----VLNDVCKGPESDCLVEAAVLGATGADSOHESQHGGL-----DQ 608
 DB 807 SKQMAHFNFGKGLQMAAKNSV-----TNDKEHEKNGATVDQKKYGTSSDE 862
 QY 609 DGEARPDALGSAALQPLLTHTVAGSPDMPDSGIYDSSVSPSSSLPLMEGLSTDTOT 668
 DB 863 MGAAKMA-----OSKLOD-----NLKQLOISLRUTEM 890
 QY 669 SSLTESVSSSS 679
 DB 891 EDTAKSFSSA 901

RESULT 14
 Q95WA7
 ID Q95WA7 PRELIMINARY; PRT: 903 AA.
 AC Q95WA7
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Circadian clock protein period.
 GN PER.
 OS Bulla gouldiana (California bubble).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia;
 OC Cephalaspidea; Bullidae; Bulla.
 OX NCBI_TaxID=114738;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Constance C.M.;
 RT "Cloning and analysis of clock genes in the marine mollusc, Bulla gouldiana."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF353619; AAK97374.1;
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000014; PAS_domain.
 DR Pfam; PF00989; PAS; 2.
 DR SMART; SM00086; PAC; 1.
 SQ SEQUENCE 903 AA; 101146 MW; 22BD873768C5324A CRC64;

Query Match 2.8%; Score 108; DB 5; Length 903;
 Best Local Similarity 19.9%; Pred. No. 1.3;
 Matches 115; Conservative 62; Mismatches 223; Indels 178; Gaps 27;

QY 214 KLEHGFKRTKQKQOTTETTSCLLQNVSPGDYIIELVDVTTRKVMH-YALKPVHSP 272
 DB 83 KLSVLPKERTGM-----DTLSTLEQ-----LVNSMQLNEKKVEHEFTPPHS- 130
 QY 273 WAGPIRAVATVPLVISAFALFVYMCCKKQENIYSHLDESSSESYTAALPRELR 332
 DB 131 -----GSFHSDDGKLSQSEMITTLKNNVVQVSPPLMEHLGY 170
 QY 333 P-----RPKVFICYSSKDGNNVVOCFAYFLQFCGEVALDWDLSLREGQREWVI 388
 DB 171 PVDWNRGRLKDFINKDMNTLN--SCIAHYSTD-----EAADNFES-----SNGTR---- 215
 QY 389 QKHESQPIIVVCSKGMKYVDK-KNYKHGGGRSGKGEFLVAVSAIAEKLQAKOS- 446
 DB 216 -----VTKEGSKYFIRKIRKLGSGFSLQNVVVFQPFMMNITSSITVELSESE 264
 QY 447 -SSAALSFIAYFD-----YSCGDVPGILDLSKY-----RLMDNLPLQ 486
 DB 265 EDGVRVRSILYLCPLNSAYNGGILPKRNFSLRHSFCNTYAHPNVALLGLFQD 324
 QY 487 CSLSLRDHGLQEP-----GOHTROGSRNRYFRSKGRSLTYA----- 524
 DB 325 FSGMSIFD--LYHDDPQQLLDIHIMLSMQPPKSGS-----IRLKTNGCYVETEW 378
 QY 525 -----ICNKHQFI--DEEDWFEKQVFPFPPPLRYREPVLEKFSGLV--- 566

DB 379 SSMFNPNSRLEFIIGQHTWIKGTNPOLFED--LFSRPDKFEL-SPELAKIOEKIVEYL 435
 QY 567 ---LNDVCKGPESDCLVEAAVLGATGADSOHESQHGGLQDGEARPDALGSAALQ 623
 DB 436 KPIQSVRAEPAP-----PMAAQTEVPPPOAQIVTQ-----TAPTQSPAARE 480
 QY 624 PLLTHTVAGSPDMPR-----DSGI-----YDSSVSPSSSLPLMEGL 661
 DB 481 PAPPPAK--PPSEKSKVDATTTEKSAVIDDGIKSIYNOLNYSNIRKFLMHP--KSF 536
 QY 662 STDOTSTSLTESVSSSGGEEPPALPKSLISGSC 699
 DB 537 SNVSDSDSVTRDSEDAINDEEMPLEIPVVKPSC 574

RESULT 15
 Q9AY10
 ID Q9AY10 PRELIMINARY; PRT: 1058 AA.
 AC Q9AY10
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Putative cas-pol polypeptide.
 GN OSUNBA0087H07.4;
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang R.A.; Frisch D.; Presting G.; Wood T.; Yu Y.; Soderlund C.;
 RA Kim H.-R.; Rambo T.; Henry D.; Simmons J.;
 RT "Rice Genomic Sequence."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC074283; AAK02020.2;
 RW POLYPROTEIN.
 SQ SEQUENCE 1058 AA; 115228 MW; 9E39B2C564FC6CE7 CRC64;

Query Match 2.8%; Score 108; DB 10; Length 1058;
 Best Local Similarity 22.1%; Pred. No. 1.7;
 Matches 85; Conservative 52; Mismatches 131; Indels 116; Gaps 21;

QY 416 HKGGGRSGKGEFLVAVSAIAEKL-----PQAKSSAALSFIAY-- 457
 DB 204 NRGSGSGRGSGDKPKPKPCQLCGKVGHTVAKCWKRFDPSTREKSTATNTSSYGIDT 263
 QY 458 --TFDYSCGDVPGILD--LSTKYRLMDNLPLQGLSHLSRDHGLQEPGHTROGSRNRY-- 512
 DB 264 NTVDSNATDHITGEMKLSVKDKYHGS-----EOVHAGGTGHEDANPAROPNLRYNH 318
 QY 513 ----PFSKSGRSIYVAICMHO-----FIDEEDPMEKQVFPF--HP-PPLR 552
 DB 319 KLEFNSK--QCAFYGYTLHGKFKCLDSTGRVYISRDV-VFDEQYIYFFANLHPNAGAR 375
 QY 553 YREPVFL-----EKFD--SGLVLDNVMCKPGP-----ESDFCLKVE 585
 DB 376 LRSEVLVLPDLLPPTQFDGGAVVNDQPMIDDPNHTNQTAETDADRGAVONSEPTGENN 435
 QY 586 AAVLGATGP-----ADSOHESQHGGLQDGEARPDALGSAALQPLLETVKAG----- 632
 DB 436 ASNGTEFGGHDHFMHGTESGSGQRTGSPHEDDAAASDAVA-----ESGNTGT 487
 QY 633 SPDMPRDSG--YDSSVSPSSSLPLMEGLSTDTOTSTSLTESVSSSGL-----GEEPP 687
 DB 488 SPAGPTAAGHAEZESQSSSISAP-----HDSPSASTPGSDASDGVAESGEGQQP 540
 QY 688 AL-PSNLLSSGSKADLCGRSYTD 710
 DB 541 MGPATRSRHGHKIP-----KMYTD 560

Mon May 19 09:52:44 2003

us-09-912-157-2_copy_36_753.rspt

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Search completed: May 19, 2003, 09:23:54
Job time : 63.3267 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 19, 2003, 09:07:58 : Search time 31.4416 Seconds
(without alignments)
1771.498 Million cell updates/sec

Title: US-09-912-157-2_COPY_336_753

Perfect score: 2210
Sequence: 1 RKQOENIYSHLDESSS.....CMLDLCRSYDELHVAFL 418

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_101002.*
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8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
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23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2210	100.0	738	22 AAU04958	Human Interleukin
2	2210	100.0	738	22 AAU11355	Human DNAX cytokin
3	2210	100.0	739	22 AAU10602	Human interleukin
4	2210	100.0	739	22 ABB07628	Human cytokine rec
5	2210	100.0	733	23 ABB07628	Human cytokine rec
6	2206	99.8	753	23 ABB07627	Human cytokine rec
7	2201	99.6	738	22 AAU09904	Human Interleukin
8	2201	99.6	738	22 AAU09951	Human Interleukin
9	2201	99.6	738	22 AAU09952	Human Interleukin
10	2197	99.4	738	22 AAU09953	Human Interleukin

11	2196	99.4	738	22 AAU09954	Human Interleukin
12	2194	99.3	738	22 AAU09956	Human Interleukin
13	2190	99.1	738	22 AAU09955	Human Interleukin
14	2190	99.1	738	22 AAU09957	Human Interleukin
15	1813.5	82.1	739	23 ABB07630	Murine cytokine re
16	984.5	44.5	554	23 AAU91330	Human novel secret
17	310	14.0	866	17 AAU04185	Human Interleukin
18	310	14.0	866	19 AAU61272	Human Interleukin
19	310	14.0	866	20 AAU92409	Human IL-17R prote
20	310	14.0	866	21 AAU99941	Human IL-17R prote
21	310	14.0	866	21 AAU97131	Human Interleukin
22	310	14.0	866	21 AAU97131	Human Interleukin
23	310	14.0	866	21 AAB03807	Human IL-17R (hCTP)
24	310	14.0	866	22 AAB02066	Human Interleukin
25	310	14.0	866	22 AAU72754	Murine Interleukin
26	289.5	13.1	864	17 AAU04184	Mouse Interleukin
27	289.5	13.1	864	19 AAU61271	Murine IL-17R prot
28	289.5	13.1	864	20 AAU92408	Murine IL-17R prot
29	289.5	13.1	864	21 AAU99935	Murine Interleukin
30	289.5	13.1	864	21 AAU97130	Murine Interleukin
31	289.5	13.1	864	21 AAU97130	Murine Interleukin
32	289.5	13.1	864	21 AAB03806	Murine IL-17R poly
33	289.5	13.1	864	22 AAB02060	Murine Interleukin
34	289.5	13.1	864	22 AAU72748	Murine Interleukin
35	271.5	12.3	539	23 AAU47457	Human IL-17 recept
36	132.5	6.0	238	20 AAU31624	Human IL-17RH matu
37	127.5	5.8	191	21 AAB15550	Human immune syste
38	127.5	5.8	296	23 ABB84242	Human secreted pro
39	127.5	5.8	385	21 AAB25795	Human secreted pro
40	127.5	5.8	385	22 AAB75381	Human IL-17 recept
41	127.5	5.8	385	23 AAU47439	Human PKO polypept
42	127.5	5.8	502	22 AAU29223	Human EST encoded
43	127.5	5.8	502	22 AAU43439	Human Interleukin
44	127.5	5.8	502	22 AAU04955	Human protein havi
45	127.5	5.8	502	22 AAE06586	

ALIGNMENTS

RESULT 1

AAU04958
ID AAU04958 standard; Protein; 728 AA.

XX AC AAU04958;

XX DT (first entry)

XX DE Human Interleukin 17 receptor, IL-17RH4.

XX KW Human; Interleukin-17 receptor; IL-17RH4; agonist; antagonist;
PRO20026; DNA 154095-2998; systemic lupus erythematosus;
rheumatoid arthritis; osteoarthritis; diabetes mellitus;
allergic disease; asthma; demyelinating disease;
degenerative cartilaginous disorder; transplantation associated disease.

XX OS Homo sapiens.

Key	Region	Location/Qualifiers
FT	19..24	/note- "N-myristoylation site"
FT	31..34	/note- "Asn is N-glycosylated"
FT	38..41	/note- "Asn is N-glycosylated"
FT	56..59	/note- "Asn is N-glycosylated"
FT	113..116	/note- "Asn is N-glycosylated"
FT	147..150	/note- "Asn is N-glycosylated"
FT	182..185	/note- "Asn is N-glycosylated"
FT		/note- "Asn is N-glycosylated"

Region: 232..235
/note="cAMP/GMP-dependent protein kinase phosphorylation site"
Modified-site: 266..269
Domain: 283..307
/note="Asn is N-glycosylated"
/note="Transmembrane domain"
Region: 312..319
/note="Tyrosine kinase phosphorylation site"
Region: 375..380
/note="N-myristoylation site"
Region: 416..424
/note="Tyrosine kinase phosphorylation site"
Region: 428..433
/note="N-myristoylation site"
Region: 429..434
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Region: 432..437
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Region: 433..436
/note="N-myristoylation site"
Region: 517..522
/note="Glycosaminoglycan attachment site"
Region: 574..579
/note="N-myristoylation site"
Region: 652..657
/note="N-myristoylation site"
Region: 707..712
/note="N-myristoylation site"
WO200146420-A2.
28-JUN-2001.
20-DEC-2000; 2000WO-US34956.
23-DEC-1999; 99US-0172096.
30-DEC-1999; 99WO-US31274.
11-JAN-2000; 2000US-0175481.
18-FEB-2000; 2000WO-US04341.
02-MAR-2000; 2000WO-US05841.
21-MAR-2000; 2000US-0191007.
21-MAR-2000; 2000WO-US07532.
02-JUN-2000; 2000WO-US15264.
22-JUN-2000; 2000US-0213087.
22-AUG-2000; 2000US-0644848.
24-AUG-2000; 2000WO-US33328.
24-OCT-2000; 2000US-0242837.
10-NOV-2000; 2000WO-US30873.
28-NOV-2000; 2000US-0253646.
01-DEC-2000; 2000WO-US32678.
(GETE) GENENTECH INC.
Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Li H, Hillan KJ, Tumas D, Van Lookeren M, Vandlen RL, Watanabe CK, Williams PM, Wood WI, Yansura DG;
WPI; 2001-451708/48.
N-PSDB; AAS09517.
Novel PRO polypeptides homologous to Interleukin-17, useful for the diagnosis and treatment of immune related disease e.g. rheumatoid arthritis and diabetes
Claim 10; Fig 18; 188pp; English.
The sequence is PRO20026 which is the human Interleukin 17 receptor, IL-17RA4, encoded by DNA 154095-2998. A composition containing ant/agonists to the PRO polypeptides or individual components are useful for treating a mammal with an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an

CC idiopathic inflammatory myopathy; Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease, an autoimmune or immune-mediated skin disease, contact dermatitis, an allergic disease e.g. food hypersensitivity, asthma, a transplantation associated disease, or a chronic inflammatory demyelinating polyneuropathy. Treating a degenerative cartilaginous disorder comprises administering a PRO1031 or PRO1122 polypeptide-agonist, or antagonist to the mammal. Numerous examples of the diseases and disorders are given in the specification.
XX
SQ Sequence 728 AA;
Query Match 100.0%; Score 2210; DB 22; Length 728;
Best Local Similarity 100.0%; Pred: No 1.7e-210;
Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RKQQNIYSHLDESSSTTTAALPRERLPRPRVFLCTSSKDGQNNVVOCPAYFL 60
Db 311 RKQQNIYSHLDESSSTTTAALPRERLPRPRVFLCTSSKDGQNNVVOCPAYFL 370
QY 61 QPCGCEVALDLWEDFSLCRGQREWIQIHESQFIIVVCSKGMKYFYDKNKKHGGG 120
Db 371 QPCGCEVALDLWEDFSLCRGQREWIQIHESQFIIVVCSKGMKYFYDKNKKHGGG 430
QY 121 RSGGKGLFLVAVSAIAEKLQAKQSSAALSKEFIATVDFSCSDVPGILDISTYRLM 180
Db 431 RSGGKGLFLVAVSAIAEKLQAKQSSAALSKEFIATVDFSCSDVPGILDISTYRLM 490
QY 181 DNLPLQCSHLRSRDLQEPQHTROGSRNTFRSKSGRSYVAICNNHOFIDEEPWFEE 240
Db 491 DNLPLQCSHLRSRDLQEPQHTROGSRNTFRSKSGRSYVAICNNHOFIDEEPWFEE 550
QY 241 KQVFPHPPLRYREPVLKPFDSGLVLDVNCVKGPSDFCLKVEAVLGAATGAPDSQHE 300
Db 551 KQVFPHPPLRYREPVLKPFDSGLVLDVNCVKGPSDFCLKVEAVLGAATGAPDSQHE 610
QY 301 SQHGGLDQDGEARPALDGSAAALPFLHTVKAQSPDMPDSDGIYDSSVSPSELPLMDG 360
Db 611 SQHGGLDQDGEARPALDGSAAALPFLHTVKAQSPDMPDSDGIYDSSVSPSELPLMDG 670
QY 361 LSTDQETSSLTSSVSSSGIGEEPPALPSSKLLSGSKADLCGRSYTDELHVAPL 418
Db 671 LSTDQETSSLTSSVSSSGIGEEPPALPSSKLLSGSKADLCGRSYTDELHVAPL 728

RESULT 2
AAU11355
ID AAU11355 standard; Protein; 738 AA.
XX AC AAU11355;
XX DT 26-MAR-2002 (first entry)

XX DE Human DNAX cytokine receptor subunit 8 (DCRS8) polypeptide.
XX KW Human; DNAX cytokine receptor subunit 8; DCRS8; phosphate labelling;
XX OS Homo sapiens.
XX Key Location/Qualifiers
XX FT Misc-difference 25 /label= Val
XX FT /note= "Encoded by GTN"

XX WO200190358-A2.
XX PD
XX PF 23-MAY-2001; 2001WO-US16767.
XX PR 24-MAY-2000; 2000US-206862P.

XX PA (SCHE) SCHERING CORP.
XX PI Gorman DM;
XX DR WPI: 2002-106198/14.
XX DR N-PSDB; AAS18134.
XX
XX Isolated antigenic human or mouse DNAX receptor subunit-like
XX polypeptide useful for detecting antibodies generated in response to
XX presence of increased protein levels or immunological disorders -
XX
XX Claim 1; Page 25; 148pp; English.
XX
XX The invention relates to primate and rodent DNAX cytokine receptor
XX subunit (DCRS) polypeptides and the polynucleotides encoding them. The
XX receptors, or their portions may be useful as phosphate labelling enzymes
XX to label general or specific substrates. The subunits may also be
XX functional immunogens to elicit recognising antibodies, or antigens
XX capable of binding antibodies. A combination, e.g., including a DCRS can
XX be used as an immunogen for the production of antisera or antibodies
XX capable of distinguishing between other cytokine receptor family members.
XX A purified DCRS can also be used as a reagent to detect antibodies
XX generated in response to the presence of elevated levels of expression,
XX or immunological disorders which lead to antibody production to the
XX endogenous receptor. This sequence represents the human DCRS
XX polypeptide.
XX
XX Sequence 738 AA;
XX
XX Query Match 100.0%; Score 2210; DB 23; Length 738;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-210;
XX Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 RKQENIYSHLDESSSTYTAALPRRLPRKPVFLCYSSKDGQNMNVQCFAYFL 60
XX 321 RKQENIYSHLDESSSTYTAALPRRLPRKPVFLCYSSKDGQNMNVQCFAYFL 380
XX
XX 61 QDFCGCEVALDWEFSLCREGQREWIQIHESQPIIIVVCSKGMKIFVDRKNTKKG 120
XX 381 QDFCGCEVALDWEFSLCREGQREWIQIHESQPIIIVVCSKGMKIFVDRKNTKKG 440
XX
XX 121 RSGSGELFVAVSAIAKLRQAKSSAALSFIAYFYDSCGDVPCILDLTKRYLM 180
XX 441 RSGSGELFVAVSAIAKLRQAKSSAALSFIAYFYDSCGDVPCILDLTKRYLM 500
XX
XX 181 DNLPLCSHLHSDRGHGLAEPQHTROGSRNRYFRSKSGSLYVAICNMQHFI 240
XX 501 DNLPLCSHLHSDRGHGLAEPQHTROGSRNRYFRSKSGSLYVAICNMQHFI 560
XX
XX 241 KQVFPHPPLRYRPLVLEKFDGLVNDVYKAPGPFDFCLKVAAVLGATGADSO 300
XX 561 KQVFPHPPLRYRPLVLEKFDGLVNDVYKAPGPFDFCLKVAAVLGATGADSO 620
XX
XX 301 SQGGGLDQGEARPDALQPLHTVTRAGSPDMRDSGIYDSSVPSSELSPLMEG 360
XX 621 SQGGGLDQGEARPDALQPLHTVTRAGSPDMRDSGIYDSSVPSSELSPLMEG 680
XX
XX 361 LSTDQETSLSESVSSSSGLGEPEPALPSKLLSSGCKADLCGRSYTDELHVA 418
XX 681 LSTDQETSLSESVSSSSGLGEPEPALPSKLLSSGCKADLCGRSYTDELHVA 738
XX

RESULT 3
AAU10602
ID AAU10602 standard; Protein; 739 AA.
XX AC AAU10602;
XX
XX (first entry)
XX Human Interleukin 17 (IL-17) receptor-like protein version 2.
XX

KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
KW hepatitis; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
KW bone disease; vascular disorder; eye disorder; cancer; human.
XX
XX Homo sapiens.
XX OS
XX WO200168859-A2.
XX
XX 20-SEP-2001.
XX
XX 15-MAR-2001; 2001WO-US08678.
XX
XX 16-MAR-2000; 2000US-189816P.
XX
XX 28-NOV-2000; 2000US-0724460.
XX
XX (AMGE-) AMGEN INC.
XX
XX Jing S;
XX
XX WPI: 2001-611392/70.
XX
XX N-PSDB; AAS16201.
XX
XX Nucleic acids encoding Interleukin 17 receptor like polypeptides,
XX useful for preventing, diagnosing and treating, e.g. leukaemia, asthma,
XX diabetes, psoriasis and glaucoma
XX
XX Claim 2; Fig 1; 158pp; English.
XX
XX The invention describes novel nucleic acids encoding Interleukin (IL) 17
XX receptor-like polypeptides useful as vaccines and in gene therapy. These
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
XX osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and
XX ophthalmological activities. The IL-17 receptor like nucleic acids and
XX proteins may be used to prevent and treat diseases associated with
XX inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
XX include, for example immune disorders (e.g. inflammation, diabetes and
XX transplant rejection), infections (e.g. hepatitis and septicemia),
XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal
XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
XX (e.g. stroke and atherosclerosis, cancers (e.g. leukaemia, myeloma and
XX breast cancer), reproductive disorders (e.g. infertility and
XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
XX DNA and its complements may also be used as diagnostic probes to detect and
XX quantitate the presence of similar nucleic acids in samples and identify
XX patients needing restorative therapy. The IL17rlp may also be used as
XX antigens in the production of antibodies against the proteins and in
XX assays to identify modulators of expression and activity. The
XX anti-IL17rlp antibodies and antagonists may also be used to down regulate
XX expression and activity. This is the amino acid sequence of human
XX Interleukin 17 (IL-17) receptor like protein described in the method of
XX the invention.
XX Note: Residues 1-288 of this sequence correspond to residues 8-296 of the
XX sequence shown in AAU10601 which is incomplete in the specification.
XX
XX Sequence 739 AA;
XX

Query Match 100.0%; Score 2210; DB 22; Length 739;
Best Local Similarity 100.0%; Pred. No. 1.8e-210;
Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 RKQENIYSHLDESSSTYTAALPRRLPRKPVFLCYSSKDGQNMNVQCFAYFL 60
XX 322 RKQENIYSHLDESSSTYTAALPRRLPRKPVFLCYSSKDGQNMNVQCFAYFL 381
XX

QY 61 QDFCGEVALDMEFSLCRGQREWVIOKIHESOFIIVVCSKGMKIFVDRKKNYKHGGG 120
 DB 382 QDFCGEVALDMEFSLCRGQREWVIOKIHESOFIIVVCSKGMKIFVDRKKNYKHGGG 441
 QY 121 RSGSGELFLVAVSAIAEKLQAKQSSSAALSKFIATVFDYSCGDPVGLDLSKYRLM 180
 DB 442 RSGSGELFLVAVSAIAEKLQAKQSSSAALSKFIATVFDYSCGDPVGLDLSKYRLM 501
 QY 181 DNLPCSLHLSRDLGQEPGQHTROGRRNYFRSKSGSLYVAICNMHOFIDEEPWF 240
 DB 502 DNLPCSLHLSRDLGQEPGQHTROGRRNYFRSKSGSLYVAICNMHOFIDEEPWF 561
 QY 241 KQVFPFPPPLRYREPVLKFDGSLVNDVCKPGPESDFCLKVEAVLGATGPADSOHE 300
 DB 562 KQVFPFPPPLRYREPVLKFDGSLVNDVCKPGPESDFCLKVEAVLGATGPADSOHE 360
 QY 301 SOHGLDQDGEARPDGSAALQPLLTHTYKAGSPDMPRDGIYDSSVPSSELSLPLMEG 621
 DB 622 SOHGLDQDGEARPDGSAALQPLLTHTYKAGSPDMPRDGIYDSSVPSSELSLPLMEG 681
 QY 361 LSTQDTSTSSVSSSGIGEEPPALPSKLLSSGCKADLCRSYTDDELHVAAPL 418
 DB 682 LSTQDTSTSSVSSSGIGEEPPALPSKLLSSGCKADLCRSYTDDELHVAAPL 739

RESULT 4

ABB07628
 ID ABB07628 standard; Protein; 739 AA.
 AC ABB07628;
 DT 2001W0-0523253 (first entry)
 DE Human cytokine receptor, Zcytor18 splice variant.
 KW Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;
 KW pulmonary alveolar proteinosis; familial periodic fever; antitumor;
 KW erythroleukemia; chromosome 3p14.3; gene therapy; splice variant.
 OS Homo sapiens.
 PN WO200208259-A2.
 PD 31-JAN-2002.
 PF 23-JUL-2001; 2001W0-0523253.
 PR 26-JUL-2000; 2000US-220747P.
 PA (Zymo) ZYMOGENETICS INC.
 PI Presnell SR, Kuestner RE, Gao Z;
 DR WPI; 2002-217048/27.
 DR N-PSDB; ABA95033, ABA95036.
 XX New cytokine receptor polypeptide designated zcytor18, useful for
 XX inhibiting cell proliferation associated with psoriasis or tumor
 XX growth, and modulating immune system by binding to endogenous zcytor18
 XX ligand
 XX Claim 1; Page 102-106; 119pp; English.

The invention relates to an isolated cytokine receptor polypeptide designated Zcytor18. The Zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumor growth. The encoding nucleic acids are useful for providing Zcytor18 in vivo by gene therapy techniques. Zcytor18 oligonucleotide probes are useful for in vivo diagnosis, and the Zcytor18 probes and primers can be used to detect and localize Zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in

CC linkage-based testing of pulmonary alveolar proteinosis, familial
 CC periodic fever and erythroleukemia, and erythroleukemia associated with
 CC polymorphisms of cytokine receptors. The present sequence represents a
 CC human Zcytor18-splice variant.
 XX Sequence 739 AA;
 SO Query Match 100.0%; Score 2210; DB 23; Length 739;
 Best Local Similarity 100.0%; Pred. No. 1.8e-210; Indels 0; Gaps 0;
 Matches 418; Conservative 0; Mismatches 0;
 QY 1 RKQKQENIYSHLDESSSTYTAALPRELRPRPKVFLCYSSKDGQNNHNVQCFAYFL 60
 DB 322 RKQKQENIYSHLDESSSTYTAALPRELRPRPKVFLCYSSKDGQNNHNVQCFAYFL 381
 QY 61 QDFCGEVALDMEFSLCRGQREWVIOKIHESOFIIVVCSKGMKIFVDRKKNYKHGGG 120
 DB 382 QDFCGEVALDMEFSLCRGQREWVIOKIHESOFIIVVCSKGMKIFVDRKKNYKHGGG 441
 QY 121 RSGSGELFLVAVSAIAEKLQAKQSSSAALSKFIATVFDYSCGDPVGLDLSKYRLM 180
 DB 442 RSGSGELFLVAVSAIAEKLQAKQSSSAALSKFIATVFDYSCGDPVGLDLSKYRLM 501
 QY 181 DNLPCSLHLSRDLGQEPGQHTROGRRNYFRSKSGSLYVAICNMHOFIDEEPWF 240
 DB 502 DNLPCSLHLSRDLGQEPGQHTROGRRNYFRSKSGSLYVAICNMHOFIDEEPWF 561
 QY 241 KQVFPFPPPLRYREPVLKFDGSLVNDVCKPGPESDFCLKVEAVLGATGPADSOHE 300
 DB 562 KQVFPFPPPLRYREPVLKFDGSLVNDVCKPGPESDFCLKVEAVLGATGPADSOHE 621
 QY 301 SOHGLDQDGEARPDGSAALQPLLTHTYKAGSPDMPRDGIYDSSVPSSELSLPLMEG 681
 DB 622 SOHGLDQDGEARPDGSAALQPLLTHTYKAGSPDMPRDGIYDSSVPSSELSLPLMEG 681
 QY 361 LSTQDTSTSSVSSSGIGEEPPALPSKLLSSGCKADLCRSYTDDELHVAAPL 418
 DB 682 LSTQDTSTSSVSSSGIGEEPPALPSKLLSSGCKADLCRSYTDDELHVAAPL 739

RESULT 5

ABB07626
 ID ABB07626 standard; Protein; 753 AA.
 AC ABB07626;
 DT 2001W0-0523253 (first entry)
 DE Human cytokine receptor, Zcytor18 amino acid sequence.
 KW Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;
 KW pulmonary alveolar proteinosis; familial periodic fever; antitumor;
 KW erythroleukemia; chromosome 3p14.3; gene therapy.
 OS Homo sapiens.
 PN WO200208259-A2.
 PD 31-JAN-2002.
 PF 23-JUL-2001; 2001W0-0523253.
 PR 26-JUL-2000; 2000US-220747P.
 PA (Zymo) ZYMOGENETICS INC.
 PI Presnell SR, Kuestner RE, Gao Z;
 DR WPI; 2002-217048/27.
 DR N-PSDB; ABA95031, ABA95032.
 XX New cytokine receptor polypeptide designated zcytor18, useful for
 XX inhibiting cell proliferation associated with psoriasis or tumor

361 LSTDQETSLTSSVSSGSGEPPALPSPKLLSSGCKADLCGRSTYDELHAAVAPL 418
 696 LSTDQETSLTSSVSSGSGEPPALPSPKLLSSGCKADLCGRSTYDELHAAVAPL 753

RESULT 7
 AAU09904
 ID AAU09904 standard; Protein: 738 AA.
 XX AAU09904;
 XX 14-FEB-2002 (first entry)
 XX Human Interleukin 17 (hIL-17) receptor like protein.
 XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone disease; vascular disorder; eye disorder; cancer; human.
 XX Homo sapiens.
 OS
 XX WO200168859-A2
 XX 2001-11-01
 XX 15-MAR-2001; 2001WO-US08678.
 XX 16-MAR-2000; 2000US-189816P.
 XX 28-NOV-2000; 2000US-0724460.
 XX (AMGE-) ANGEN INC.
 XX JIng S;
 XX WPI: 2001-611392/70.
 XX N-PSDB; AAS15346.
 XX Nucleic acids encoding Interleukin 17 receptor like polypeptides,
 XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
 XX diabetes, psoriasis and glaucoma.
 XX Claim 2; Page 152-154; 158pp; English.
 XX The invention describes novel nucleic acids encoding Interleukin (IL) 17
 XX receptor like polypeptides useful as vaccines and in gene therapy. These
 XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
 XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 XX osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and
 XX ophthalmological activities. The IL-17 receptor like nucleic acids and
 XX proteins may be used to prevent and treat diseases associated with
 XX inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These
 XX include, for example immune disorders (e.g. inflammation, diabetes and
 XX transplant rejection), infections (e.g. hepatitis and septicemia),
 XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal
 XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 XX (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
 XX breast cancer), reproductive disorders (e.g. infertility and
 XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 XX DNA and its complements may also be used as diagnostic probes to detect and
 XX quantitate the presence of similar nucleic acids in samples and identify
 XX patients needing restorative therapy. The IL17rp may also be used as
 XX antigens in the production of antibodies against the proteins and in
 XX assays to identify modulators of expression and activity. The
 XX anti-IL17rp antibodies and antagonists may also be used to down regulate
 XX expression and activity. This is the amino acid sequence of the human

CC Interleukin 17 (IL-17) receptor like protein described in the method of
 CC the invention:
 XX Sequence 738 AA;
 Query Match 99.6%; Score 2201; DB 22; Length 738;
 Best Local Similarity 99.8%; Pred. No. 1.4e-209;
 Matches 416; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RKQENIYSHLDESESSSTTAALPRRLPRKPVLYCTSSKDGQNHVYVQCFAYPL 60
 DB 322 RKQENIYSHLDESESSSTTAALPRRLPRKPVLYCTSSKDGQNHVYVQCFAYPL 381
 QY 61 QDFCCEVALDLWEDFSLCREGQRENVQIKIHESQFIIVVCSKMKYFVDKKNYKKGKG 120
 DB 382 QDFCCEVALDLWEDFSLCREGQRENVQIKIHESQFIIVVCSKMKYFVDKKNYKKGKG 441
 QY 121 RSGGGEFLFVAVSAIAEKLRQAKSSAALSKFTAVFYDSCGDVPGILDSTYRLM 180
 DB 442 RSGGGEFLFVAVSAIAEKLRQAKSSAALSKFTAVFYDSCGDVPGILDSTYRLM 501
 QY 181 DNLPLQCSHLHSRDHQLQEPQTRQSGRRNFRSKSGSLYVAICNMHOFIDEEPWF 240
 DB 502 DNLPLQCSHLHSRDHQLQEPQTRQSGRRNFRSKSGSLYVAICNMHOFIDEEPWF 561
 QY 241 KQVFPHPPPLRYREPVLKFDGSLVNDVCKPGPESDFCLAYEAAVIGATGAPDSQHE 300
 DB 562 KQVFPHPPPLRYREPVLKFDGSLVNDVCKPGPESDFCLAYEAAVIGATGAPDSQHE 621
 QY 301 SQHGGLDQGGARPALDGSAAQLPILHTVYKAGSPDMPRDSGIYDSSVPSSELSPLMEG 360
 DB 622 SQHGGLDQGGARPALDGSAAQLPILHTVYKAGSPDMPRDSGIYDSSVPSSELSPLMEG 681
 QY 361 LSTDQETSLTSSVSSGSGEPPALPSPKLLSSGCKADLCGRSTYDELHAAVAP 417
 DB 682 LSTDQETSLTSSVSSGSGEPPALPSPKLLSSGCKADLCGRSTYDELHAAVAP 738

RESULT 8
 AAU09951
 ID AAU09951 standard; Protein: 738 AA.
 XX AAU09951;
 XX (first entry)
 XX Human Interleukin 17 (hIL-17) receptor like protein-substitution #1.
 XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 KW mutin.
 XX Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 XX Misc-difference 45 /label= Gly, Pro or Ala
 XX WO200168859-A2.
 XX 20-SEP-2001.
 XX 15-MAR-2001; 2001WO-US08678.
 XX 16-MAR-2000; 2000US-189816P.
 XX 28-NOV-2000; 2000US-0724460.

(AMGE-) AMGEN INC.

Jing S:

WPI: 2001-611392/70.

Nucleic acids encoding Interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma

Claim 18; Page 7; 158pp; English.

The invention describes novel nucleic acids encoding Interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, osteopathic, osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17r) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also be used as diagnostic probes to detect and quantify the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17r may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-IL17r antibodies and antagonists may also be used to down regulate expression and activity.

Note: This sequence is not given in the specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AA009904) and has been created according to information given in claim 18.

Sequence 738 AA:

Query Match 99.6%; Score 2201; DB 22; Length 738;
Best Local Similarity 99.8%; Pred. NO. 1.4e-209;
Matches 416; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKQENIYSHLDESSSTYTAALPRRLPRPKVFLCYSSKDGQGNHNVVQCFAYFL 60
DB 322 RKQENIYSHLDESSSTYTAALPRRLPRPKVFLCYSSKDGQGNHNVVQCFAYFL 381
QY 61 QDFCCFVALDLWDFSLCREGQREWIQIHESQFIIVCGSKGMYFDDKRYKHGGG 120
DB 382 QDFCCFVALDLWDFSLCREGQREWIQIHESQFIIVCGSKGMYFDDKRYKHGGG 441
QY 121 RGSKGELFLVAVSAIAEKLQAKQSSAALSKEFLVDFYSCBGPVGLDLSTYRLM 180
DB 442 RGSKGELFLVAVSAIAEKLQAKQSSAALSKEFLVDFYSCBGPVGLDLSTYRLM 501
QY 181 DMLPOLCSHLHSRDLQEPQTRGSRNRTFRSKRSRSLYVAICNHHQFIDEEPDPWE 240
DB 502 DMLPOLCSHLHSRDLQEPQTRGSRNRTFRSKRSRSLYVAICNHHQFIDEEPDPWE 561
QY 241 KQFVFPHPPLRYREPVLKFDGLVNDVCKPGPSDFCLKYEAVLGLATGPDQSQHE 300
DB 562 KQFVFPHPPLRYREPVLKFDGLVNDVCKPGPSDFCLKYEAVLGLATGPDQSQHE 621
QY 301 SQBGLDQDGEARPDGSAALQPLHTYKAGSPDMPDSDGIVDSSVPSSELSPLMGG 360
DB 622 SQBGLDQDGEARPDGSAALQPLHTYKAGSPDMPDSDGIVDSSVPSSELSPLMGG 681
QY 361 LSTDQETSSITSSVSSSGIGEEPPALPSKLLSSGCKADLACRSYTDLHAVAP 417

DB 682 LSTDQETSSITSSVSSSGIGEEPPALPSKLLSSGCKADLACRSYTDLHAVAP 738

RESULT 9

AA009952

ID AA009952 standard; Protein; 738 AA

XX AC AA009952;

XX 14-FEB-2002 (first entry)

XX Human Interleukin 17 (hIL-17) receptor like protein substitution #2.

XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
XX anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
XX hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
XX anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
XX vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;
XX hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
XX bone disease; vascular disorder; eye disorder; cancer; human; mutant;
XX mutein.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 227

XX /Label- Phe, Leu, Val, Ile, Ala, Tyr

XX WO200168859-A2

XX 15-MAR-2001; 2001WO-0508678

XX 16-MAR-2000; 2000US-189816P

XX 28-NOV-2000; 2000US-0724460

XX (AMGE-) AMGEN INC.

XX Jing S;

XX WPI: 2001-611392/70

XX Nucleic acids encoding Interleukin 17 receptor like polypeptides,
XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
XX diabetes, psoriasis and glaucoma

XX Claim 19; Page 7; 158pp; English.

XX The invention describes novel nucleic acids encoding Interleukin (IL) 17
XX receptor like polypeptides useful as vaccines and in gene therapy. These
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
XX osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and
XX ophthalmological activities. The IL-17 receptor like nucleic acids and
XX proteins may be used to prevent and treat diseases associated with
XX inappropriate IL-17 receptor like polypeptide (IL17r) expression. These
XX include, for example immune disorders (e.g. inflammation, diabetes and
XX transplant rejection), infections (e.g. hepatitis and septicemia),
XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal
XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
XX (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
XX breast cancer), reproductive disorders (e.g. infertility and
XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
XX DNA and its complements may also be used as diagnostic probes to detect and
XX quantify the presence of similar nucleic acids in samples and identify
XX patients needing restorative therapy. The IL17r may also be used as

CC antigens in the production of antibodies against the proteins and in
CC assays to identify modulators of expression and activity. The
CC anti-IL17 receptor-like polypeptides may also be used to down regulate
CC expression and activity.
CC Note: This sequence is not given in the specification but is based on the
CC human Interleukin 17 (IL-17) receptor like protein sequence (AA09904)
CC and has been created according to information given in claim 19.
XX
SQ Sequence 738 AA.

Query Match 99.6%; Score 2201; DB 22; Length 738;
Best Local Similarity 99.8%; Pred. No. 1.4e-209;
Matches 416; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RKQENIYSHLDESSSTTTAALPRRLPRPKVFLCYSKDGQNNHNVQCFAYEL 60
DB 322 RKQENIYSHLDESSSTTTAALPRRLPRPKVFLCYSKDGQNNHNVQCFAYEL 381
QY 61 QDFCGCEVALDWEFSLCRGQREWIYQKHESQFIIVVCSKGMKYFVCKNKYKRGGG 120
DB 382 QDFCGCEVALDWEFSLCRGQREWIYQKHESQFIIVVCSKGMKYFVCKNKYKRGGG 441
QY 121 RSGSGELFLVAVSAIAEKLRQAKQSSAALSKFIATVFDYSCGDVPGILDSTYRLM 180
DB 442 RSGSGELFLVAVSAIAEKLRQAKQSSAALSKFIATVFDYSCGDVPGILDSTYRLM 501
QY 181 DNLPLCSLHSDRGLOEPQGTROGSRNRYFRSKGRSLYVAICNNHOFIDEEPWF 240
DB 502 DNLPLCSLHSDRGLOEPQGTROGSRNRYFRSKGRSLYVAICNNHOFIDEEPWF 561
QY 241 KQVFPFPPPLRYREPLEKFDGLVNDVCKPGPESDFCLKVAAPVLGATGPADSQHE 300
DB 562 KQVFPFPPPLRYREPLEKFDGLVNDVCKPGPESDFCLKVAAPVLGATGPADSQHE 621
QY 301 SOHGLDQGEARPALDGSALQPLHTYKAGSPDMPDSGIYDSSVPSSELSPLMEG 360
DB 622 SOHGLDQGEARPALDGSALQPLHTYKAGSPDMPDSGIYDSSVPSSELSPLMEG 681
QY 361 LSTQDTTSLTSSVSSSGLEGEPPALPSKLLSGCKADLGCRSTYDELHAPV 417
DB 682 LSTQDTTSLTSSVSSSGLEGEPPALPSKLLSGCKADLGCRSTYDELHAPV 738

RESULT 10
AA09953
ID AA09953 standard; Protein: 738 AA.
XX
AC AA09953;
XX
DT 14-EP-2003 (first entry)
XX
DE Human Interleukin 17 (hIL-17) receptor like protein substitution #3.
XX
KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-picrobial;
KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
KW mutelin.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 363
FT /label= Ser, Thr, Ala, Cys
XX
PN WO200168859-A2.
XX
PD 20-SEP-2001.
XX

PF 15-MAR-2001; 2001WO-US08678
XX
PR 16-MAR-2000; 2000US-189816P
PR 28-NOV-2000; 2000US-0724460
XX
PA (AMGE-) AMGEN INC.
XX
PI Jing S;
XX
DR WPI; 2001-611392/70.
XX
PT Nucleic acids encoding interleukin 17 receptor-like polypeptides,
PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
PT diabetes, psoriasis and glaucoma.
XX
PS Claim 20; Page -; 158pp; English.
XX
CC The invention describes novel nucleic acids encoding interleukin (IL) 17
CC receptor like polypeptides useful as vaccines and in gene therapy. These
CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and
CC ophthalmological activities. The IL-17 receptor like nucleic acids and
CC proteins may be used to prevent and treat diseases associated with
CC inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
CC include, for example immune disorders (e.g. inflammation, diabetes and
CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
CC breast cancer), reproductive disorders (e.g. infertility and
CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
CC DNA and its complements may also be used as diagnostic probes to detect and
CC quantitate the presence of similar nucleic acids in samples and identify
CC patients needing restorative therapy. The IL17rlp may also be used as
CC antigens in the production of antibodies against the proteins and in
CC assays to identify modulators of expression and activity. The
CC anti-IL17rlp antibodies and antagonists may also be used to down regulate
CC expression and activity.
CC Note: This sequence is not given in the specification but is based on the
CC human Interleukin 17 (IL-17) receptor like protein sequence (AA09904)
CC and has been created according to information given in claim 20.
XX
SQ Sequence 738 AA;

Query Match 99.4%; Score 2197; DB 22; Length 738;
Best Local Similarity 99.5%; Pred. No. 3.4e-209;
Matches 415; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 RKQENIYSHLDESSSTTTAALPRRLPRPKVFLCYSKDGQNNHNVQCFAYEL 60
DB 322 RKQENIYSHLDESSSTTTAALPRRLPRPKVFLCYSKDGQNNHNVQCFAYEL 381
QY 61 QDFCGCEVALDWEFSLCRGQREWIYQKHESQFIIVVCSKGMKYFVCKNKYKRGGG 120
DB 382 QDFCGCEVALDWEFSLCRGQREWIYQKHESQFIIVVCSKGMKYFVCKNKYKRGGG 441
QY 121 RSGSGELFLVAVSAIAEKLRQAKQSSAALSKFIATVFDYSCGDVPGILDSTYRLM 180
DB 442 RSGSGELFLVAVSAIAEKLRQAKQSSAALSKFIATVFDYSCGDVPGILDSTYRLM 501
QY 181 DNLPLCSLHSDRGLOEPQGTROGSRNRYFRSKGRSLYVAICNNHOFIDEEPWF 240
DB 502 DNLPLCSLHSDRGLOEPQGTROGSRNRYFRSKGRSLYVAICNNHOFIDEEPWF 561
QY 241 KQVFPFPPPLRYREPLEKFDGLVNDVCKPGPESDFCLKVAAPVLGATGPADSQHE 300
DB 562 KQVFPFPPPLRYREPLEKFDGLVNDVCKPGPESDFCLKVAAPVLGATGPADSQHE 621

QY 301 SOHGLDQDGEARPDGSAALQPLHTVKGSPDMPDRSGIYDSSVPSSELSIPLMEG 360
 DB 622 SOHGLDQDGEARPDGSAALQPLHTVKGSPDMPDRSGIYDSSVPSSELSIPLMEG 681
 QY 361 LSTDTSTSLTESVSSSGIGEEPPALPSKLLSSGCKADIGCRSYTDELHAPV 417
 DB 682 LSTDTSTSLTESVSSSGIGEEPPALPSKLLSSGCKADIGCRSYTDELHAPV 738

RESULT 11
 AAU09954
 ID AAU09954 standard; Protein; 738 AA.
 AC AAU09954
 XX
 XX 14-FEB-2002 (first entry)
 XX Human Interleukin 17 (hIL-17) receptor like protein substitution #4.
 XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KW vascular; cytosolic; anti-leukaemic; anti-infertility; ophthalmological;
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 KW mutin.
 XX Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 374 /label= Val, Ile, Met, Leu, Phe, Ala, Nle
 FT
 XX WO200168859-A2.
 XX 15-MAR-2001; 2001WO-US08678.
 XX 16-MAR-2000; 2000US-189816P.
 PR 28-NOV-2000; 2000US-0724460.
 XX (AMGE-) AMGEN INC.
 XX Jing S.
 XX WPI; 2001-611392/70.
 XX Nucleic acids encoding interleukin 17 receptor like polypeptides,
 FT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
 FT diabetes, psoriasis and glaucoma.
 XX Claim 21; Page -; 158pp; English.
 XX The invention describes novel nucleic acids encoding interleukin (IL) 17
 CC receptor like polypeptides useful as vaccines and in gene therapy. These
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 CC osteopathic, vascular, cytosolic, anti-leukaemic, anti-infertility and
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and
 CC proteins may be used to prevent and treat diseases associated with
 CC inappropriate IL-17 receptor like polypeptide (IL17rip) expression. These
 CC include, for example immune disorders (e.g. inflammation, diabetes and
 CC transplant rejection), infections (e.g. hepatitis and septicemia),
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and

CC breast cancer), reproductive disorders (e.g. infertility and
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 CC DNA and its complements may also be used as diagnostic probes to detect and
 CC quantitate the presence of similar nucleic acids in samples and identify
 CC patients needing restoration therapy. The IL17rip may also be used as
 CC antigens in the production of antibodies against the proteins and in
 CC assays to identify modulators of expression and activity. The
 CC anti-IL17rip antibodies and antagonists may also be used to down regulate
 CC expression and activity.
 CC Note: This sequence is not given in the specification but is based on the
 CC human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)
 CC and has been created according to information given in claim 21.
 XX Sequence 738 AA;
 SQ

Query Match 99.4%; Score 2196; DB 22; Length 738;
 Best Local Similarity 99.5%; Pred. No. 4.3e-209;
 Matches 415; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RKQOENIYSHLDESSSESYTAALPRERLRPRKPVFLCYCKDQONHNVVOCFAFL 60
 DB 322 RKQOENIYSHLDESSSESYTAALPRERLRPRKPVFLCYCKDQONHNVVOCFAFL 381
 QY 61 QPCGCEVALDWEDEFSLCRBQREWIQIHESQFIIVVCSKGMKYFVDDKNYKHGGG 120
 DB 382 QPCGCEVALDWEDEFSLCRBQREWIQIHESQFIIVVCSKGMKYFVDDKNYKHGGG 441
 QY 121 RSGCKGELFLVAVSAIAEKLRQAKQSSSAALSFKFIATVDFYDCEGDVPGILDSTKYRLM 180
 DB 442 RSGCKGELFLVAVSAIAEKLRQAKQSSSAALSFKFIATVDFYDCEGDVPGILDSTKYRLM 501
 QY 181 DNLPLCSHLHSDRGLOPQOHTROGSRNRYFSKSGSLYVAICNNHOFIDEPOWFE 240
 DB 502 DNLPLCSHLHSDRGLOPQOHTROGSRNRYFSKSGSLYVAICNNHOFIDEPOWFE 561
 QY 241 KQVFPPEPPLRYREPVLKFDGSLVLDVNMCKPSPESDFCLKVEAAVIGATGADSOHE 300
 DB 562 KQVFPPEPPLRYREPVLKFDGSLVLDVNMCKPSPESDFCLKVEAAVIGATGADSOHE 621
 QY 301 SOHGLDQDGEARPDGSAALQPLHTVKGSPDMPDRSGIYDSSVPSSELSIPLMEG 360
 DB 622 SOHGLDQDGEARPDGSAALQPLHTVKGSPDMPDRSGIYDSSVPSSELSIPLMEG 681
 QY 361 LSTDTSTSLTESVSSSGIGEEPPALPSKLLSSGCKADIGCRSYTDELHAPV 417
 DB 682 LSTDTSTSLTESVSSSGIGEEPPALPSKLLSSGCKADIGCRSYTDELHAPV 738

RESULT 12
 AAU09956
 ID AAU09956 standard; Protein; 738 AA.
 XX
 XX AAU09956;
 XX
 XX 14-FEB-2002 (first entry)
 XX Human Interleukin 17 (hIL-17) receptor like protein substitution #6.
 DE Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KW vascular; cytosolic; anti-leukaemic; anti-infertility; ophthalmological;
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 KW mutin.
 XX Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 515 /label= Asp, Glu
 FT

XX PN WO200168859-A2.
XX PD 20-SEP-2001.
XX PF 15-MAR-2001; 2001WO-US08678.
XX PR 16-MAR-2000; 2000US-189816P.
XX PR 28-NOV-2000; 2000US-0724460.
XX PA (AMGE-) AMGEN INC.
XX PI Jing S;
XX DR WPI; 2001-611392/70.
XX FT Nucleic acids encoding interleukin 17 receptor like polypeptides,
XX FT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
XX FT diabetes, psoriasis and glaucoma.
XX PS Claim 23; Page -: 158pp; English.
XX CC The invention describes novel nucleic acids encoding interleukin (IL) 17
XX CC receptor like polypeptides useful as vaccines and in gene therapy. These
XX CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
XX CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
XX CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
XX CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and
XX CC ophthalmological activities. The IL-17 receptor like nucleic acids and
XX CC proteins may be used to prevent and treat diseases associated with
XX CC inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
XX CC include, for example immune disorders (e.g. inflammation, diabetes and
XX CC transplant rejection), infections (e.g. hepatitis and septicemia),
XX CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
XX CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
XX CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
XX CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
XX CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
XX CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
XX CC breast cancer), reproductive disorders (e.g. infertility and
XX CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
XX CC DNA and its complements may also be used as diagnostic probes to detect and
XX CC quantitate the presence of similar nucleic acids in samples and identify
XX CC patients needing restorative therapy. The IL17rlp may also be used as
XX CC antigens in the production of antibodies against the proteins and in
XX CC assays to identify modulators of expression and activity. The
XX CC anti-IL17rlp antibodies and antagonists may also be used to down regulate
XX CC expression and activity.
XX CC Note: This sequence is not given in the specification but is based on the
XX CC human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)
XX CC and has been created according to information given in claim 23.
XX XI Sequence 738 AA;

Query Match 99.3%; Score 2194; DB 22; Length 738;
Best Local Similarity 99.5%; Pred. No. 6.8e-209;
Matches 415; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 RKQENIYSHLDEESSESTYTAALPRRLPRPKVFLCYSSKQDNMNVQCFAYFL 60
DB 322 RKQENIYSHLDEESSESTYTAALPRRLPRPKVFLCYSSKQDNMNVQCFAYFL 381
QY 61 QDFCCGVALDLWEDFSLCREGQRENVJQKHESQFIIVVCSKGMKIFDYDKNKHGGG 120
DB 382 QDFCCGVALDLWEDFSLCREGQRENVJQKHESQFIIVVCSKGMKIFDYDKNKHGGG 441
QY 121 RSGSGELFLVAVSAIAELKQAKOSSAALSKEFIIVFYDSCEGDPVGLDLSKFKRLM 180
DB 442 RSGSGELFLVAVSAIAELKQAKOSSAALSKEFIIVFYDSCEGDPVGLDLSKFKRLM 501
QY 181 DNLPLCSHLRSRDLQPGQHTQGRNRYFRSKRSRLYVAINCMEHQFIDEPWF 240
DB 502 DNLPLCSHLRSRDLQPGQHTQGRNRYFRSKRSRLYVAINCMEHQFIDEPWF 561

QY 241 KQFVPPHPPRLRYEPVLEKFDGLVNDVCKPGPESDFCLKVEAAVLGATGADSOHE 300
DB 562 KQFVPPHPPRLRYEPVLEKFDGLVNDVCKPGPESDFCLKVEAAVLGATGADSOHE 621
QY 301 SOHGLDQDGEARPALDGSAAALPILHTVKAGSPDMPDPSGIYDSSVPSSELSPLMEG 360
DB 622 SOHGLDQDGEARPALDGSAAALPILHTVKAGSPDMPDPSGIYDSSVPSSELSPLMEG 681
QY 361 LSTDQTTSSITSSVSSSSGIGEEPPALPSKLLSSGSKADLACRSTTDELHAPV 417
DB 682 LSTDQTTSSITSSVSSSSGIGEEPPALPSKLLSSGSKADLACRSTTDELHAPV 738
RESULT 13
AAU09955
ID AAU09955 standard; Protein; 738 AA.
XX AC AAU09955;
XX DT 14-FEB-2002 (first entry)
XX DE Human Interleukin 17 (hIL-17) receptor like protein substitution #5.
XX KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
XX KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
XX KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
XX KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
XX KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;
XX KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
XX KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
XX KW mutin.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 385 /label= Cys, Ser, Ala
XX FT WO200168859-A2.
XX PD 20-SEP-2001.
XX PF 15-MAR-2001; 2001WO-US08678.
XX PR 16-MAR-2000; 2000US-189816P.
XX PR 28-NOV-2000; 2000US-0724460.
XX PA (AMGE-) AMGEN INC.
XX PI Jing S;
XX DR WPI; 2001-611392/70.
XX FT Nucleic acids encoding interleukin 17 receptor like polypeptides,
XX FT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
XX FT diabetes, psoriasis and glaucoma.
XX PS Claim 23; Page -: 158pp; English.
XX CC The invention describes novel nucleic acids encoding interleukin (IL) 17
XX CC receptor like polypeptides useful as vaccines and in gene therapy. These
XX CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
XX CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
XX CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
XX CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and
XX CC ophthalmological activities. The IL-17 receptor like nucleic acids and
XX CC proteins may be used to prevent and treat diseases associated with
XX CC inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
XX CC include, for example immune disorders (e.g. inflammation, diabetes and
XX CC transplant rejection), infections (e.g. hepatitis and septicemia),
XX CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal

CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
 CC breast cancer), reproductive disorders (e.g. infertility and
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 CC DNA and its complements may also be used as diagnostic probes to detect and
 CC quantitate the presence of similar nucleic acids in samples and identify
 CC patients needing restorative therapy. The IL17rip may also be used as
 CC antigens in the production of antibodies against the proteins and in
 CC assays to identify modulators of expression and activity. The
 CC anti-IL17rip antibodies and antagonists may also be used to down regulate
 CC expression and activity.
 CC Note: This sequence is not given in the specification but is based on the
 CC human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)
 CC and has been created according to information given in claim 22.
 XX Sequence 738 AA;

Query Match 99.1%; Score 2190; DB 22; Length 738;
 Best Local Similarity 99.5%; Pred. No. 1.7e-208;
 Matches 415; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RKQOENIYSHLDEESSESTYTAALPRRLPRPKVFLCYSSKDGQNMNVVQCFAYFL 60
 DB 322 RKQOENIYSHLDEESSESTYTAALPRRLPRPKVFLCYSSKDGQNMNVVQCFAYFL 381
 QY 61 QDFGCEVALDWEFSLCRGQREWVQIKHESQFIIVVCSKGMKYFDKKNYKHGGG 120
 DB 382 QDFGCEVALDWEFSLCRGQREWVQIKHESQFIIVVCSKGMKYFDKKNYKHGGG 441
 QY 121 RSGKGELFLVAVSAEKLQAKOSSAALSFIATFYDSCGDFVGLDLSTKRYLM 180
 DB 442 RSGKGELFLVAVSAEKLQAKOSSAALSFIATFYDSCGDFVGLDLSTKRYLM 501
 QY 181 DNLPLQCSHLSDHGLQFPGQTRGSGRRNYFRSKGRSLYVAICNMHOFIDEEPWF 240
 DB 502 DNLPLQCSHLSDHGLQFPGQTRGSGRRNYFRSKGRSLYVAICNMHOFIDEEPWF 561
 QY 241 KQVFPPFPPLRYREPVLKFGSLVLDVNMCKPQSDCLVAAVLGATGADSDQHE 300
 DB 562 KQVFPPFPPLRYREPVLKFGSLVLDVNMCKPQSDCLVAAVLGATGADSDQHE 621
 QY 301 SQHGLDQDGEARALDGSAAALQPLHVTYKAGSPDMRDSGIYDSSVPSSELSPLMEG 360
 DB 622 SQHGLDQDGEARALDGSAAALQPLHVTYKAGSPDMRDSGIYDSSVPSSELSPLMEG 681
 QY 361 LSTQDTTSSLTSSVSSGSGEERPPALPSKLLSSGSKADLGCRSYDDELHVAAP 417
 DB 682 LSTQDTTSSLTSSVSSGSGEERPPALPSKLLSSGSKADLGCRSYDDELHVAAP 738

RESULT 14

AAU09957
 ID AAU09957 standard; Protein; 738 AA.

XX AAU09957;

XX 14-FEB-2002 (first entry)

XX Human Interleukin 17 (hIL-17) receptor like protein substitution #7.

DE Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 XX mutein.

OS Homo sapiens.

OS Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 602 /Label- Cys, Ala, Ser

XX W0200168859-A2.

XX 20-SEP-2001.

XX 15-MAR-2001; 2001WO-US086678.

XX 16-MAR-2000; 2000US-189816P.

XX 28-NOV-2000; 2000US-074460.

XX (AMGE-) AMGEN INC.

XX Jing S;

XX MPI; 2001-611392/70.

XX Nucleic acids encoding interleukin 17 receptor like polypeptides,
 XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
 XX diabetes, psoriasis and glaucoma

XX Claim 24; Page -: 158pp; English.

XX The invention describes novel nucleic acids encoding interleukin (IL) 17
 XX receptor like polypeptides useful as vaccines and in gene therapy. These
 XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
 XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 XX osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
 XX ophthalmological activities. The IL-17 receptor like nucleic acids and
 XX proteins may be used to prevent and treat diseases associated with
 XX inappropriate IL-17 receptor like polypeptide (IL17rip) expression. These
 XX include, for example immune disorders (e.g. inflammation, diabetes and
 XX transplant rejection), infections (e.g. hepatitis and septicemia),
 XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal
 XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 XX (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
 XX breast cancer), reproductive disorders (e.g. infertility and
 XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 XX DNA and its complements may also be used as diagnostic probes to detect and
 XX quantitate the presence of similar nucleic acids in samples and identify
 XX patients needing restorative therapy. The IL17rip may also be used as
 XX antigens in the production of antibodies against the proteins and in
 XX assays to identify modulators of expression and activity. The
 XX anti-IL17rip antibodies and antagonists may also be used to down regulate
 XX expression and activity.

XX Note: This sequence is not given in the specification but is based on the
 XX human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)
 XX and has been created according to information given in claim 24.

XX Sequence 738 AA;

Query Match 99.1%; Score 2190; DB 22; Length 738;

Best Local Similarity 99.5%; Pred. No. 1.7e-208;

Matches 415; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RKQOENIYSHLDEESSESTYTAALPRRLPRPKVFLCYSSKDGQNMNVVQCFAYFL 60

DB 322 RKQOENIYSHLDEESSESTYTAALPRRLPRPKVFLCYSSKDGQNMNVVQCFAYFL 381

QY 61 QDFGCEVALDWEFSLCRGQREWVQIKHESQFIIVVCSKGMKYFDKKNYKHGGG 120

DB 382 QDFGCEVALDWEFSLCRGQREWVQIKHESQFIIVVCSKGMKYFDKKNYKHGGG 441

QY 121 RSGKGELFLVAVSAEKLQAKOSSAALSFIATFYDSCGDFVGLDLSTKRYLM 180

DB 442 RSGKGELFLVAVSAEKLQAKOSSAALSFIATFYDSCGDFVGLDLSTKRYLM 501

QY 181 DNLPLQCSHLSDHGLQFPGQTRGSGRRNYFRSKGRSLYVAICNMHOFIDEEPWF 240

DB 502 DNLPLQCSHLSDHGLQFPGQTRGSGRRNYFRSKGRSLYVAICNMHOFIDEEPWF 561

QY 241 KQVFPPFPPLRYREPVLKFGSLVLDVNMCKPQSDCLVAAVLGATGADSDQHE 300

DB 562 KQVFPPFPPLRYREPVLKFGSLVLDVNMCKPQSDCLVAAVLGATGADSDQHE 621

QY 301 SQHGLDQDGEARALDGSAAALQPLHVTYKAGSPDMRDSGIYDSSVPSSELSPLMEG 360

DB 622 SQHGLDQDGEARALDGSAAALQPLHVTYKAGSPDMRDSGIYDSSVPSSELSPLMEG 681

QY 361 LSTQDTTSSLTSSVSSGSGEERPPALPSKLLSSGSKADLGCRSYDDELHVAAP 417

DB 682 LSTQDTTSSLTSSVSSGSGEERPPALPSKLLSSGSKADLGCRSYDDELHVAAP 738

Db 442 RSGGKGLFLVAVSAIAEKLAKQSSAALSKFIAVTEDYSCBQDVGILDLSTYRLM 501
 QY 181 DNLPLCSLHSDRGDLQEPQHTROGSRNTFRSKGSLYVAICNNHOFIDEEPDMTE 240
 Db 502 DNLPLCSLHSDRGDLQEPQHTROGSRNTFRSKGSLYVAICNNHOFIDEEPDMTE 561
 QY 241 KQVPPHPPPLRYREPVLKFDGSLVNDVCKPGPESDFCLKVEAVLGTATGAPDSQHE 300
 Db 562 KQVPPHPPPLRYREPVLKFDGSLVNDVCKPGPESDFCLKVEAVLGTATGAPDSQHE 621
 QY 301 SQGGGLDQGEARPALDGSAAQLPILHTYKAGSPDMPRDSGIYDSSVPSSELSLPMRG 360
 Db 622 SQGGGLDQGEARPALDGSAAQLPILHTYKAGSPDMPRDSGIYDSSVPSSELSLPMRG 681
 QY 361 LSTDQETSSLTESVSSSGGEEPPALPSKLLSGGCKDGLGCRSYTDELHNAVAP 417
 Db 417 LSTDQETSSLTESVSSSGGEEPPALPSKLLSGGCKDGLGCRSYTDELHNAVAP 478

RESULT 15

ID ABB07630 standard; Protein; 739 AA.

AC ABB07630;

DT  first entry)

DE Murine cytokine receptor, zcytor18.

KW Cytokine receptor; zcytor18; cell proliferation; antiproliferative; human;
 KW pulmonary alveolar proteinosis; familial periodic fever; antitumor;
 KW erythroleukemia; chromosome 3p14.3; gene therapy; mouse.

OS Mus sp.

PN W0200208259-A2.

PD 31-JAN-2002.

PF 23-JUL-2001; 2001WO-US23253.

PR 26-JUL-2000; 2000US-220747P.

PA (ZYMO) ZYMOGENETICS INC.

PI Presnell SR, Kuestner RE, Gao Z;

PP WPI; 2002-217048/27.

DR N-PSDB; ABA95037, ABA95038.

FT New cytokine receptor polypeptide designated zcytor18, useful for
 FT inhibiting cell proliferation associated with psoriasis or tumor
 FT growth, and modulating immune system by binding to endogenous zcytor18
 FT ligand

PS Claim 1: Page 111-115; 119pp; English.

CC The invention relates to an isolated cytokine receptor polypeptide
 CC designated zcytor18. The zcytor18 polypeptides can be expressed by
 CC standard recombinant methodology. The polypeptides can be used to inhibit
 CC cell proliferation associated with psoriasis or tumor growth. The
 CC encoding nucleic acids are useful for providing zcytor18 in vivo by gene
 CC therapy techniques. zcytor18 oligonucleotide probes are useful for in
 CC vivo diagnosis, and the zcytor18 probes and primers can be used to detect
 CC and localize zcytor18 gene expression in tissue samples. The probes are
 CC also useful for detecting gross aberrations in chromosome 3 in which
 CC zcytor18 gene resides. The zcytor18 polynucleotides can also be used in
 CC linkage-based testing of pulmonary, alveolar proteinosis, familial
 CC periodic fever, and erythroleukemia, and erythroleukemia associated with
 CC polymorphisms of cytokine receptors. The present sequence represents a
 CC murine zcytor18 amino acid sequence.

XX Sequence 739 AA;

Query Match 182118 Score 1813.5; DB 23; Length 739;
 Best Local Similarity 83.1%; Pred. No. 4.9e-171;
 Matches 350; Conservative 25; Mismatches 39; Indels 7; Gaps 4;
 QY 1 RKQKENIYSHLDEESSESTTAALPRERLRPRKVFICTYSSKQGNHNVVQCFAIFL 60
 Db 323 RKQKENIYSHLDEESSESTTAALPRERLRPRKVFICTYSSKQGNHNVVQCFAIFL 382
 QY 61 QDFGCEVALDLMEFSLCREGOREWVOKIHESQFIYVCSKGMKIFDYDKKNYKHGGG 120
 Db 383 QDFGCEVALDLMEFSLCREGOREWVOKIHESQFIYVCSKGMKIFDYDKKNYKHGGG 442
 QY 121 RSGSGKGLFLVAVSAIAEKLAKQSSAALSKFIAVTEDYSCBQDVGILDLSTYRLM 180
 Db 443 RSGSGKGLFLVAVSAIAEKLAKQSSAALSKFIAVTEDYSCBQDVGILDLSTYRLM 502
 QY 181 DNLPLCSLHSDRGDLQEPQHTROGSRNTFRSKGSLYVAICNNHOFIDEEPDMTE 239
 Db 503 DNLPLCSLHSDRGDLQEPQHTROGSRNTFRSKGSLYVAICNNHOFIDEEPDMTE 559
 QY 240 KQVPPHPPPLRYREPVLKFDGSLVNDVCKPGPESDFCLKVEAVLGTATGAPDSQHE 299
 Db 560 KQVPPHPPPLRYREPVLKFDGSLVNDVCKPGPESDFCLKVEAVLGTATGAPDSQHE 619
 QY 300 --ESQGGGLDQGEARPALDGSAAQLPILHTYKAGSPDMPRDSGIYDSSVPSSELSLPL 357
 Db 620 YLESHQVGLDQDTEAQPCSDAPALQPLHAYKAGSPSEMPRDSGIYDSSVPSSELSLPL 679
 QY 358 MEGSLTDQETSSLTESVSSSGGEEPPALPSKLLSGGCKDGLGCRSYTDELHNAVAP 417
 Db 680 MEGSLTDQETSSLTESVSSSGGEEPPALPSKLLSGGCKDGLGCRSYTDELHNAVAP 738
 QY 418 L 418
 Db 739 L 739

Search completed: May 19, 2003, 09:20:02
 Job time : 32.4416 secs

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OK protein - protein search, using sw model

Run on: May 19, 2003, 09:08:53 ; Search time 8.48731 Seconds
(without alignments)
2042.709 Million cell updates/sec

Title: US-09-912-157-2_COPY_336_753
Perfect score: 2210
Sequence: 1 RKQOENYSHLDESSSS.....CFADLGRSYTDELHNAVL 418

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	308	13.9	866	1 IL17R_HUMAN	Q96f46 homo sapien
2	289.5	13.1	864	1 IL17R_MOUSE	Q60943 mus musculus
3	127.5	5.8	502	1 IL17S_MOUSE	Q60943 mus musculus
4	126	5.7	718	1 YSO2_CAEEL	Q10128 caenorhabdi
5	110.5	5.0	499	1 IL17S_MOUSE	Q9j1p3 mus musculus
6	105.5	4.8	592	1 STB3_MOUSE	Q60770 mus musculus
7	99.5	4.5	794	1 STB3_MOUSE	Q60821 mus musculus
8	96.5	4.4	746	1 ABL_MLVAB	P00521 abelson mur
9	96	4.3	660	1 HT31_ARATH	Q04996 arabidopsis
10	95	4.3	933	1 PRGR_HUMAN	P06401 homo sapien
11	94.5	4.3	841	1 IE63_MCMVS	Q59154 murine cyto
12	93.5	4.2	806	1 RMIL_CHICK	Q04982 gallus gall
13	93.5	4.2	807	1 RMIL_COTJA	P34908 coturnix co
14	92.5	4.2	347	1 SH33_MOUSE	Q82421 mus musculus
15	92.5	4.2	548	1 IDD_MOUSE	P38154 mus musculus
16	92.5	4.2	830	1 JIP2_MOUSE	Q9ere9 mus musculus
17	92.5	4.2	2314	1 JIP2_MOUSE	P23471 homo sapien
18	92	4.2	864	1 STP2_PIG	Q02799 sus scrofa
19	92	4.2	883	1 PCGB_MOUSE	Q61361 mus musculus
20	91.5	4.1	351	1 RM14_CAEEL	P20271 caenorhabdi
21	91	4.1	883	1 PCGB_RAT	P55068 rattus norv
22	91	4.1	2038	1 FSH_DRONE	P13709 drosophila
23	90.5	4.1	895	1 ANDR_MACFA	Q97952 caecilia fasc
24	90	4.1	579	1 MALT_AEDAE	P13080 aedes aegypt
25	90	4.1	803	1 Z151_HUMAN	Q13105 homo sapien
26	89.5	4.0	766	1 STB6_YEAST	Q36085 saccharomyc
27	88.5	4.0	797	1 SHK3_HUMAN	Q9bhb0 homo sapien
28	88.5	4.0	1992	1 TRIB_HUMAN	Q14669 homo sapien
29	88.5	4.0	2373	1 CCAB_HUMAN	Q95180 homo sapien
30	88	4.0	229	1 VE4_HPV08	P06425 human papill
31	88	4.0	638	1 GYRB_BACSU	P05652 bacillus su
32	88	4.0	770	1 TLE1_MOUSE	Q62440 mus musculus
33	88	4.0	782	1 CFSB_MOUSE	Q35218 mus musculus

34	88	4.0	2364	1 PGCA_BOVIN	P13608 bos taurus
35	87.5	4.0	2220	1 CAB1_HUMAN	Q9v6j0 homo sapien
36	87.5	4.0	2339	1 CCAB_RABIT	Q05152 oryctolagus
37	87	3.9	587	1 REL_MOUSE	P15307 mus musculus
38	87	3.9	984	1 EPBL_CHICK	Q07494 gallus gall
39	86.5	3.9	393	1 HMG2_DRONE	Q24537 drosophila
40	86.5	3.9	641	1 SGT1_MOUSE	Q9cs74 mus musculus
41	86.5	3.9	725	1 ADDB_MOUSE	Q9qyb8 mus musculus
42	86.5	3.9	741	1 Z288_HUMAN	Q9hc78 homo sapien
43	86.5	3.9	1047	1 HIRA_DRONE	Q17468 drosophila
44	86.5	3.9	1581	1 PPRB_HUMAN	Q15648 h peroxisom
45	86	3.9	291	1 SH33_RAT	Q35180 rattus norv

ALIGNMENTS

RESULT 1
ID IL17R_HUMAN STANDARD; PRT: 866 AA.
AC Q96f46: Q43844;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-17 receptor precursor (IL-17 receptor).
GN IL17R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=I-cell;
RX MEDLINE=98033683; PubMed=9367539;
RA Yao Z., Spriggs M.K., Derry J.M.J., Strockbine L., Park L.S.,
VandenBos T., Zappone J., Painter S.L., Armitage R.J.;
RT "Molecular characterization of the human interleukin (IL)-17
receptor."
RT Cytokine 9:794-800(1997).
RL [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -- FUNCTION: Receptor for IL17. Binds its ligand with low affinity,
CC suggesting that additional components are involved in IL17-induced
CC signaling.
CC -- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -- TISSUE SPECIFICITY: Widely expressed.
CC -- PTM: Glycosylated.

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EMBL: U58917; AAB99730.1;
EMBL: BC011624; AB011624.1;
Genew; BCNC:5985; IL17R.
MIM; 605461;
DR Receptor; Transmembrane; Signal; Glycoprotein.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 866 INTERLEUKIN-17 RECEPTOR.
FT DOMAIN 32 320 EXTRACELLULAR (POTENTIAL).
FT TRANSME 321 341 POTENTIAL.
FT DOMAIN 342 866 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 810 818 POLY-GLU.
FT CARBOHYD 43 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 367 V -> A (IN REF. 1).
 FT CONFLICT 580 H -> R (IN REF. 1).
 SQ SEQUENCE 866 AA; 96131 MW; 283308ED330B0C9 CRC64;

Query Match 13.9%; Score 308; DB 1; Length 866;
 Best Local Similarity 28.3%; Pred. No. 1.9e-15;
 Matches 127; Conservative 60; Mismatches 173; Indels 88; Gaps 20;

QY 14 ESESSTYTAALPRELRPRP---KVFICYSSKDGONHNVVOCFAFYFLODFCGCEVA 69
 DB 353 EKYSDTYTDTGLVADLPPPLPKPKWIIYSA-DHELYVYVLAQFLLTACGTEVA 411
 QY 70 LDLMEDFSLCREGQREW---IQKHESQFIIVVCSGKMYFYVDKKNYKHGGG----- 120
 DB 412 LDLEEQAISAGVMTWVGRQKQEMYESKIIIVLCRGT---AKWQALLGRGAPVRL 467
 QY 121 ---RGSKGELFVAVSAIAEKLRQAKOSSAALSKEFIATVF-DYSCGIDVPGILDSTK 176
 DB 468 KDCHEKPVGDLETAAMNMLPDKR---PACFGTYVVCYFSEVSCDGVDPDLGAPR 522
 QY 177 YRLMDNLPLQCSHLRSDHGLQEPGQ---SRRTFRSKRSLSYVAICNHQFIDE 234
 DB 523 YPLMDRFEV---YFIQDLEMFGRHVRVSGELSDGNTLRSPPGRLRALDRFDMQVH 580
 QY 235 EDPNFE-----KQVPPHPPLRYEPVLEKFDGLVLDVYVCKPGPESDFCLKVEA 286
 DB 581 CPDMECENYSADQDAPSLDEEV-FEPLPLP-GTGVKRAPLVRE-PGSQACLAIDP 637
 QY 287 AVLGATGAPDQSHR-----SOHGLDQDGEARPLDQSA---ALQ 323
 DB 638 LVGEEGAANVALEPHLPQPGQAPQPLTLVLAEEGALVAVTEPGLADGAVRLA 597
 QY 324 -----PLHTVKGSPDMRDSGYDSSVPSSELSPLMEGLSTDTQETSLTESVSS 377
 DB 698 GEGEACPLIGSGAG-----RNSVLF---LVPDPSPL-GGSTPMASPLDLPEDVR- 745
 QY 378 SSGLEEPPALPSKLLSGSCADLGC 405
 DB 746 -----EHLGLMLSLPQSLSCQAGGC 768

RESULT 2

IL17_MOUSE
 ID IL17_MOUSE STANDARD; PRT; 864 AA.
 AC Q60943;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-17 receptor precursor (IL-17 receptor).
 GN IL17R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymic lymphoma;
 RX MEDLINE=96111969; Pubmed=8777726;
 RA Xao Z., Fanslow W.C., Seidlin M.F., Rousseau A.M., Painter S.L.,
 RA Comeau M.R., Cohen J.I., Spriggs M.K.;
 RT "Herpesvirus Saimiri encodes a new cytokine, IL-17, which binds to a
 RT novel cytokine receptor";
 RL Immunity 3:811-821(1995).
 CC -1- FUNCTION: Receptor for IL17. Binds its ligand with low affinity,
 CC suggesting that additional components are involved in IL17-induced
 CC signaling (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC
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 or send an email to license@isb-sib.ch)

EMBL; J01993; AAC52357.1;
 DR MGD; MGI:107399; IL17r;
 KW Receptor; Transmembrane; Signal; Glycoprotein.
 FT SIGNAL 1..31 POTENTIAL.
 FT CHAIN 32..864 INTERLEUKIN-17 RECEPTOR.
 FT DOMAIN 32..322 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 323..343 POTENTIAL.
 FT DOMAIN 344..864 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 809..814 POLY-GUJ.
 FT CARBOHYD 54..54 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 79..79 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 206..206 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 225..225 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 242..242 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 265..265 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 308..308 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 864 AA; 97807 MW; 343FD51AA687DA31 CRC64;

Query Match 13.1%; Score 289.5; DB 1; Length 864;
 Best Local Similarity 25.8%; Pred. No. 4.5e-14;
 Matches 120; Conservative 75; Mismatches 170; Indels 101; Gaps 21;

QY 14 ESESSTYTAALPRELRPRP---KVFICYSSKDGONHNVVOCFAFYFLODFCGCEVA 69
 DB 355 EKHGDSKINGILPVADLPPPLPRKVMIVISA-DHELYVYVLAQFLLTACGTEVA 413
 QY 70 LDLMEDFSLCREGQREWVTK-----IHESQFIIVVCSGKMYFYVDKKNYKHGGG----- 119
 DB 414 LDLEEVIVSEGVNTWVGRQKQEMYESKIIIVLCRGT---TQKRAILGWAEPAV 468
 QY 120 ---RGSKGELFVAVSAIAEKLRQAKOSSAALSKEFIATVFYDSC-EGDVPGLDLS 174
 DB 469 QLRCDHWKPADLFTAAMNMLPDKR---PACFGTYVVCYFSEVSCDGVDPDLNIT 523
 QY 175 YRLMDNLPLQCSHLRSDHGLQEPGQ---HTROGSRRTFRSKRSLSYVAICNHQFI 232
 DB 524 SRYPLMDRFEV---YFIQDLEMFGRHVRVSGELSDGNTLRSPPGRLKAVLRQEMQ 581
 QY 233 DEEPDNFEKQFVFPHP---PPLR---YREPVLEKFDGLVLDVYVCKPGPESDFCLAVE 285
 DB 582 TQCPDMFERENICLADGQDLPLSLDEEVEDPPLPP-GGGIVKQOQFVRELPSDGLVVD 639
 QY 286 AAVLGATGAPDQSHRSGHGLDQD-----GEARPLDQSAALQPLH 327
 DB 640 VCV-----SEESRMAKLDQPLQPELVAVTLQSWVLAQVPA---AHVVEPLHL 688
 QY 328 TVKAGSPDNP---RDS-----GIYDSSV---PSELSPL-----MEGLSTDTQ 366
 DB 689 PDGSGAAALQPMTEDEACPLGVGRNSILCLPVDSDLLPCLSTPMSPDHQDARSL 748
 QY 367 ETSSLSVESVSSGLGEEPPP-----ALPSKLLSGSCADLGC 404
 DB 749 ESLMLSVLQQLSGQPLSWPRPEVVLGCTPSEEQRSQVSDQG 794

RESULT 3

IL17S_HUMAN
 ID IL17S_HUMAN STANDARD; PRT; 502 AA.
 AC Q9NRM6; Q9BP20; Q9NR4; Q9NRMS;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-17B receptor precursor (IL-17B receptor) (IL-17 receptor
 DE homolog 1) (IL-17Rhl) (IL17Rhl) (Cytokine receptor CR4).
 GN IL17B OR EVI27.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 [1]
 NCBI_TaxID=9606;
 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 MEDLINE-20737223; PubMed-10815801.
 Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A., Copeland N.G.,
 Shaughnessy J.D. Jr.,
 "EV127 encodes a novel membrane protein with homology to the IL17
 receptor."
 Oncogene 19:2098-2109(2000).
 [2]
 SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF N-TERMINUS.
 TISSUE-Lung;
 MEDLINE-20317118; PubMed-10749887;
 Shi Y., Ulrich S.J., Zhang J., Connolly K., Wargozorzewski K.J.,
 Barber M.C., Wang W., Mathen K., Hodge V., Fisher C.L., Olsen H.,
 Ruben S.M., Knyazev I., Cho I.H., Kao V., Wilkinson K.A.,
 Carrell J.A., Ebner R.;
 "A novel cytokine receptor-ligand pair. Identification, molecular
 characterization, and in vivo immunomodulatory activity."
 J. Biol. Chem. 275:19167-19176(2000).
 [3]
 SEQUENCE FROM N.A. (ISOFORM 1).
 Zhang W., Cao X.;
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [4]
 SEQUENCE FROM N.A. (ISOFORM 1).
 TISSUE-Cervix;
 Strausberg R.;
 Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 [5]
 FUNCTION.
 PubMed-11058597;
 Lee J., Ho W.H., Maruoka M., Corpuz R.T., Baldwin D.T., Foster J.S.,
 Goddard A.D., Iwasura D.G., Vandien R.L., Wood W.I., Gurney A.L.;
 "IL-17E, a novel proinflammatory ligand for the IL-17 receptor homolog
 IL-17R1."
 J. Biol. Chem. 276:1660-1664(2001).
 [6]
 FUNCTION: Receptor for the proinflammatory cytokines IL17B and
 IL17E. May play a role in controlling the growth and/or
 differentiation of hematopoietic cells.
 [7]
 SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
 Secreted (isoform 2).
 [8]
 ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here), and 2; are
 produced by alternative splicing.
 [9]
 TISSUE SPECIFICITY: Expressed in several endocrine tissues, mostly
 in fetal and adult liver, kidney, pancreas, testis, colon, brain
 and small intestine; not detected in peripheral blood leukocytes,
 lymphoid organs, and most cell lines.
 [10]
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 [11]
 EMBL; AF208110; AAF86051.1;
 EMBL; AF208111; AAF86052.1;
 EMBL; AF212365; AAF78776.1;
 EMBL; AF250309; AAK37428.1;
 EMBL; BC000980; AAH00980.1;
 Genbank; HGNC:18015; IL17BR.
 MIM; 603458;
 Receptor; Transmembrane; Signal; Glycoprotein; Alternative splicing.
 [12]
 SIGNAL
 1 17
 CHAIN 18 502 INTERLEUKIN-17B RECEPTOR
 DOMAIN 18 292 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 293 313 POTENTIAL.
 DOMAIN 314 502 CYTOPLASMIC (POTENTIAL).
 CARBOHYD 67 67 N-LINKED (GLCNAC...) (POTENTIAL).
 CARBOHYD 103 103 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 156 156 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 283 283 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARSPLIC 250 288 LTPYPPGSGSDICRHGTGVTGACGGVPPPLDNKSKRG
 FT S: (IN ISOFORM 2).
 FT VARSPLIC 289 502 MISSING (IN ISOFORM 2).
 FT CONFLICT 6 6 L -> I (IN REF. 1).
 FT CONFLICT 422 426 LFPLA -> SSPCL (IN REF. 2).
 FT CONFLICT 427 502 MISSING (IN REF. 2).
 FT CONFLICT 468 468 L -> F (IN REF. 1).
 SQ SEQUENCE 502 AA: 55884 MW: 6287586FAAE49CC-CRC64;
 Query Match 5.8%; Score 127.5; DB 1; Length 502;
 Best Local Similarity 24.6%; Pred. No. 0.03; 92; Indels 15; Gaps 4;
 Matches 45; Conservative 31; Mismatches 92; Indels 15; Gaps 4;
 QY 8 IYSHLDESSSESYTAALPRELRPRKVFYCYSSKQGNHNVVOCFAIFLQPCGE 67
 DB 312 MRRHERIKTSFTTT-----LLPIKLVVYVPEICFHH--TICFTFELQHCSE 362
 QY 68 VALDLWEDSLCREGQREYVQIKHESQFIIVCGSKGMYFVDKKNYKHGGSGSGKE 127
 DB 363 VILEKWKKKIAENGVPVOMLATOKKAAKRVYLLSDNVNSVCDGTCCKSGSPSENSQ-D 421
 QY 128 LFLVAVSAIAEKLRQKSSAALSFAVYDYSCEGDPVGLDLSYTRIAMNLPQIC 187
 DB 422 LFLAFLNLCSDLR-----SQIHLKHYVYVYFREIDTNDQTNALSVCPKTHMKATAPC 476
 QY 188 SHL 190
 DB 477 AEL 479

RESULT 4

YS02_CAEEL
 ID YS02_CAEEL STANDARD; PRT: 718 AA.
 AC Q10128;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Hypothetical 81.6 kDa protein F56D1.2 in chromosome II precursor.
 GN F56D1.2
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Chisoe S., Wilson R.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 CC
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 CC
 CC EMBL; U39997; AAA81100.1;
 DR WormPep; F56D1.2; CE01970.
 KW Hypothetical protein; Transmembrane; Signal.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 718 HYPOTHETICAL PROTEIN F56D1.2.
 FT TRANSMEM 373 393 POTENTIAL.
 SQ SEQUENCE 718 AA: 81622 MW: 4289E056288417AA CRC64;
 Query Match 5.7%; Score 126; DB 1; Length 718;
 Best Local Similarity 21.1%; Pred. No. 0.06;
 Matches 82; Conservative 64; Mismatches 149; Indels 94; Gaps 19;

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CC EMBL; U19321; AAG69913.1;
CC DR EMBL; D30798; BAA19478.1;
CC DR MGI; 107362; Strp3.
CC DR InterPro; IPR001619; Sec1-like.
CC DR Pfam; PF00995; Sec1; 1.
CC KW Protein transport.
CC SQ SEQUENCE 592 AA; 67942 MW; 7874871DEL07871A CRC64;

Query Match 4.88; Score 105.5; DB 1; Length 592;
Best Local Similarity 18.84; Pred. No. 1.6;
Matches 89; Conservative 60; Mismatches 145; Indels 179; Gaps 21;

QY 6 ENYSHLDEESSESYTAALPRRLPRKPVLCYSSKQGNMNVVQCFAYFLQDFC- 64
DB 63 ENYKREPVQMKALYF-----ISPTKSVDCFLRDFGSKKKYKAAIYFTDFCP 115
QY 65 -----GCE-----VALDLWEDFSLC-----REGQSWVIO 89
DB 116 DSLFNKIKASCKSIRCKEINISFYQESQVTLVDYDPAFYCYSPDPSNASKKEVME 175
QY 90 KIHESQFIIVVC-----SKGMKY-----FYDKK---NYK--HKGGRGSGKG 126
DB 176 AMAEQ--IVTVCATLDENGVRYKSKPLDNASKLAQLVEKKLDEYIKIDKGLIKGTQS 233
QY 127 ELFLV-----AVSAIAEKLQAKQSSAALSFIAYFD-----YSCRG-DVPGI 170
DB 234 QLLIDRGDFPVSIVHEL-----TFQAMATDLPIDNTYIKYKTDGKREAV 281
QY 171 L-----DLSTKYR-----LMDNLPQCSHLASRDHGLQEPQONTQGRSRRYFRSKGRS 220
DB 282 LEEDDQVRYRHHRAVIAVLEETPKLMEISSTK-----KATEGT 322
QY 221 LVVAICNNHOFIDEEPWFQKVPVPPPLRYREPVLKFF----- 261
DB 323 SLSALTQMKMPHFRAQISKQV-----HLNAECCMKFKLKEIKTEQDIALGTD 377
QY 262 -----DSGLVANDVCKGSPEDSCLVAEAVLGATGAPDSQHSQHGGLDQGEARP 314
DB 378 AEGQRVDSMLVLLPVL--NKHNDCKIRAVLLYIFGNGTTEEN----- 422
QY 315 ALDGSAAQLPILHTVAKGSDMPRD--SGIYDSSVPSESLPLMEGLSTDOT 366
DB 423 -----LDRLIHNKTEDSDMIRNSHLGVPVIPPVPPQAKPLKDRSAET 468

RESULT 7
Z131_MOUSE
ID Z151_MOUSE STANDARD; PRT; 794 AA.
AC Q60699;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Zinc finger protein 151 (Polyomavirus late initiator promoter binding
DE protein) (LP-1) (Zinc finger protein 213).
GN ZNF151 OR ZFP100.
OS Mus musculus (Mouse).
OC Eumetazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP Rapp L., Carmichael G.G.;
RA Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RX STRAIN=CBA; TISSUE=Kidney;
RA MEDLINE=96003919; PubMed=7575457;
RA Schulz T.C., Hopwood B., Rathjen P.D., Wells J.R.E.;

RT "An unusual arrangement of 13 zinc fingers in the vertebrate gene
RT Z13".
RL Biochem. J. 311:219-224(1995).
CC FUNCTION: MAY-FUNCTION AS-A HOUSEKEEPING DNA-BINDING PROTEIN THAT
CC REGULATES THE EXPRESSION OF SPECIFIC GENES.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- TISSUE SPECIFICITY: FOUND IN ALL THE EMBRYONIC AND ADULT TISSUES
CC EXAMINED.
CC -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
CC FINGER PROTEINS.
CC -1- SIMILARITY: CONTAINS 1 BTB/POL DOMAIN.
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CC EMBL; U22396; AAG4848.1;
CC DR EMBL; U14556; AAR85493.1;
CC DR HSSP; P08046; IALH.
CC MGD; MGI:107410; Zfp100.
CC InterPro; IPR002110; BTB_PoZ.
CC InterPro; IPR000822; Znf_C2H2.
CC Pfam; PF00096; zf-C2H2; 13.
CC Pfam; PF00651; BTB; 1.
CC PRINTS; PR00048; ZINC_FINGER.
CC PRODOM; PD000003; Znf_C2H2; 1.
CC SMART; SM00225; BTB; 1.
CC SMART; SM00355; Znf_C2H2; 13.
CC PROSITE; PS00097; BTB; 1.
CC PROSITE; PS00028; ZINC_FINGER_C2H2_1; 13.
CC PROSITE; PS0157; ZINC_FINGER_C2H2_2; 13.
CC KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
CC Nuclear protein; Repeat.
FT DOMAIN 1 104 BTB.
FT ZN_FING 297 730 ZINC FINGERS.
FT ZN_FING 297 319 C2H2-TYPE.
FT ZN_FING 325 347 C2H2-TYPE.
FT ZN_FING 353 375 C2H2-TYPE.
FT ZN_FING 381 403 C2H2-TYPE.
FT ZN_FING 409 431 C2H2-TYPE.
FT ZN_FING 437 459 C2H2-TYPE.
FT ZN_FING 465 487 C2H2-TYPE.
FT ZN_FING 493 515 C2H2-TYPE.
FT ZN_FING 519 543 C2H2-TYPE.
FT ZN_FING 549 571 C2H2-TYPE.
FT ZN_FING 577 599 C2H2-TYPE.
FT ZN_FING 605 628 C2H2-TYPE.
FT ZN_FING 708 730 C2H2-TYPE.
FT CONFLICT 507 507 G -> A (IN REF. 2).
FT CONFLICT 573 573 N -> K (IN REF. 2).
SQ SEQUENCE 794 AA; 86664 MW; FFF885E5DEB7ED CRC64;

Query Match 4.58; Score 99.5; DB 1; Length 794;
Best Local Similarity 20.68; Pred. No. 6.5;
Matches 71; Conservative 41; Mismatches 146; Indels 87; Gaps 15;
QY 64 CGCEVALDMEDESICREGQEWYQIKTHESQFIIVVCSSGMR-YFVKKNTKHKGGGRG 122
DB 24 CDCFIYVD-GVDF-----KAHKA--VLAACSEYFKMLFVDQDQVHVHLDISNA 67
QY 123 SGKGLFVAVSAIAEKLQAKQSS-----AALSKFIATVFDYSCEDVPGLDLSL 175
DB 68 AGLQ-----VLEFMTAKLSLSPENVDDVLAVASFQMQ-----DIVT 106
QY 176 KYRLMDMLPOLCSHL-HSRDHGLQEPQGH-----TROGSRNFRSKSGRSLY 222
DB 107 ACHTLAKSLAEPSSTTGESADASAVESGDKRAKDEKAAATMLSLRGQARSSSTGFGRELK 166
QY 223 VAICNNHOFIDEEPWFQKVPVPPPLRYREPVLKFFQSGGLVAVLMVCKPSPESDFCL 282

DB 167 EERQAGASSAGTQKADAPREPP-----VELKPDPTSSMA- 206
 QY 283 KVEAVILGATGADSHSGHGLDGEARPALDGSALLOPLHTVTRAGSPDMPDUG 342
 DB 207 AAREALSSSSQMEVEPASK--ECQEEGAGPATYKRGMR-LONGEPPEENEESA 263
 QY 343 IYDSSVPSLSLP---LMEGLSTDTOTETSLTESVSSSGLEE 384
 DB 264 GTDS---GOELGEGONLSTGTGRTESKAYGSIHKEDCGKE 305

RESULT 8
 ABL_MLVAB STANDARD; PRT; 746 AA. #
 AC P00521; 1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE Tyrosine-protein kinase transforming protein ABL (BC 2.7.1.112).
 GN V-ABL.
 OS Abelson murine leukemia virus.
 OC Viruses; Retroviral viruses; Retroviridae; Mammalian type C retroviruses.
 OX NCBI_TaxID=11788;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83221648; PubMed=6304726;
 RA Reddy E.P., Smith M.J., Srinivasan A.;
 RT "Nucleotide sequence of Abelson murine leukemia virus genome:
 structural similarity of its transforming gene product to other onc
 gene products with tyrosine-specific kinase activity";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:3623-3627(1983).
 RN [2]
 RP REVISIONS TO 588-746.
 RA Reddy E.P., Smith M.J., Srinivasan A.;
 RL Proc. Natl. Acad. Sci. U.S.A. 80:7372-7372(1983).
 RN [3]
 RP SEQUENCE OF 233-327 FROM N.A.
 RX MEDLINE=83245023; PubMed=6191223;
 RA Groffen J., Heisterkamp N., Reynolds F.H. Jr., Stephenson J.R.;
 RT "Homology between phosphotyrosine acceptor site of human c-abl and
 RT viral oncogene products";
 RL Nature 304:167-169(1983).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 CC tyrosine phosphate.
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-ABL
 CC POLYPEPTIDE.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. ABL
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.

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DR EMBL; V01541; NOT ANNOTATED_CDS.
 DR EMBL; K00010; AAA6470.1;
 DR PIR; A00627; YWVGCM.
 DR HSP; P00519; 2ABL.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.

SMART; SM00219; TYRK; 1.
 DR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
 DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
 DR PROSITE; PS00001; SH2; 1.
 KW Polyprotein; Tyrosine-protein kinase; Transferase; Oncogene;
 SH2 domain; 13 103
 FT DOMAIN 128 379 PROTEIN KINASE.
 FT DOMAIN 128 379
 SQ SEQUENCE 746 AA; 81872 MW; B9072FF5F9257 CRC64;
 Query Match 4.4%; Score 96.5; DB 1; Length 746;
 Best Local Similarity 20.7%; Pred No. 10; Mismatches 165; Indels 127; Gaps 19;
 Matches 90; Conservative 52;
 QY 49 HNNVQCF-----YFLQDFGCGEVALDWFDFSCRGQREWVQKHESQFIIV 100
 DB 181 HPLVOLLGVCTREPPFYIITEFTYGNLLD-----YLRCNRQEVSAVV--LLTMATQ 232
 QY 101 CSKGMKIFVKKYKHKG-GGRSGGKGLFVAVSAIA-EKLQAKOSSAALSKEF---- 154
 DB 233 ISSAMEY-LEKKNFTHDLAARNCLVGNLKVADFGLSRLMTGDTTAAHAGAKFKPKW 291
 QY 155 ----TAVFYDSCGDV-----PGILDSTAYRLMDNLPQLCSLHS 192
 DB 292 TAPESLATNFKSISKDWAGVLLHNIYMGSPYGI-DLSQVTELE----- 339
 QY 193 RDHGLQEPQHTROGSRNRYR-----SKSGSLVVAICNMHOFIDEE---PWTFEX 241
 DB 340 KQYRKERP-----EGCPKVTYELARACWQNPFSRFAEIHQAFETMFQESSISDEVK 394
 QY 242 QF-----VFFHPPLRYRPEVLEKFGSLGLVMDVMCK---PGPESDFCLK 283
 DB 395 ELGKSTRGGAGSMLOAPLPETKTRCRAAEQKASPSLPKLRQVYATSPSSGLSHK 454
 QY 284 VEAUVGATG---PADSQ-----HESQGGDLDQGEARPAL 316
 DB 455 KEATKGSAGMGTPATAEPAPPNNKVLKSKASEMRVRRHKHSESPGRD---KGLAK 511
 QY 317 DGSAAQLPLLTHTVTRAGSPDMPDUGIYDSSVPSSELSPLMEGLSTDTOTETSLTESV 376
 DB 512 LKPAPPPPPACTGKAGKPAQSPQEAAGEAGGPTKTKCTSLANDAVNTDPTKAGPGGE--- 568
 QY 377 SSSGLGEEPPALP 390
 DB 569 ---GLKRPVPPSPV 579

RESULT 9
 HT31_ARATH STANDARD; PRT; 660 AA.
 ID HT31_ARATH
 AC Q04996;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE Homeobox protein HAT3.1.
 GN HAT3.1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94035169; PubMed=8106082;
 RA Schindler U., Beckmann H., Casimiro A.R.;
 RT "HAT3.1, a novel Arabidopsis homeodomain protein containing a
 RT conserved cysteine-rich region";
 RL Plant J. 4:137-150(1993).
 CC -1- FUNCTION: BINDS ONLY TO LARGE DNA FRAGMENTS. RECOGNIZES A DNA
 CC FRAGMENT CARRYING 8 COPIES OF BOX7 MOTIF OF THE LIGHT-INDUCED
 CC CAB-E PROMOTER OF NICOTIANA PLUMBAGINIFOLIA. ALSO RECOGNIZES
 CC THE BOX7M1 MOTIF.

CC 1- SUBCELLULAR LOCATION: Nuclear.
 CC 2- TISSUE SPECIFICITY: PRIMARILY DETECTED IN ROOT TISSUE.
 CC 3- SIMILARITY: BELONGS TO THE PHD-ASSOCIATED HOMEBOX FAMILY.
 CC 4- SIMILARITY: CONTAINS 1 PHD-TYPE ZINC-FINGER.
 CC 5- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.
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 CC
 DR EMBL: X69512; CAAG263.1;
 DR HSP: P41778; 1006.
 DR TRANSFAC: T04111;
 DR InterPro: IPR001356; Homeobox.
 DR InterPro: IPR001963; Znf_PHD.
 DR Pfam: PF00046; homeobox; 1.
 DR Pfam: PF00628; PHD; 1.
 DR ProDom: PD000010; Homeobox; 1.
 DR ProDom: PD000389; HOX; 1.
 DR SMART: SM00249; PHD; 1.
 DR PROSITE: PS00027; HOMEBOX_1; 1.
 DR PROSITE: PS00071; HOMEBOX_2; 1.
 DR PROSITE: PS01359; ZF_PHD_1; 1.
 DR PROSITE: PS00016; ZF_PHD_2; 1.
 KW Homeobox; DNA-binding; Nuclear protein; Transcription regulation;
 KW zinc-finger.
 FT ZN_FING 202 259 PHD-TYPE
 FT DNA_BIND 551 610 HOMEBOX
 SQ SEQUENCE 660 AA; 73604 MW; A3B265CD394DA138 CRC64;
 Query Match 4.3%; Score 96; DB 1; Length 660;
 Best Local Similarity 21.4%; Pred. No. 9.4;
 Matches 79; Conservative 49; Mismatches 139; Indels 112; Gaps 18;
 QY 103 KGMFYVDKRYKHK-----GGRGSGKGLFLVAVSAIAEKLRQAKSSAALSKEI 155
 Db 120 KRLRYFLNRYEQSLDAYSLSGWGS-----LEKIRPEKELERATKE--- 164
 QY 156 AVTDYSCGVDGPIGLDLYKYLNDLNPQLCSHLHSRQGLQEPGQHTQGSRRYFRS 215
 Db 165 -----ILRSKLDFQHLDTLCARGLSPSLFTDGEI-----SSEDFCA 206
 QY 216 KSG-RSLTV-----AICN-----MHQFIDEPPDFEKFQVFPHPPLRYREPYLE-KFDS 263
 Db 207 KCGSKDLSVDNDIILCDGFCDRGFQYCYLEPP--LRKEDIP--PDGSGMLCPGCDCKDSD 262
 QY 264 GLVLDNVCKPSPESDCLAV-----BAVLGATGAD-----SQHES 301
 Db 263 LOLLNDSLGTFYSVSDWEKIFPEAAALVGGQNLCDLPSADSDEEDYDPCILNDNEN 322
 QY 302 QHGGLDQGEARPALDGS-----AALQPLIYTKAGS-----PSDPRDSGIYD 345
 Db 323 DEGDSD-DNEESNEDSGSDTEFTASDEMIESFKGKDKMDVNALPSDSDSDDD-YD 380
 QY 346 SVSPSELSPLMGLSTDTSTESLITSVSSSGLGE-----EPPALPSKLLS 395
 Db 381 PDAPTC-----DKESSNSDCTSDTDELETFSKGDENQQAEDYPLEDPGRTGQLQ 434
 QY 396 SGSCRADLG 404
 Db 435 DAILEDVVG 443
 RESULT 10
 PRG: HUMAN
 ID PRG: HUMAN STANDARD; PRT; 933 AA.
 AC P06401; Q9UPF7;
 DT 01-JAN-1988 (rel. 06, Created)
 DT 16-OCT-2001 (rel. 40, Last sequence update)

DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE Progesterone receptor (PR).
 GN PGR OR NR3C3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RI MEDLINE=90228361; PubMed=2328727.
 RA Kastner P., Krust A., Turcotte B., Stroop U., Tori L., Gronemeyer H.,
 RA Chambon P.
 RA "Two distinct estrogen-regulated promoters generate transcripts
 RA encoding the two functionally different human progesterone receptor
 RA forms A and B."
 RL EMBL: J191603; 1614(1990).
 RN [2]
 RN SEQUENCE FROM N.A.
 RI MEDLINE=87184565; PubMed=3551956;
 RA Misrahi M., Atger M., D'Aurion L., Loosfelt H., Meriel C.,
 RA Fridlansky F., Guichon-Mantel A., Galibert F., Milgrom E.,
 RA "Complete amino acid sequence of the human progesterone receptor
 RA deduced from cloned cDNA."
 RL Biochem. Biophys. Res. Commun. 143:740-748(1987).
 RN [3]
 RN SEQUENCE FROM N.A.
 RI Kieback D.G., Agoulnik I.U., Tong X.-W.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 682-933.
 RP MEDLINE=98282128; PubMed=9620806;
 RA Williams S.P., Sigler P.B.;
 RA "Atomic structure of progesterone complexed with its receptor."
 RL Nature 393:392-396(1998).
 CC 1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
 CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
 CC 2- SUBCELLULAR LOCATION: Nuclear.
 CC 3- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A AND B (SHOWN HERE); ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC 4- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC 5- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
 CC NR3 SUBFAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: X51730; CAAG6019.1;
 DR EMBL: M15716; AAA60081.1;
 DR EMBL: AF016381; AAD01587.1;
 DR PIR: A03245; QREUP.
 DR PIR: S09971; S09971.
 DR PDB: 1A28; 15-JUL-98.
 DR TRANSFAC: T00696;
 DR GeneW: HGNC:8910; PGR.
 DR MIM: 264080;
 DR InterPro: IPR000536; Hormone_rec_lig.
 DR InterPro: IPR000128; Progesterone_receptor.
 DR InterPro: IPR001723; Steroid_receptor.
 DR InterPro: IPR001628; Znf_C4steroid.
 DR Pfam: PF00104; hormone_rec; 1.
 DR Pfam: PF00105; zf-C4; 1.
 DR Pfam: PF02161; Prog_receptor; 1.
 DR PRINTS: PR00398; STERHORMONER.
 DR PRINTS: PR00047; STROIDFINGER.
 DR ProDom: PD000035; Znf_C4steroid; 1.
 DR SMART: SM00430; HOL1; 1.

KW Transcription regulation.
 SQ SEQUENCE 841 AA; 92706 MW; 9F18372739D723E4 CRC64;
 Query Match 4.3%; Score 94.5; DB 1; Length 841;
 Best Local Similarity 23.1%; Pred. No. 16;
 Matches 58; Conservative 25; Mismatches 73; Indels 95; Gaps
 QY 152 SRDGLQEQCTROGSR-----NFRSKGSRSLVAICNMH----- 229
 DB 536 SRRSANTGRSRGRGSRGEAQRNGSHHSKSEPT--VSSYTVGQNGARGDSAPSRK 593
 QY 230 -QFIDEEPWFQK---FVFPHPPPLRYREPVLKFDGSLVLDVMYKPGSPDFCLKVE 285
 DB 594 SQSQSQSQPPTTKSKSKTAAMPPPP---SP-----CSPSPAS----- 627
 QY 286 AAVLGATGPADESQESQHGGLDQGEARPALDGAALQPLLTTVKAGSPSNKPRD---SG 342
 DB 628 -----RERRRSKSPSSPPRP--HDPSPGPAFAAEKELATAG 661
 QY 343 IYDSSVPS-SELSLPLMGLSLTDOTETSSLTSSVSSSGGEEPPA-----LPSKLL 394
 DB 662 DEDGVSFGECVSATRGSSADESSSSSSSSSSSS--DEESDVDCRELDQSKRL 720
 QY 395 SSG---SKAD 402
 DB 721 EEALERCERD 731
 RESULT 12
 RMIL CHICK
 ID RMIL CHICK STANDARD; PRT; 806 AA.
 AC 004982;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE RMIL serine/threonine-protein kinase (EC 2.7.1.37).
 GN C-RMIL.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Choroauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocytes, and Fibroblast;
 RX MEDLINE=9331227; PubMed=8323553;
 RA Calogeralet I., Burnier J.V., Eyche A., Felder M., Catthy G.,
 RA Marx M.;
 RT "Genomic organization and nucleotide sequence of the coding region of
 RT the chicken c-Rmil(8-raf-1) proto-oncogene.";
 RL Biochem. Biophys. Res. Commun. 193:1324-1331(1993).
 CC -! NEURAL CELLS MAY PLAY A ROLE IN TRANSDUCING SPECIFIC SIGNALS IN
 CC NEURAL CELLS.
 CC -! CATALYTIC ACTIVITY: ATP + a protein - ADP + a phosphoprotein.
 CC -! SUBCELLULAR LOCATION: Nuclear.
 CC -! ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A.
 CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -! TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEURAL TISSUE.
 CC -! PM: PHOSPHORYLATED.
 CC -! SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -! MIL/RAF SUBFAMILY.
 CC -! SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
 CC BINDING DOMAIN.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: X57052; CAA47436.1;

DR PIR: JN0612; JN0612.
 DR HSP: P04049; 1PAR.
 DR InterPro: IPR002219; DAG_PE-BIND.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003116; RBD.
 DR InterPro: IPR004040; STY_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00130; DAG_PE-BIND; 1.
 DR Pfam: PF02196; RBD; 1.
 DR Pfam: PF00008; DAGPEDOMAIN.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00109; Cl; 1.
 DR SMART: SM00455; RBD; 1.
 DR SMART: SM00221; STYK; 1.
 DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE: PS00081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW Proto-oncogene; Transferase; Serine/threonine-protein kinase;
 KW ATP-binding; Nuclear protein; Alternative splicing; Zinc;
 KW Phorbol-ester binding; Phosphorylation.
 FT DOMAIN 122 129 POLY-SER.
 FT DOMAIN 235 280 PHORBOL-ESTER AND DAG BINDING.
 FT DOMAIN 248 280 CYS-RICH.
 FT DOMAIN 497 757 PROTEIN KINASE.
 FT NP_BIND 503 511 ATP (BY SIMILARITY).
 FT BINDING 523 523 ATP (BY SIMILARITY).
 FT ACT_SITE 616 616 BY SIMILARITY.
 FT VARSPIC 393 432 MISSING (IN SHORT ISOFORM).
 SQ SEQUENCE 806 AA; 89365 MW; 8F3FAD5274FB75C CRC64;

Query Match 4.2%; Score 93.5; DB 1; Length 806;
 Best Local Similarity 19.3%; Pred. No. 19;
 Matches 107; Conservative 55; Mismatches 165; Indels 227; Gaps 27;

QY 16 SSESSTYALPRERLRPRK---VFLCYSSKQG-----QHNNV 53
 DB 5 SSGSSAGSLENGDEPPPPVLCGACGSGGDPAPPEVWNIKMIKTQHEAL 64
 QY 54 QCFAYFLDRCG---CFVALDWDPS--LCRGGREVIQIHESQPIVVCCKM 107
 DB 65 -----LDKPGGHNPPSYLAEYETSKLDALQRE--QQLES 103
 QY 108 FVKKKTKHKGGRGSGGELFVAVSAIAEKLRQAKQSSAALSFKFIAYV---FDYSCE 164
 DB 104 -----GNGTDFSVSSASTDTVAVSSSSSLVAPSSLSVYQNPDTMSRN 147
 QY 165 GD-----VPG-----ILDLSTKYRLMDNL-POLCSHLSDHGLQE 199
 DB 148 NPKSPQPIVRFVLPNKTQTVVPCGTVTRDSLKALMRGLIPECCAVYRIQD-GEKK 206
 QY 200 P-----GQH-----TRGSRNRYFSKSGSLVATCN----- 227
 DB 207 PIGWDTISWLTGEELFVLEVNVLTHNEVRKTFE-----LAPCDFCRKLLFQG 258
 QY 228 -----MHQFDREPD-----WFEKQFVPEHP-----PPLRYREP 256
 DB 259 FRCQCYGKFKQRCSTEVPLCMVNTDQLDLFLVSKFFEHPISQEITTGTTAGSGYP 318
 QY 257 VLEKFDGLVNDVCMKPGSPESDCLKYEAVALGATGADPSQHSQHGGLDQDGPALP 316
 DB 319 SVPPSDS--VGPPIPLSPSPKSI-----PIQPFPADEDEHNGQGRDSSA----- 366
 QY 317 DGSNAALPLLR--TVKAGSPDMPRGIDYSSVPSSLSLPLMEGLSDTQET--SSITE 373
 DB 367 -----PNVHITIEPVNDILRDQVGRGEGAPLQ-----LARCRLYQRTSPPLH 415
 QY 374 SV-----SSSGLGEEPPALPKLLS-----SGSKAD- 402
 DB 416 SVPIEIVDFEPGPFVFRGTSAGLSATPPASLFGSLTNVKALQKSPGPKRERKSSSSDR 475

QY 403 -----LGGERSYDDE 411
 DB 476 NPMKTLGRDSSDD 489

RESULT 13
 RML_COTJA STANDARD; PRT; 807 AA.
 AC P34908;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE RML serine/threonine-protein kinase (EC 2.7.1.37).
 GN C-RML;
 OS Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Coturnix;
 OX NCBI_TaxID=93934;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94319540; Pubmed=1620546; Laugier D.,
 RA Eychene A., Barnier J.V., Dezelee P., Mari M., Laugier D.,
 RA Calogeraki I., Calothy G.,
 RT "Quail neuroretina c-Rml(B-rat) proto-oncogene cDNAs encode two
 RL proteins of 93.5 and 95 kDa resulting from alternative splicing.",
 RL Oncogene 7:1315-1323(1992).
 CC -1- FUNCTION: MAY PLAY A ROLE IN TRANSDUCING SPECIFIC SIGNALS IN
 CC NEURAL CELLS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein - ADP + a phosphoprotein.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEURAL TISSUE.
 CC -1- PTM: PHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -1- SIMILARITY: BELONGS TO THE MIL/RAF SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
 CC BINDING DOMAIN.

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 DR EMBL: M80846; AAA49493.1;
 DR EMBL: M80845; AAA49492.1;
 DR HSP: P04049; 1PAR.
 DR InterPro: IPR002219; DAG_PE-bind.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003116; RBD.
 DR InterPro: IPR004040; STY_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00130; DAG_PE-BIND; 1.
 DR Pfam: PF02196; RBD; 1.
 DR PRINTS: PR00008; DAGPEDOMAIN.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00109; Cl; 1.
 DR SMART: SM00455; RBD; 1.
 DR SMART: SM00221; STYK; 1.
 DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE: PS00081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW Proto-oncogene; Transferase; Serine/threonine-protein kinase;
 KW ATP-binding; Nuclear protein; Alternative splicing; Zinc;
 KW Phorbol-ester binding; Phosphorylation.
 FT DOMAIN 122 129 POLY-SER.

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FT DOMAIN 235 280 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 248 280 CYS-RICH.
FT DOMAIN 497 757 PROTEIN KINASE.
FT NP_BIND 503 511 ATP (BY-SIMILARITY).
FT BINDING 523 523 ATP (BY-SIMILARITY).
FT ACT_SITE 616 616 BY-SIMILARITY.
FT VARSPLIC 393 432 MISSING (IN SHORT ISOFORM).
SO SEQUENCE 807 AA; 89521 MW; 1F9700A65242FB7 CRC64;

Query Match: 4.2%; Score 93.5; DB 1; Length 807;
Best Local Similarity 19.3%; Pred. No. 19;
Matches 107; Conservative 55; Mismatches 165; Indels 127; Gaps 27;

QY 16 SSSSTYTAALPRELRPRK---VFCTSSKDG-----QNMNVV 53
Db 5 SSGSAGASLNGMEPEPPPPVGLGACGAGGGDPAPEEVNWKQMLTQERIAL 64
QY 54 QCPAYFLQPCG---CEVALDMEPS---LCRGGQREWVQKTHESQFIYVCSKGMKY 107
Db 65 -----LDKFGGHERPPSYILEAYEYTSKDALQORE---QQLLES- 103
QY 108 FVDKKNYKKGGRSGGGLFLVAVSAIAELKROAKQSSAALSKEFTAVT---FDVSC 164
Db 104 -----GNGTDFSVSSASTDTVASSSSSLVAPSSLSYQNTDMRN 147
QY 165 GD-----VPG-----ILDSTKYRLMDNL-POLCSHLSDRGLQ 199
Db 148 NPKSPQPIRVFLPNKORTVPPARCGVTVRDSLKALAMRGLIPECCAVTRIQD-GEKK 206
QY 200 P-----GQH-----TROGSRNFRSKGRSRYVAICH----- 227
Db 207 PIGMDTISLWGLHELVLENVPLTHNFVKTEFT-----LACDPCRLKLFQ 258
QY 228 -----WQFIDEEDP-----WPEQVFPHP-----PPLRYREP 256
Db 259 FRCQTGKGFHRCSTEVPLMCVNYDQDILLFVSKEFFHRSIQETTLGTTPASGYP 318
QY 257 VLEKFDGLVNDVNMCKPESDFCLKEVAALVIGATGPADSOHESQHGGLDQGEARPAL 316
Db 319 SVTPSDS---VGPPILPSPSPSKSI-----PIQPPERPADEHRNQFQRDSSA 366
QY 317 DGSAAQLPLH---TVKAGSPDNDRSGIYDSSVPSSLSLPLMEGLSTQDET-SSLTE 373
Db 367 -----PNVHTNTEPNIDLDLDQGVGEGAPLQO-----LMCLKRYSTRPSPPLH 415
QY 374 SV-----SSSGLGEEPPALPSKLLS-----SGCKAD- 402
Db 416 SVTSEIVDFECPVFRGSTAGLSTPPASLPGSLTNVAKLQSPQORERKSSSEDR 475
QY 403 -----LCRSYTD 411
Db 476 NRMKTLGRDSSDD 489

RESULT 14
SH33_MOUSE
ID SH33_MOUSE STANDARD; PRT; 347 AA.
AC Q62421;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE SH3-containing GRB2-like protein 3 (SH3 domain protein 2C) (SH3p13).
GN SH3L3 OR SH3D2C OR SH3D3C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo.
RX MEDLINE=98294438; PubMed=9630982;
RA Sparks A.B., Hoffman N.G., McConnell S.J., Fowlkes D.M., Kay B.K.;
RT *Cloning of ligand targets: systematic isolation of SH3

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domain-containing proteases.
Nat. Biotechnol. 14:741-744(1996).
-1- FUNCTION: MAY PLAY A REGULATORY ROLE IN SYNAPTIC VESICLE RECYCLING
CC (BY-SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH SYNAPTOTANIN AND DYNAMIN 1.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE ENDOPHILIN FAMILY.
CC
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CC
CC EMBL; 058887; AAC72268.1;
CC RSP; P29355; ISEM.
CC MGD; MGI:700011; SH3D2C2.
CC InterPro; IPR001452; SH3.
CC Pfam; PF00018; SH3; 1.
CC PRINTS; PR00452; SH3DOMAIN.
CC ProDom; PD000066; SH3; 1.
CC SMART; SM00326; SH3; 1.
CC PROSITE; PS00002; SH3; 1.
CC SH3 domain; Coiled coil; Multigene family.
KW SH3 domain; Coiled coil; COILED COIL (POTENTIAL).
FT DOMAIN 180 201
FT DOMAIN 285 344 SH3
FT DOMAIN 273 276 POLY-SER.
FT SEQUENCE 347 AA; 38934 MW; A2174642F853B5EB CRC64;
Query Match: 4.2%; Score 92.5; DB 1; Length 347;
Best Local Similarity 20.7%; Pred. No. 78;
Matches 63; Conservative 43; Mismatches 122; Indels 77; Gaps 12;

QY 94 SQFIYVCSKGMKYFVDKKNYKKGKGG-----RSGKGEFLVAVSAIAE-KLRQAK 145
Db 44 SKAVAILSKATEYFLQNPAYRAKGLMNTVSKLKGQVATGYPTQEGLLGDOMLKRYKE 103
QY 146 --SSAALSXFIAYFYDSCGDPGILDLSKYRLMDNLPCLSHLSDRGLQEPQGH 203
Db 104 LGEDSAFGNSLDVVGKALMAEVKDSLDINVKQTFIDPLQLL-----QKDLKEIGHH 157
QY 204 TR--QGSRRNYFRSKS-----GESLYVAICHMHQFIDEEDP----- 238
Db 158 LKLEGRRLDYKRRKRVKIPPEEIRQAVEKEESKELASRNFLENDEYQVSQALV 217
QY 239 FEKQVFPHPPLRYEPVLEKFDGLVNDVNMCKPESDFCLK---VEAAVLGATGPA 295
Db 218 FVEAALDYH-----RQSTEILQELQSKLELRISLASKVKREFMPKPVNKSSTDANGVGS 273
QY 296 DSOHESQHGGLDQGEARPALDGSAAALQPLLTVTKAGSPDNDRSGIYDSSVPSSLSL 355
Db 274 SS---SKTPGTD-----TPADQPCGRGLDPE-PENEGEL 304
QY 356 PLMEG 360
Db 305 GFKEG 309

RESULT 15
SH3_MOUSE
ID SH3_MOUSE STANDARD; PRT; 548 AA.
AC P98154; Q61844;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Integral membrane protein DCCR2/IDD precursor (Seizure-related
DE membrane-bound adhesion protein).
DE
GN IDD OR DCCR2 OR DGSC OR SE212 OR SE2-12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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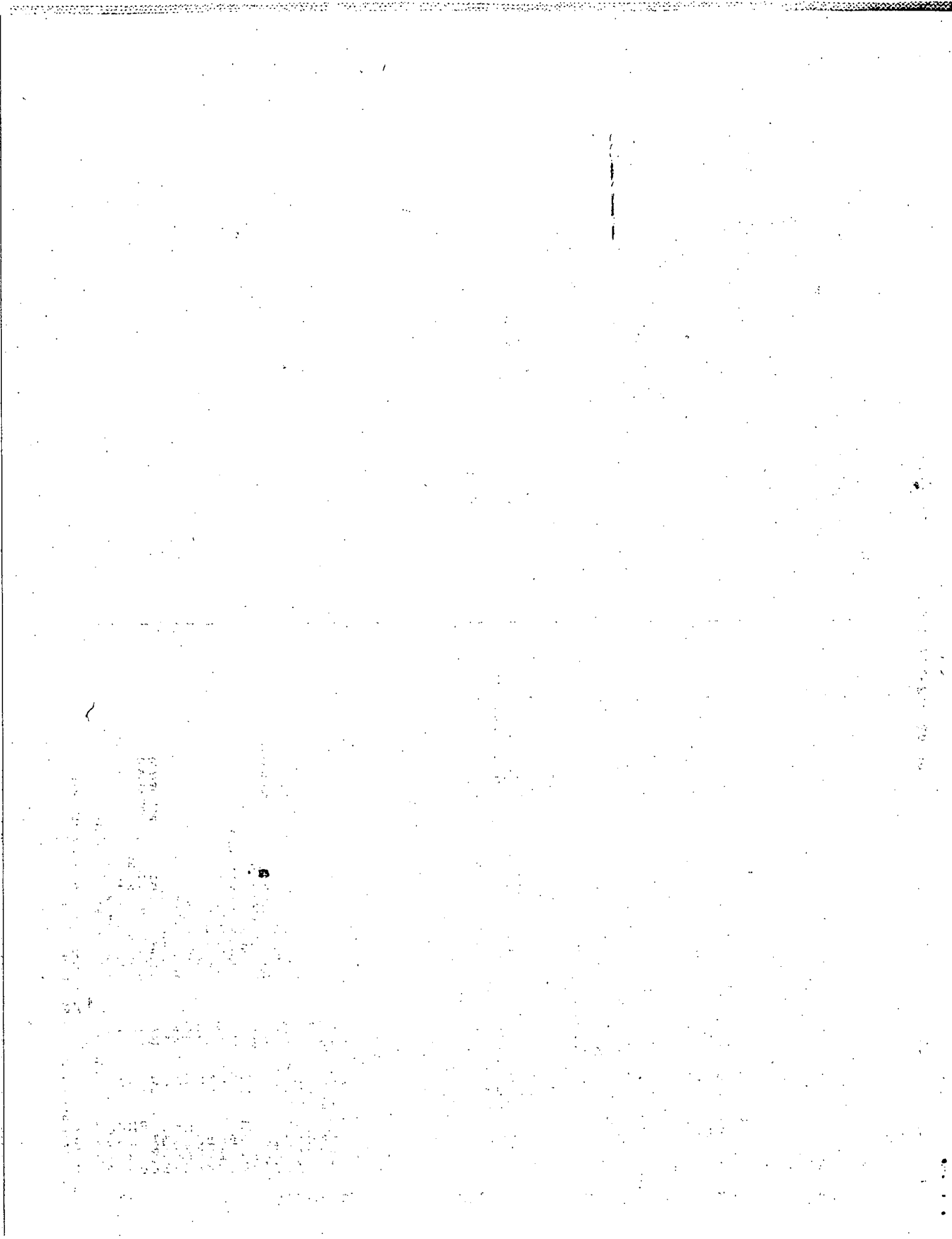
OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Embryo;
 RX MEDLINE=97262110; PubMed=9107688;
 RA Taylor C., Wadley R., O'Donnell H., Roberts C., Mattel M.-G.,
 RA Kimbly W.L., Wynshaw-Boris A., Scambler P.J.;
 RT "Cloning and mapping of murine Dgcr2 and its homology to the Sez-12
 RT seizure-related protein.";
 RL Mamm. Genome 8:371-375(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain cortex;
 RX MEDLINE=96212927; PubMed=8630060;
 RA Kajiwara K., Nagasawa H., Shimizu-Nishikawa S., Ookura T.,
 RA Kimura M., Sugaya E.;
 RT "Cloning of Sez-12 encoding seizure-related and membrane-bound
 RT adhesion protein.";
 RL Biochem. Biophys. Res. Commun. 222:144-148(1996).
 CC -1- FUNCTION: PROBABLY PLAYS A ROLE IN NEURAL CREST CELL MIGRATION.
 CC MAY PLAY A ROLE IN DELIVERY OF EXTRACELLULAR SIGNALS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS IN VARIOUS ORGANS WITH LOW
 CC ABUNDANCE.
 CC -1- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
 CC -----
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 CC -----
 DR EMBL; X95480; CAA6749.1; -;
 DR EMBL; D78641; BA01460.1; -;
 DR HSSP; P01130; IAJJ.
 DR MGI; 892866; Dgsc.
 DR InterPro; IPR002172; LDL_recept_A.
 DR InterPro; IPR001304; Lectin_C.
 DR InterPro; IPR001007; VWFC.
 DR Pfam; PF00057; ldl_recept_a; 1.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR SMART; SM00192; LDLA; 1.
 DR SMART; SM00214; VWFC; 1.
 DR PROSITE; PS01208; VWFC; 1.
 DR PROSITE; PS01209; LDLRA_1; 1.
 DR PROSITE; PS00068; LDLRA_2; 1.
 DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
 KW Receptor; Glycoprotein; Transmembrane; Lectin; Signal.
 FT SIGNAL; 1
 FT CHAIN; 24
 FT DOMAIN; 25 548
 FT TRANSMEM; 348 366
 FT DOMAIN; 367 548
 FT DOMAIN; 28 68
 FT DOMAIN; 113 239
 FT DOMAIN; 268 331
 FT DISULFID; 30 44
 FT DISULFID; 37 57
 FT CARBOHYD; 51 66
 FT CARBOHYD; 147 147
 FT CARBOHYD; 194 194
 FT CONFLICT; 67 67
 FT CONFLICT; 108 111
 FT CONFLICT; 370 370
 SQ SEQUENCE 546 AA; 50697 MW; 77AF5C839F6B817 CRC64;

Query Match
 Best Local Similarity

4.28; Score 92.5; DB 1; Length 548;
 19.58; Pred. No. 14;

Matches 87; Conservative 48; Mismatches 114; Indels 197; Gaps 24;
 QY 73 WEDESLCEQORE-WYQKHESQFIIVVCSKMKYFDKKNKTKHKGSGSGKG--ELF 129
 DB 176 MKD-----ORKLW-----GYQYVITGRNHSLEGRWEVAFKGSPEVF 212
 QY 130 L-----VAVSATAEK-----LRQAKOSSAALSKEFIAYI----- 158
 DB 213 LPDPIIFASAMSENDNVFCALQCFHFPTLRHDLRSHWAESGSEKSFCLKRSQTCVDI 272
 QY 159 -----EYSCSEGDPVGLDLSTKYRLMDNLPLCL-SHLHSDRHGLQEPQOHTRO--- 206
 DB 273 KDNVVDGFFFTFKGDDPCL--SCTCHR--GEPEMVAALCERPOGQOQYKRDPECK 327
 QY 207 -----GSRNRYFRSKSGRSLTVaic-----NM 228
 DB 328 FMCILDPDGS--SLFDSMASGMRLVWSCISSEFLILSLFLFVHRLAQRRIERIESLIGANL 385
 QY 229 HOF-----IDEEPDMFEKQFVPPH-----PPPLRYREPVLKPFDSG 264
 DB 386 HFNGLRRIPCFDYGPDPGCTGLPLHLSDDGEGTFHFDPPTTAYKYPMQDPD- 444
 QY 265 LVLDNVCKPGPSDFCLKVEAVLGTGTPADSGHESQHGGLQDGEARPAIDGSAALQP 324
 DB 445 -----PPPYEASINPDSVY---DPADDD-----AFEP 470
 QY 325 LIHTVKAQSPDMPRDSGI-----YDSSVPSSELSPLMEGLSTQDTETSSL-----TE 373
 DB 471 -----VEASLPA--PRDGGIEGALPHRLDQPLPPAETSLADLE---DSTDSSALLVPPD 520
 QY 374 SVSSSSGLGEEPPA---LPSKLSS 396
 DB 521 PAQSGSTPATEAPFGGRUPRASLNT 546

Search completed: May 19, 2003, 09:21:01
 Job time : 14.4873 secs



GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 19, 2003, 09:17:08 ; Search time 11.3807 Seconds
(without alignments)
1080.669 Million cell updates/sec

Title: US-09-912-157-2_COPY_336_753
Perfect score: 2210
Sequence: 1 RKQOENIYSHDESSSS.....CRKDLGCRSYTDELNAVPL 418

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 1: Issued Patents AA:*

- 2: /cgn2_5/ptodata/1/1aa/5A-COMB.pep.*
- 3: /cgn2_5/ptodata/1/1aa/5B-COMB.pep.*
- 4: /cgn2_5/ptodata/1/1aa/6A-COMB.pep.*
- 5: /cgn2_5/ptodata/1/1aa/6B-COMB.pep.*
- 6: /cgn2_5/ptodata/1/1aa/6C-COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	310	14.0	866	2	US-08-620-694A-10
2	310	14.0	866	3	US-09-022-255-10
3	310	14.0	866	3	US-09-022-696-10
4	310	14.0	866	3	US-08-978-773-4
5	310	14.0	866	3	US-09-022-253-10
6	310	14.0	866	3	US-09-022-260-10
7	310	14.0	866	4	US-09-022-259-10
8	310	14.0	866	4	US-09-022-257-10
9	289.5	13.1	864	3	US-08-620-694A-2
10	289.5	13.1	864	3	US-09-022-255-2
11	289.5	13.1	864	3	US-09-022-696-2
12	289.5	13.1	864	3	US-08-978-773-2
13	289.5	13.1	864	3	US-09-022-253-2
14	289.5	13.1	864	4	US-09-022-260-2
15	289.5	13.1	864	4	US-09-022-259-2
16	289.5	13.1	864	4	US-09-022-257-2
17	95	4.3	933	4	US-08-764-870-14
18	95	4.3	933	4	US-08-980-115-14
19	92.5	4.2	347	4	US-08-630-915A-32
20	92.5	4.2	2308	2	US-08-015-973-1
21	92.5	4.2	2308	2	US-08-448-164-1
22	92.5	4.2	2308	4	US-08-081-929-2
23	92.5	4.2	2314	4	US-09-816-703A-2
24	91.5	4.1	828	2	US-08-993-228-21
25	90	4.1	803	4	US-09-063-035-2
26	88.5	4.0	830	4	US-09-562-737-31
27	88.5	4.0	2353	4	US-08-984-709A-50

28	88	4.0	410	4	US-08-725-758A-4	Sequence 4, Appl1
29	88	4.0	426	4	US-08-725-758A-2	Sequence 2, Appl1
30	87.5	4.0	683	4	US-09-620-412C-357	Sequence 357, App
31	87.5	4.0	830	4	US-09-562-737-34	Sequence 34, Appl
32	87	3.9	830	4	US-09-562-737-32	Sequence 32, Appl
33	87	3.9	951	1	US-08-162-809-2	Sequence 2, Appl1
34	86.5	3.9	617	4	US-09-188-930-303	Sequence 303, App
35	86.5	3.9	1581	4	US-09-110-517-2	Sequence 2, Appl1
36	86.5	3.9	2101	1	US-08-466-390-4	Sequence 4, Appl1
37	86.5	3.9	2101	1	US-08-470-950-4	Sequence 4, Appl1
38	86.5	3.9	2101	1	US-08-467-781-4	Sequence 4, Appl1
39	86.5	3.9	2101	1	US-08-195-487-4	Sequence 4, Appl1
40	86.5	3.9	2101	2	US-08-483-924-4	Sequence 4, Appl1
41	86.5	3.9	2101	4	US-09-452-294-1	Sequence 1, Appl1
42	86.5	3.9	2101	5	PCT-US93-06160-4	Sequence 4, Appl1
43	86	3.9	878	4	US-09-141-212-8	Sequence 8, Appl1
44	86	3.9	878	4	US-09-561-138-8	Sequence 8, Appl1
45	86	3.9	879	4	US-09-141-212-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-08-620-694A-10
Sequence 10, Application US/08620694A
Patent No. 5869286
GENERAL INFORMATION:
APPLICANT: YAO, Zhengbin
APPLICANT: Spriggs, William
TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620.694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-620-694A-10
Query Match: 14.0%; Score 310; DB 2; Length 866;

Best Local Similarity 28.3%; Pred. No. 8.9e-24;
Matches 127; Conservative 60; Mismatches 173; Indels 88; Gaps 20;

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QY 14 EESSESTYTAALPRERLRPR---KVFCTSSKDGQNMNVVOCFAFLQDQCGCEVA 69
DB 353 EYSDTKYTDGLPADLPPKPKRWIISA-DHPLYDVVLFKFAQLLTACGTEVA 411
QY 70 LDLEWDFSLCRGQREWY---IQKHESQFIIVVCSKGMKFFVDKKNYKHGGG--- 120
DB 412 LDLEWDFSLCRGQREWY---IQKHESQFIIVVCSKGMKFFVDKKNYKHGGG--- 120
QY 121 ---RSGSGELFLVAVSAIAEKLQAKSSAALSKEFIATVF-DYSCGDVPGILDSTK 176
DB 468 RCDHGKPVGDLFTAAANNMILPDKR---PACFGTVVCTSEVSCDGDVDFGAPR 522
QY 177 YRLMDLNPOLCSHLHSDHGLQEPQHTROG--SRNRYFRSKSGRSLYVAICNMHOFIDE 234
DB 523 YPLMDRFEVY---YFRIDLEMFQPMHVRGELSGDNTLSPGGRQLRAALDRFDQVVR 580
QY 235 EPDRFE-----KQVFPHPPLRYREPVLEKFDGLVNDVMCKPGPESDFCLKVEA 286
DB 581 CPDWFECENLYSADDDQAPSLDEEV-FEPLLP--GTGIVKRAPLVRE-PGSOACLAIDP 637
QY 287 AVLGATGPADSOHE-----SQRGGLDQDGEARPALDGS---ALQ 323
DB 638 LVGEEGAANAKLEPHLQPGQAPQPOPLTVLAABEGALVAAPVPGPLADGAARLALA 697
QY 324 -----PLHTVAGSPDMRDSGYDSSVPSSLSPLMEGLSTDTQTETSSLTSESVS 377
DB 698 GEACPLGSPAG-----RNSVLF--LPVDPDSPL--GSSTPMASPDLLPEDVR- 745
QY 378 SSGLEGEPPALPSKLLSGCKADLGC 405
DB 746 -----EHLEGLMSLFEQSLSQAQGGC 768
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RESULT 2

US-09-022-255-10
Sequence 10, Application US/09022255
Patent No. 6072033

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,255
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695

REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-255-10

Query Match 14.0%; Score 310; DB 3; Length 866;

Best Local Similarity 28.3%; Pred. No. 8.9e-24;

Matches 127; Conservative 60; Mismatches 173; Indels 88; Gaps 20;

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QY 14 EESSESTYTAALPRERLRPR---KVFCTSSKDGQNMNVVOCFAFLQDQCGCEVA 69
DB 353 EYSDTKYTDGLPADLPPKPKRWIISA-DHPLYDVVLFKFAQLLTACGTEVA 411
QY 70 LDLEWDFSLCRGQREWY---IQKHESQFIIVVCSKGMKFFVDKKNYKHGGG--- 120
DB 412 LDLEWDFSLCRGQREWY---IQKHESQFIIVVCSKGMKFFVDKKNYKHGGG--- 120
QY 121 ---RSGSGELFLVAVSAIAEKLQAKSSAALSKEFIATVF-DYSCGDVPGILDSTK 176
DB 468 RCDHGKPVGDLFTAAANNMILPDKR---PACFGTVVCTSEVSCDGDVDFGAPR 522
QY 177 YRLMDLNPOLCSHLHSDHGLQEPQHTROG--SRNRYFRSKSGRSLYVAICNMHOFIDE 234
DB 523 YPLMDRFEVY---YFRIDLEMFQPMHVRGELSGDNTLSPGGRQLRAALDRFDQVVR 580
QY 235 EPDRFE-----KQVFPHPPLRYREPVLEKFDGLVNDVMCKPGPESDFCLKVEA 286
DB 581 CPDWFECENLYSADDDQAPSLDEEV-FEPLLP--GTGIVKRAPLVRE-PGSOACLAIDP 637
QY 287 AVLGATGPADSOHE-----SQRGGLDQDGEARPALDGS---ALQ 323
DB 638 LVGEEGAANAKLEPHLQPGQAPQPOPLTVLAABEGALVAAPVPGPLADGAARLALA 697
QY 324 -----PLHTVAGSPDMRDSGYDSSVPSSLSPLMEGLSTDTQTETSSLTSESVS 377
DB 698 GEACPLGSPAG-----RNSVLF--LPVDPDSPL--GSSTPMASPDLLPEDVR- 745
QY 378 SSGLEGEPPALPSKLLSGCKADLGC 405
DB 746 -----EHLEGLMSLFEQSLSQAQGGC 768
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RESULT 3

US-09-022-696-10
Sequence 10, Application US/09022696
Patent No. 6072037

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,696

FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/620,694
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USN 08/410,535
 FILING DATE: 23 MARCH 1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,695
 REFERENCE/DOCKET NUMBER: 2617-B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)587-0430
 TELEFAX: (206)
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 866 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-022-696-10

Query Match 14.0% Score 310; DB 3; Length 866;
 Best Local Similarity 28.3%; Pred. No. 8.9e-24;
 Matches 127; Conservative 60; Mismatches 173; Indels 88; Gaps 20;

QY 14 ESSESTYTAALPRELRPRP----KVFICYSSKDGQNMVYVCFAYFLQDFCGCEVA 69
 Db 353 EKYSDTKYDGLPAADLPPLPKPKWIIYSA-DHPLYVDVVLKFAQLLACGTEVA 411
 QY 70 LQWEDFSICREGQREWV----IQIHESQFIIVVCSKGMKFDKKNYKHGGG----- 120
 Db 412 LQLEQALISAGVWTVGKQKQENVESKIIIVLCSSGTR----AKQALLGRGAPVRL 467
 QY 121 ----RSGKGELFLVAVSAIAEKLRQAKSSAALSFKFIATVF-DYSCGDVPGILDLSK 176
 Db 468 RCDHGKPVGDILFTAMNNMLDPFKR-----PACFGTYVVCYFSEVSCDGVDFLGAAPR 522
 QY 177 YRLMDNLPOLCSHLHSRDHGLQEPQHTROG--SRNRYFRSKSGRSLYVAICNMHOFIDE 234
 Db 523 YPLMDRFEV--YFRIDLEMPQGRMHRVSGELSGDNTLRSFGQRLRAALDRFRDQVR 580
 QY 235 EPDQFE-----KQVFPHPPLRYREPVLKFDGSLVLDVNCVKPGSDFCCLKVEA 286
 Db 581 CPDMFECENLYSADQDQAPSLDEEV-FEPLLP--GTGIVKRAPLVRE-PGSOACLAIDP 637
 QY 287 AVLGATGPADSQHE-----SQHGLDQDGEARPAALDQSA---ALQ 323
 Db 638 LVGEGGAAVAKLEPHLQPRGPAPQPLHTLVLAEEGALVAVAEPGLADGAARLALA 697
 QY 324 -----PLHVTKAGSPDMRDSGLYDSSVPSSELSIPLMEGLSTDTQETTSLSYSS 377
 Db 698 GEGEACPLGSGFAG-----RNSVLF---LPVDPESPL--GSSTPMASFDLLPEDVR- 745
 QY 378 SSGLEGEPPALPSKLLSSGSKADLGC 405
 Db 746 -----EHLEGLMLSLFEQSLSCQAQGGC 768

RESULT 4
 US-08-978-773-4
 ; Sequence 4, Application US/08978773
 ; Patent No. 6083906
 ; GENERAL INFORMATION:
 ; APPLICANT: Troutt, Anthony
 ; TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immuner Corporation
 ; STREET: 51 University Street

CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER-READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: ApplePowerMacintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/978,773
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USSN 60/052,525
 FILING DATE: 27 NOVEMBER 1996
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2623-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)587-0430
 TELEFAX: (206)
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 866 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-978-773-4

Query Match 14.0% Score 310; DB 3; Length 866;
 Best Local Similarity 28.3%; Pred. No. 8.9e-24;
 Matches 127; Conservative 60; Mismatches 173; Indels 88; Gaps 20;

QY 14 ESSESTYTAALPRELRPRP----KVFICYSSKDGQNMVYVCFAYFLQDFCGCEVA 69
 Db 353 EKYSDTKYDGLPAADLPPLPKPKWIIYSA-DHPLYVDVVLKFAQLLACGTEVA 411
 QY 70 LQWEDFSICREGQREWV----IQIHESQFIIVVCSKGMKFDKKNYKHGGG----- 120
 Db 412 LQLEQALISAGVWTVGKQKQENVESKIIIVLCSSGTR----AKQALLGRGAPVRL 467
 QY 121 ----RSGKGELFLVAVSAIAEKLRQAKSSAALSFKFIATVF-DYSCGDVPGILDLSK 176
 Db 468 RCDHGKPVGDILFTAMNNMLDPFKR-----PACFGTYVVCYFSEVSCDGVDFLGAAPR 522
 QY 177 YRLMDNLPOLCSHLHSRDHGLQEPQHTROG--SRNRYFRSKSGRSLYVAICNMHOFIDE 234
 Db 523 YPLMDRFEV--YFRIDLEMPQGRMHRVSGELSGDNTLRSFGQRLRAALDRFRDQVR 580
 QY 235 EPDQFE-----KQVFPHPPLRYREPVLKFDGSLVLDVNCVKPGSDFCCLKVEA 286
 Db 581 CPDMFECENLYSADQDQAPSLDEEV-FEPLLP--GTGIVKRAPLVRE-PGSOACLAIDP 637
 QY 287 AVLGATGPADSQHE-----SQHGLDQDGEARPAALDQSA---ALQ 323
 Db 638 LVGEGGAAVAKLEPHLQPRGPAPQPLHTLVLAEEGALVAVAEPGLADGAARLALA 697
 QY 324 -----PLHVTKAGSPDMRDSGLYDSSVPSSELSIPLMEGLSTDTQETTSLSYSS 377
 Db 698 GEGEACPLGSGFAG-----RNSVLF---LPVDPESPL--GSSTPMASFDLLPEDVR- 745
 QY 378 SSGLEGEPPALPSKLLSSGSKADLGC 405
 Db 746 -----EHLEGLMLSLFEQSLSCQAQGGC 768

RESULT 5
 US-09-022-253-10
 ; Sequence 10, Application US/09022253
 ; Patent No. 6096305

GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,253
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694
FILING DATE: 21-MARCH-1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-253-10
Query Match 14.0%; Score 310; DB 3; Length 866;
Best Local Similarity 28.3%; Pred. No. 8.9e-24;
Matches 127; Conservative 60; Mismatches 173; Indels 88; Gaps 20;
QY 14 EESSESTYTAALPERLRPR-----KVFICYSSKDGQNNHNVOCFAVFLQDFGCEVA 69
DB 353 EKYSDRYDGLPADLPPPLPKRWIIYSA-DHPLYVDVLFKFAQLLTACGTEVA 411
QY 70 LDWEDFSICRGQREW---IQKHESQFIIVVCSKGMKYFVDKKNYKHGG-----120
DB 412 LDLEEQAISEAGVMTWVGROKQENVSNSKIIVLCRGT-----AKWQALLGKAPVRL 467
QY 121 ---RSGKGELFLVAVSAIAELKRAQKSSAALSFKFIATF-DYSCGDVPGILDSTK 176
DB 468 RCDGKPGVGLDFTAAANMLLPDKR-----PACFTYVVCYFSEVSCDGDVDFLGAAPR 522
QY 177 YRLMNPQLCSLHESDGLQEPQHTROG--SRNRYFSKSGSLVYICNMBEQFIDE 234
DB 523 YPLADREFEY--YFRIDLEMPQGMHVRVGLSGDNLKPSGRLRAALDRFDMQVR 580
QY 235 EPWFFE-----KQVFPFHPPLRYREPVELEKFDGLVNDVMCKPSPEDFCLKVEA 286
DB 581 CPDWFECENYSADDQADSLAEV-FEPLLP-GTGIYKRAPIVRE-PGSAQLADP 637
QY 287 AVLGATPANSQHE-----SQGGGLDQGEARPALDGA---ALQ 323

DB 638 LVGEGGAANAKLEPHLQPRGPAPQPLETLVLAEEGALVAANVEPGLADGAARLALA 697
QY 324 -----PLHTVTKAGSPDMRDSGIYDSVSPSSLSPLAEGSLTDOTETSSLTSSVSS 377
DB 698 GRGEACPLGSPGAG-----RNSVLF--LVPDPSPL--GSSTPMASPDLLPEDVR- 745
QY 378 SSGLOEPEPPALPSKLLSSGSCADLGC 405
DB 746 -----EHLEGLATLSLFEQSLSCQAQGC. 768
RESULT 6
US-09-022-260-10
Sequence 10, Application US/09022260
Patent No. 6100235
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,260
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-260-10
Query Match 14.0%; Score 310; DB 3; Length 866;
Best Local Similarity 28.3%; Pred. No. 8.9e-24;
Matches 127; Conservative 60; Mismatches 173; Indels 88; Gaps 20;
QY 14 EESSESTYTAALPERLRPR-----KVFICYSSKDGQNNHNVOCFAVFLQDFGCEVA 69
DB 353 EKYSDRYDGLPADLPPPLPKRWIIYSA-DHPLYVDVLFKFAQLLTACGTEVA 411
QY 70 LDWEDFSICRGQREW---IQKHESQFIIVVCSKGMKYFVDKKNYKHGG-----120
DB 412 LDLEEQAISEAGVMTWVGROKQENVSNSKIIVLCRGT-----AKWQALLGKAPVRL 467
QY 121 ---RSGKGELFLVAVSAIAELKRAQKSSAALSFKFIATF-DYSCGDVPGILDSTK 176

Db 468 RCDHGKPGDGLFTAAANNMLPDKR-----PACFGTVVVCYFSEVSCDGDVDFLFGAAPR 522
QY 177 RLMDNLPOLCSHLSDHGLQBPQHTROG--SRNFRKSGRSGLTYAICNMHQFIDE 234
Db 523 YPLMDRFEV--YFIODLEMGPCGRMHRVGLSGDNYLSPGGRQLRAALDRFRDQVR 580
QY 235 EPDWEF-----KQVFPFHPPLRYREPYLEKFDGSLVNDVMCKPGPESDFCLAYEA 286
Db 581 CPDWEFCENLYSADDODAPSLDEEV-FEPLPP-GTGIKRAPLVRE-PGSOACLAIDP 637
QY 287 AVLKATGPADSOHE-----SOHGGLDQDGEARPAIDGSA---ALQ 323
Db 638 LVGEGGAANAKLEPHLOPQOPAPQPLHTLVLAAREGALVAAREPGPLADGAAYRLALA 697
QY 324 -----PLHTVYKAGSPDMPDSDGYDSSVPSSELSLPLMEGLSDTOTETSLTESVSS 377
Db 698 GEGEACPLGSPGAG-----RNSVLF---LPVDPEDSPL--GSSTPMASPOLLPEDYR- 745
QY 378 SSGLEGEPPALPSKILSSGCKADLGC 405
Db 746 -----EHLGLMLSLFQSLSCQAQGGC 768

RESULT 7

US-09-022-259-10
; Sequence 10, Application US/09022259
; Patent No. 6191104
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,259
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-259-10

Query Match: 14.0%; Score 310; DB 4; Length 866;
Best Local Similarity: 28.39; Pred. No. 8.9e-24;
Matches: 127; Conservative 60; Mismatches 173; Indels 88; Gaps 20;
QY 14 EESSESTTIALPRLRPRP-----KVFYCYSKDQNMNVQCFAYFLQDPGCGEVA 69
Db 353 EKYSDDTKTDTGPAADLPPLPKRVKVIYISA-DPLIYDVVILKFAOFLLTACGTEVA 411
QY 70 LDWEDEFSLRCQREW-----IOKIHESOFITVCSKGMKIFVDKKNYKKGCG- 120
Db 412 LDLEEQALSEAGVTWYGRQKQEMVESNSKIIVLCRGTR---AKQALLGRGAPVRL 467
QY 121 ---RGSKGKELFVAVSAIAELKROAKOSSAALSFEIATVE-DYSCBDDVPGILDSTK 176
Db 468 RCDHGKPGDGLFTAAANNMLPDKR-----PACFGTVVVCYFSEVSCDGDVDFLFGAAPR 522
QY 177 RLMDNLPOLCSHLSDHGLQBPQHTROG--SRNFRKSGRSGLTYAICNMHQFIDE 234
Db 523 YPLMDRFEV--YFIODLEMGPCGRMHRVGLSGDNYLSPGGRQLRAALDRFRDQVR 580
QY 235 EPDWEF-----KQVFPFHPPLRYREPYLEKFDGSLVNDVMCKPGPESDFCLAYEA 286
Db 581 CPDWEFCENLYSADDODAPSLDEEV-FEPLPP-GTGIKRAPLVRE-PGSOACLAIDP 637
QY 287 AVLKATGPADSOHE-----SOHGGLDQDGEARPAIDGSA---ALQ 323
Db 638 LVGEGGAANAKLEPHLOPQOPAPQPLHTLVLAAREGALVAAREPGPLADGAAYRLALA 697
QY 324 -----PLHTVYKAGSPDMPDSDGYDSSVPSSELSLPLMEGLSDTOTETSLTESVSS 377
Db 698 GEGEACPLGSPGAG-----RNSVLF---LPVDPEDSPL--GSSTPMASPOLLPEDYR- 745

RESULT 8

US-09-022-257-10
; Sequence 10, Application US/09022257
; Patent No. 6197525
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,257
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-257-10

Query Match 14.04; Score 310; DB 4; Length 866;
Best Local Similarity 28.34; Pred. No. 8.9e-24;
Matches 127; Conservative 60; Mismatches 173; Indels 88; Gaps 20;

QY 14 EESSESSTTAALPRERLRPRP-----KVFICYSKDQNMNVVQCFAYFLQDFCGCEVA 69
DB 353 EKYSDTKYTDGLPDLPPPLPKRKVMIIYSA-DHPLIVDVVYLKFAQLLTACGTVA 411
QY 70 LDLWEDFSLCREGQRENV-----IQIHESOFIIVVCSKGMKIFVDKKNYKHGGG----- 120
DB 412 LDLLEQQAISAGVMTWVGROKQEMVESNSKIIVLCSTGTR-----AKWQALLGRGAPVRL 467
QY 121 ---RSGSGELFVAVSAIAEKLRQAKOSSAALSKEIANTF-DYSCGDVPGILDSTK 176
DB 468 RCDGKPVGDLDFTAMNMILPDFKR-----PACFTGVVCFVSEVSDGDVDFLFGAAPR 522
QY 177 YELMDNLPOLCSHLHSRDGLQBPQOHTQSG--SRNRYFRSKSGRSIYVAICNMHQFI 234
DB 523 YPLMDRFEV--YFIQDLEMFPGRMHVRGELSDNTLSPGPGRLAALDRFRDMOVR 580
QY 235 EDPWFE-----KQVPPHPPPLATREPVLEKFDGLVNDVMCKPGPSDFCLVEA 286
DB 581 CPDWFECENLYSADQDAPSLDEEV-FEPLLP-GTGVKRAPLYRE-PGQACLAIDP 637
QY 287 AVLGATGPADSOHE-----SOHGGLDQDGEAKPALDGA---ALQ 323
DB 638 LVGEGGAHVAAKPHLPQRPQAPQPLHTLVLAEEGALVAAVPEPGIADGAARLALA 697
QY 324 -----PLHVTVKAAGSPMDRSGIYSSVPSSELSLPLMEGLSTDTOTETSLTSEVSS 377
DB 698 GEGEACPLLGSFGAG-----RNSVLF-----LVDPEDSPL--GSGTPMASPDLLPEDVR- 745
QY 378 SSGLEEEPPALPKSLSSGSCADLGC 405
DB 746 -----EHLEGLMLSLFQSLSCQAQGGC 768

RESULT 9
US-08-620-694A-2

Sequence 2, Application US/08620694A
Patent No. 5869286

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

APPLICANT: Fauslow, William

TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-620-694A-2

Query Match 13.18; Score 289.5; DB 2; Length 864;

Best Local Similarity 25.88; Pred. No. 1.4e-21;
Matches 120; Conservative 75; Mismatches 170; Indels 101; Gaps 21;

QY 14 EESSESSTTAALPRERLRPRP-----KVFICYSKDQNMNVVQCFAYFLQDFCGCEVA 69
DB 355 EKHGDSKINGILPVADLTTPPLPRKVMIIYSA-DHPLIVVYLKFAQLLTACGTVA 413
QY 70 LDLWEDFSLCREGQRENVQK-----IHESOFIIVVCSKGMKIFVDKKNYKHGGG----- 119
DB 414 LDLLEQVISEVGVMTWVGROKQEMVESNSKIIVLCSTG-----TQAKKAILGWAEPV 468
QY 120 -----GRSGKGEFLVAVSAIAEKLRQAKOSSAALSKEIANTFDTSC-EGDVPGILDLS 174
DB 469 QLRCDEMKPAGDLFTAMNMILPDFKR-----PACFTGVVCFVSEVSDGDVDFLFGAAPR 523
QY 175 -TKYELMDNLPOLCSHLHSRDGLQBPQOHTQSG--SRNRYFRSKSGRSIYVAICNMHQFI 232
DB 524 SRYPLMDRFEV--YFIQDLEMFPGRMHVRGELSDNTLSPGPGRLAALDRFRDMOVR 581
QY 233 EDPWFEKQVFPFHR-----PPLR--YREPVLEKFDGLVNDVMCKPGPSDFCLVEA 285
DB 582 TQCPDWFECENLYSADQDAPSLDEEV-FEPLLP-GGGLVKKQPLVREL-SDGCLVVD 639
QY 286 AAVLGATGPADSOHESQHGGLDQD-----GEARPALDGSAAALQPLH 327
DB 640 VCV-----SEESRMAKLPQLPQRELVANTLQSMVLPAPQVPA---ARVVEPLHL 688
QY 328 TVKAGSPDMP--RDS-----GIYDSSV--PSSELSLPL-----MEGLSTDOT 366
DB 689 PDGGAQAQLPWTETSEACPLGVORNSILCLPVSDDLPLCLSTPMKSPDHLOGDAEQL 748
QY 367 -ETSSLTSEVSSSGGLCEEEPP-----ALPSKLLSSGSCADLGC 404
DB 749 ESLMLSVLQQLSGQPLESWPRPEVVLGCTPPEEQRSQVSDQG 794

RESULT 10

US-09-022-255-2

Sequence 2, Application US/09022255

Patent No. 6072033

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

APPLICANT: Fauslow, William

TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,255
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-255-2

Query Match 13.1%; Score 289.5; DB 3; Length 864;
Best Local Similarity 25.8%; Pred. No. 1.4e-21;
Matches 120; Conservative 75; Mismatches 170; Indels 101; Gaps 21;

QY 14 EESSESSTYTAALPRELRPRP-----KVFLCYSSKQGNHNVVQCFAYFLQDFGCEVA 69
DB 355 EKHGDSKINGILPVADLTPPLPRKVIWYSA-DHPLVVEVLKFAQLITACGTEVA 413
QY 70 LDLMEDFSLCREGQRENVIOK-----IHESQFIIVVCSKGMKVFVDKNNKHKGG-----119
DB 414 LDLEEQVISEVGMVWVSQRQENVESNSKIIILCSRG-----TQAKWKAILGWAEPV 468
QY 120 -----GRSGGGEFLVAVSAIAEKLQAKQSSAALSKEFIATVFDYSC-EGDVPGLDLS 174
DB 469 QLRCDHWKPAQDLTAANNILPDFKR-----PACFTYVVCYFSGICSERDVPDLNIT 523
QY 175 TYRLMDNLPLQCSLHSDHGLQEPGQ--HTROGSRNRYFRSGRSRSLVIAICNNHQFI 232
DB 524 SRYPLMDRFEV--YFRIDLEMFEPGRMHVRLTGDNTYQSPGRQLKEAVLRFQEWQ 581
QY 233 DEEDPWFKEQVFPHP-----PPLR---YREPVLEKFGSLVNDVCKPGPSDFCLKVE 285
DB 582 TQCPDWFREMLCAQDQLPSLDEEVEDPULPP-GGIVKQOPLVREL-SDGLVVD 639
QY 286 AAVLGATGAPDSQHSQHGGLDQD-----GEARPALDGSAAALQPLH 327
DB 640 VCV-----SEESMAKLDLPQWQRELVAHTLQSMVLPABQVPA---ARVVEPLH 688
QY 328 TVKAGSPDMD-RDS-----GIYDSSV---PSELSLPL-----HEGLSTDT 366
DB 689 PGCSAAQLPWTEDSACPLVQVNSILCLPVDSDDLPICTPMMSPDHQLQAGARBL 748
QY 367 ETSLSITESVSSSGIGREPP-----ALPSKILLSGSGCKADIG 404

Db 749 ESMKLSVLAQSLGQPLESMRPEVVLGCTPSEERQSGVQSDG 794
RESULT 11-696-2
US-09-022-696-2
Sequence 2, Application US/09022696
Patent No. 6072037
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fenslow, William
TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,696
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-696-2

Query Match 13.1%; Score 289.5; DB 3; Length 864;
Best Local Similarity 25.8%; Pred. No. 1.4e-21;
Matches 120; Conservative 75; Mismatches 170; Indels 101; Gaps 21;

QY 14 EESSESSTYTAALPRELRPRP-----KVFLCYSSKQGNHNVVQCFAYFLQDFGCEVA 69
DB 355 EKHGDSKINGILPVADLTPPLPRKVIWYSA-DHPLVVEVLKFAQLITACGTEVA 413
QY 70 LDLMEDFSLCREGQRENVIOK-----IHESQFIIVVCSKGMKVFVDKNNKHKGG-----119
DB 414 LDLEEQVISEVGMVWVSQRQENVESNSKIIILCSRG-----TQAKWKAILGWAEPV 468
QY 120 -----GRSGGGEFLVAVSAIAEKLQAKQSSAALSKEFIATVFDYSC-EGDVPGLDLS 174
DB 469 QLRCDHWKPAQDLTAANNILPDFKR-----PACFTYVVCYFSGICSERDVPDLNIT 523
QY 175 TYRLMDNLPLQCSLHSDHGLQEPGQ--HTROGSRNRYFRSGRSRSLVIAICNNHQFI 232
DB 524 SRYPLMDRFEV--YFRIDLEMFEPGRMHVRLTGDNTYQSPGRQLKEAVLRFQEWQ 581
QY 233 DEEDPWFKEQVFPHP-----PPLR---YREPVLEKFGSLVNDVCKPGPSDFCLKVE 285

Db 582 TOCPWFRENLCLADGDLPSLDEVEFEDPLPP--GGIVKQOPLVRLP--SDGCLVVD 639
QY 286 AAVLGATGPADSHESQHGGLDQ-----GEARPALDGSAAOPLH 327
Db 640 VCV-----SEESRMALDQPLQAPRELVAHTLQSNVLPABQVPA---ABVVEPLH 688
QY 328 TVKAGSPDMP--RDS-----GIYDSSV---PSSELSLPL-----MEGLSTDT 366
Db 689 PDGSAALQPLMTEDEACPLGVQRNSILCLPVDSDLPCLCTPMNSPDHLOGDAREQL 748
QY 367 ETSSLTESVSSSGLGEEPP-----ALPSKLLSSGCKADLG 404
Db 749 ESLMLSVLQSLGQPLSPREVLGCTPSEERQSVQSDQG 794

RESULT 12

US-08-978-773-2
Sequence 2, Application US/08978773
Patent No. 6083906
GENERAL INFORMATION:
APPLICANT: Troutt, Anthony
TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple PowerMacintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,773
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 60/052,525
FILING DATE: 27 NOVEMBER 1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2623-A
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-978-773-2

Query Match 13.18; Score 289.5; DB 3; Length 864;
Best Local Similarity 25.88; Pred. No. 1.4e-21;
Matches 120; Conservative 75; Mismatches 170; Indels 101; Gaps 21;
QY 14 EESSESSTTALPRERLRPP-----KVFLCYSKDQGNHNVVOCFAFLQDFCGGEVA 69
Db 355 EKGDDSKINGLPLVADUTPLPRKVIWISA-DHPLVEVLVLFQAQFLITACGTEVA 413
QY 70 LDLEWDFSLCRGQREWIQK-----IHESOFILVVCCKGMYFVKKNYKRGK-----119
Db 414 LDLEWDFSLCRGQREWIQK-----IHESOFILVVCCKGMYFVKKNYKRGK-----119
QY 120 -----GRGSKGELFLVANSATKRLQAKOSSNALSRIANTFYDYS-EGDVPGLDLS 174

Db 469 QLRCDHKPAGDLFTAAMRMILPDKR-----PACFTVTVCFSGICSERDVPULFNIT 523
QY 175 TKYRLMNLPLQCSHLHSDHGLQBPQO---HTROGSRNFFSKSGRSILYVAICNMHOPI 232
Db 524 SRYPLADREFEV---YFIODLEMFPGRMHVRRLATGDNLTLOSPSGROLKAVLRPQEMO 581
QY 233 DEEDPMEKOFVPHF---PPLR---YREPVLEKFDGLVADVMCKPSPESDFCLAVE 285
Db 582 TOCPWFRENLCLADGDLPSLDEVEFEDPLPP--GGIVKQOPLVRLP--SDGCLVVD 639
QY 286 AAVLGATGPADSHESQHGGLDQ-----GEARPALDGSAAOPLH 327
Db 640 VCV-----SEESRMALDQPLQAPRELVAHTLQSNVLPABQVPA---ABVVEPLH 688
QY 328 TVKAGSPDMP--RDS-----GIYDSSV---PSSELSLPL-----MEGLSTDT 366
Db 689 PDGSAALQPLMTEDEACPLGVQRNSILCLPVDSDLPCLCTPMNSPDHLOGDAREQL 748
QY 367 ETSSLTESVSSSGLGEEPP-----ALPSKLLSSGCKADLG 404
Db 749 ESLMLSVLQSLGQPLSPREVLGCTPSEERQSVQSDQG 794

RESULT 13

US-09-022-253-2
Sequence 2, Application US/09022253
Patent No. 6096305
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: No. 6096305e1 Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,253
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694
FILING DATE: 21-MARCH-1996
APPLICATION NUMBER: USN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-253-2

Query Match 13.18; Score 289.5; DB 3; Length 864;
Best Local Similarity 25.88; Pred. No. 1.4e-21;
Matches 120; Conservative 75; Mismatches 170; Indels 101; Gaps 21;

QY 14 EESSESTYTAALPRERLRPRP---KVFLCYSSKQONNNVVOCAFYFLQDFCGCEVA 69
DB 355 EKGGDDSKINGILPVADLPPLPRKVIWISA-DHPLYVEVLKFAQLITACGTEVA 413
QY 70 LDLMEDFSLCRGQREWIQK---IHESQFIIVVCSKGMKIFYDKNKKHGG-----119
DB 414 LDLMEDFSLCRGQREWIQK---IHESQFIIVVCSKGMKIFYDKNKKHGG-----119
QY 120 ---GRSGGKELFLVAVSAIAEKLQAKQSSAALSKFIAVYFDYSC-EGDVPGLDLS 174
DB 469 QLRCDHWKPGADLFTAMNMLPDKR---PACFGTYVVCYFSGICSERDVPDLNIT 523
QY 175 TKYRLMDNLQCLSHLSRDHGLQPGQ---HTROGSRNNYFRSKSGSLYVAICNHOFI 232
DB 524 SRIPLMDREFEV---YRIQDLEFEPGRMHVRELTDNTLQSPSGRLKEAVLRFQMO 581
QY 233 DEEDPWFKEQFVFFHP---PPLR---YREPVLEKFDGLVNDVCKPGPESDFCLAYE 285
DB 582 TOCPDWFERNICLADGQDPLSDEVEFDPLPP-GGGIVKQOPLVREL-SDGCLVVD 639
QY 286 AAVLGATGPADSOHSGHGLDQD-----GEARPALDGSAAALQPLH 327
DB 640 VCV-----SEESRMALDQPLQRELVAHTLQSMVLPAEQVPA---AHVVEPLHL 688
QY 328 TVRAGSPDMP---RDS-----GIYDSSV---PSSLSLPL-----MEGLSTDT 366
DB 689 PDGSGAAOLPMTEDSEACPLLVQVNSILCLPVDSDLLPCTPMSDPHLOQDAREQL 748
QY 367 ETSLSLTVSSSSGGLGEEPP-----ALPSKLLSSGSKADLG 404
DB 749 ESLMLSLVLOQSLSGQPLESWPRPEVLEGCTPSEERQSVQSDQG 794

RESULT 14
US-09-022-260-2
; Sequence 2, Application US/09022260;
; Patent No. 6100235
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fauslow, William
; TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,260
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO.: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-260-2

Query Match 13.18; Score 289.5; DB 3; Length 864;
Best Local Similarity 25.88; Pred. No. 1.4e-21;
Matches 120; Conservative 75; Mismatches 170; Indels 101; Gaps 21;

QY 14 EESSESTYTAALPRERLRPRP---KVFLCYSSKQONNNVVOCAFYFLQDFCGCEVA 69
DB 355 EKGGDDSKINGILPVADLPPLPRKVIWISA-DHPLYVEVLKFAQLITACGTEVA 413
QY 70 LDLMEDFSLCRGQREWIQK---IHESQFIIVVCSKGMKIFYDKNKKHGG-----119
DB 414 LDLMEDFSLCRGQREWIQK---IHESQFIIVVCSKGMKIFYDKNKKHGG-----119
QY 120 ---GRSGGKELFLVAVSAIAEKLQAKQSSAALSKFIAVYFDYSC-EGDVPGLDLS 174
DB 469 QLRCDHWKPGADLFTAMNMLPDKR---PACFGTYVVCYFSGICSERDVPDLNIT 523
QY 175 TKYRLMDNLQCLSHLSRDHGLQPGQ---HTROGSRNNYFRSKSGSLYVAICNHOFI 232
DB 524 SRIPLMDREFEV---YRIQDLEFEPGRMHVRELTDNTLQSPSGRLKEAVLRFQMO 581
QY 233 DEEDPWFKEQFVFFHP---PPLR---YREPVLEKFDGLVNDVCKPGPESDFCLAYE 285
DB 582 TOCPDWFERNICLADGQDPLSDEVEFDPLPP-GGGIVKQOPLVREL-SDGCLVVD 639
QY 286 AAVLGATGPADSOHSGHGLDQD-----GEARPALDGSAAALQPLH 327
DB 640 VCV-----SEESRMALDQPLQRELVAHTLQSMVLPAEQVPA---AHVVEPLHL 688
QY 328 TVRAGSPDMP---RDS-----GIYDSSV---PSSLSLPL-----MEGLSTDT 366
DB 689 PDGSGAAOLPMTEDSEACPLLVQVNSILCLPVDSDLLPCTPMSDPHLOQDAREQL 748
QY 367 ETSLSLTVSSSSGGLGEEPP-----ALPSKLLSSGSKADLG 404
DB 749 ESLMLSLVLOQSLSGQPLESWPRPEVLEGCTPSEERQSVQSDQG 794

RESULT 15
US-09-022-259-2
; Sequence 2, Application US/09022259
; Patent No. 6191104
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fauslow, William
; TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/022,259
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/620,694
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USN 08/410,535
 FILING DATE: 23 MARCH 1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,695
 REFERENCE/DOCKET NUMBER: 2617-B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 587-0430
 INFORMATION FOR SEQ. ID NO. 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 864 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-022-259-2

Query Match 13.18; Score 289.5; DB 4; Length 864;
 Best Local Similarity 25.8; Pred. No. 1.4e-21;
 Matches 120; Conservative 75; Mismatches 170; Indels 101; Gaps 21;

QY	14	EESESSTYALPRERLRPR-----KVFCTSSKDGQNHNNVQCFAFLQDFCGCEVA	69
DB	355	ERHGDSDKINGILPVADITPPPLPRVWIVTSA-DHPLVYVVLKFAQLITACGTEVA	413
QY	70	LDLWEDFSLCRGQREWVQK-----IHESQFIIVCSKGMKYFDKKNYKHGG-----	119
DB	414	LDLLEQVISEVGVNTWVRQKQMVESKIIILCSRG-----TQAKRAILGNAPAV	468
QY	120	-----GRSGKGELFVAVSAIAEKLQAKQSSAALSFIATYFDYSC-EGDVPGLDLS	174
DB	469	QLACDHWKPGDGLFTAAANNMLDPFKR-----PACFGTVVCFISGICSERDVPDLFNIT	523
QY	175	TYRLADNLPLCSLHSDHGLQEGC--HTROGSRNRYPSKSGSLYALCNHOFI	232
DB	524	SRPLMDREEV--YRIQDLEMPFGMHVRELTDGNTLQSPGKOLKAVLRFOEQ	581
QY	233	DEPDWFEKQVFFHP-----PPLR---YREPVLKFDGLVNDVCKPGPESDFCLAYE	285
DB	582	TOCPDWFENERCLADGGQLSLDEEVEFDPLLP--GGGIVKQOPLVRELFP--SDGCLVVD	639
QY	286	AAVLGATGPADSOHESQHGGLDQD-----GEARPALDGSAAALOPLLH	327
DB	640	VCV-----SEESRMALDPQLWQRELVAITLQSNVLPACQYPA---AHVVEPLHL	688
QY	328	TVAGSPDMP--RDS-----GIYDSV---PSELSLPL-----NEGLSTDQT	366
DB	689	PDGSGAAQLPMTEDSEACPLLGVRNSITLCLPVDSDDLPLCTPMNSPDLQDAREQL	748
QY	367	ETSLTESVSSSGIGREEPP-----ALPSKLLSGSCKADLG	404
DB	749	ESLMLSVLQSLSGQPLESWPRPVEVLGGCTPSEERQSVQSDQG	794

Search completed: May 19, 2003, 09:26:28
 Job time : 15.3807 secs